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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:02 ; Search time 184.09 Seconds  
(without alignments)  
3.621 Million cell updates/sec

Title: PEP1-MOD8A  
Perfect score: 46  
Sequence: 1 SLFEGIDAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues  
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	89.1	9	21	RAY44199
2	41	89.1	9	22	AAH97601
3	41	89.1	10	21	RAY44200
4	41	89.1	10	22	AAH97602
5	40	87.0	10	22	AAH97603
6	40	87.0	554	21	AAH88409
7	40	87.0	554	21	AAH88410
8	40	87.0	554	21	AAH88412
9	40	87.0	554	21	AAH88413
10	40	87.0	624	21	AAH23252
11	40	87.0	634	11	AAH03930

12	40	87.0	640	11	AAH03929	Homo sapiens HSP
13	40	87.0	640	18	AAH10065	Human heat shock p
14	40	87.0	640	21	AAH23653	Human heat shock p
15	40	87.0	640	21	AAH88408	Human heat shock p
16	40	87.0	640	21	AAH88411	Human heat shock p
17	40	87.0	641	14	AAH43004	Mature mouse sperm
18	40	87.0	641	19	AAH54349	Human heat shock 7
19	40	87.0	641	21	AAH23652	Human heat shock p
20	40	87.0	641	22	AAH82534	Human heat shock p
21	40	87.0	642	21	AAH23650	Rat heat shock pro
22	40	87.0	647	11	AAH03928	Xenopus laevis HSP
23	39	84.8	643	18	AAH28995	Marmoset intracell
24	39	84.8	665	21	AAH58386	Lung cancer associ
25	37	80.4	91	21	AAH02174	Human secreted pro
26	37	80.4	253	21	AAH24333	Arabidopsis thalia
27	37	80.4	279	21	AAH24332	Arabidopsis thalia
28	37	80.4	342	21	AAH24331	Arabidopsis thalia
29	37	80.4	646	11	AAH03927	Rat HSP (rathsp70)
30	37	80.4	646	19	AAH54364	Heat shock cognate
31	37	80.4	646	20	AAH17407	Human heat shock c
32	37	80.4	646	20	AAH17408	Mouse heat shock c
33	37	80.4	646	21	AAH23649	Mouse heat shock p
34	37	80.4	646	21	AAH23651	Human heat shock p
35	37	80.4	646	22	AAH82535	Human heat shock p
36	37	80.4	656	18	AAH01638	Candida albicans h
37	37	80.4	890	21	AAH22938	GFP-HSC70 fusion p
38	36	78.3	633	14	AAH43002	Mouse SLIP1 homolo
39	35	76.1	412	22	AAH61974	S. avermitilis ORF
40	35	76.1	558	22	AAH01251	B. subtilis dihydr
41	35	76.1	646	11	AAH03931	Zea mays HSP (mzeh
42	35	76.1	647	20	AAH31380	T. gondii antigen
43	35	76.1	647	22	AAH49099	Toxoplasma gondii
44	34	73.9	98	19	AAH77538	Staphylococcus aur
45	34	73.9	100	22	AAH02055	Synthetic human ta

## ALIGNMENTS

RESULT 1  
AAH44199  
ID AAY44199 standard; peptide; 9 AA.  
XX AC AAY44199;  
XX DT 15-FEB-2000 (first entry)  
XX DE Heat shock protein 70 amino acid residues 286-294.  
XX KW Human; heat shock protein 70; hsp70; identification; tumour; mutation;  
KW T cell response; amplification; vector; bacterium; cancer; allele;  
KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;  
KW immune defence; immunogenicity; specificity; human leucocyte antigen.

OS Homo sapiens.  
XX WO9954464-A1.  
XX PD 28-OCT-1999.  
XX PF 22-APR-1999; 99WO-FR00957.  
XX PR 22-APR-1998; 98FR-0005033.  
XX PA (INSR) INST ROUSSY GUSTAVE.  
XX PI Triebel F, Gaudin C;  
XX DR WPI; 2000-013251/01.  
XX PT Identifying mutant peptides from heat-shock protein 70, for treatment  
XX of cancer -



PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-294 of the human  
 CC heat shock protein 70 (hsp70). The invention relates to a method of  
 CC identifying peptides, derived from hsp70 that stimulate a tumour-specific  
 CC T cell response. Identification of the hsp70 peptides that have at least  
 CC one mutation or alteration compared with the native sequence, and induce  
 CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70  
 CC encoding DNA from one or more tumours; (ii) cloning the amplified  
 CC sequences into a vector that can be replicated in bacteria;  
 CC (iii) sequencing fragments in each cultured bacterial colony to identify  
 CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
 CC mutant peptides identified. The peptides, optionally formulated with an  
 CC agent that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic  
 CC T lymphocytes in a cell culture and/or induce these cells to secrete  
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
 CC tumour necrosis factor), particularly where the cells are used to  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles.

XX Sequence 9 AA;

Query Match 89.1%; Score 41; DB 21; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 4.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 ||||| |  
 Db 1 slfegidly 9

RESULT 2

AA97601  
 ID AAB97601 standard; peptide; 9 AA.  
 XX  
 AC AAB97601;  
 XX  
 DT 30-JUL-2001 (first entry)  
 XX  
 DE Heat shock protein 70 (HSP70) peptidic fragment 1.  
 XX  
 KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129190-A1.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-EP09530.  
 XX  
 PR 15-OCT-1999; 99EP-0120484.  
 XX  
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.  
 XX  
 PI Abastado JP, Bartholeyns J;  
 XX  
 DR WPI; 2001-290909/30.  
 XX  
 PT Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -  
 XX  
 XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 1 relating to position 286-294 of

CC human, heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX Sequence 9 AA;

Query Match 89.1%; Score 41; DB 22; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 4.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 ||||| |  
 Db 1 slfegidly 9

RESULT 3

AA44200  
 ID AAY44200 standard; peptide; 10 AA.  
 XX  
 AC AAY44200;  
 XX  
 DT 15-FEB-2000 (first entry)  
 XX  
 DE Heat shock protein 70 amino acid residues 286-295.  
 XX  
 KW Human; heat shock protein 70; hsp70; identification; tumour; mutation;  
 KW T cell response; amplification; vector; bacterium; cancer; allele;  
 KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;  
 KW immune defence; immunogenicity; specificity; human leucocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954464-A1.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 22-APR-1999; 99WO-FR00957.  
 XX  
 PR 22-APR-1998; 98FR-0005033.  
 XX  
 PA (INSR) INST ROUSSY GUSTAVE.  
 XX  
 PI Triebel F, Gaudin C;  
 XX  
 DR WPI; 2000-013251/01.  
 XX  
 PT Identifying mutant peptides from heat-shock protein 70, for treatment  
 PT of cancer -  
 XX  
 PS Claim 10; Page 6; 56pp; French.

CC This peptide corresponds to amino acid residues 286-295 of the human  
 CC heat shock protein 70 (hsp70). The invention relates to a method of  
 CC identifying peptides, derived from hsp70 that stimulate a tumour-specific  
 CC T cell response. Identification of the hsp70 peptides that have at least  
 CC one mutation or alteration compared with the native sequence, and induce  
 CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70  
 CC encoding DNA from one or more tumours; (ii) cloning the amplified  
 CC sequences into a vector that can be replicated in bacteria;  
 CC (iii) sequencing fragments in each cultured bacterial colony to identify



CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
 CC mutant peptides identified. The peptides, optionally formulated with an  
 CC agent that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic  
 CC T lymphocytes in a cell culture and/or induce these cells to secrete  
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
 CC tumour necrosis factor). Particularly where the cells are used to  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles.

XX  
 SQ Sequence 10 AA;

Query Match 89.1%; Score 41; DB 21; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.031;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 Db | | | | | | |  
 1 slfegidiy 9

RESULT 4  
 AAB97602  
 ID AAB97602 standard; peptide; 10 AA.  
 AC AAB97602;  
 XX  
 DT 30-JUL-2001 (first entry)  
 XX  
 DE Heat shock protein 70 (HSP70) peptidic fragment 2.  
 XX  
 KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129190-A1.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-EP09530.  
 XX  
 PR 15-OCT-1999; 99EP-0120484.  
 XX  
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;  
 XX  
 DR WPI; 2001-290909/30.  
 XX  
 PT Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -  
 XX  
 PS Claim 8; Page 15; 21pp; English.

CC The amino acid sequence of fragment 2 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX  
 SQ Sequence 10 AA;

Query Match 89.1%; Score 41; DB 22; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.031;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 Db | | | | | | |  
 1 slfegidiy 9

RESULT 5  
 AAB97603  
 ID AAB97603 standard; peptide; 10 AA.  
 XX  
 AC AAB97603;  
 XX  
 DT 30-JUL-2001 (first entry)  
 XX  
 DE Heat shock protein 70 (HSP70) peptidic fragment 3.  
 XX  
 KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 3.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129190-A1.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-EP09530.  
 XX  
 PR 15-OCT-1999; 99EP-0120484.  
 XX  
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;  
 XX  
 DR WPI; 2001-290909/30.  
 XX  
 PT Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -  
 XX  
 PS Claim 8; Page 15; 21pp; English.

CC The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX  
 SQ Sequence 10 AA;



Query Match 87.0%; Score 40; DB 22; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 1 slfegidfy 9

## RESULT 6

AAAY88409  
 ID AAY88409 standard; Protein: 554 AA.

XX AC AAY88409;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI; 2000-264458/23.

XX DR N-PSDB; AAA15621.

XX PT Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

XX PT

XX PS Examples; Fig 2; 11pp; Japanese.

XX CC This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 87.0%; Score 40; DB 21; Length 554;  
 Best Local Similarity 88.9%; Pred. No. 4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 200 slfegidfy 208

## RESULT 7

AAAY88410  
 ID AAY88410 standard; Protein: 554 AA.

XX AC AAY88410;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI; 2000-264458/23.

XX DR N-PSDB; AAA15622.

XX PT Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

XX PT

XX PS Disclosure; Fig 3; 11pp; Japanese.

XX CC This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 87.0%; Score 40; DB 21; Length 554;  
 Best Local Similarity 88.9%; Pred. No. 4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 200 slfegidfy 208

## RESULT 8

AAAY88412  
 ID AAY88412 standard; Protein: 554 AA.

XX AC AAY88412;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI; 2000-264458/23.



XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
PT  
XX  
PS Disclosure; Fig 5; 11pp; Japanese.  
XX  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
SQ Sequence 554 AA;

Query Match 87.0%; Score 40; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEEGIDAY 9  
DB 200 slifegidfy 208

RESULT 9  
ID AAY88413 standard; Protein; 554 AA.  
XX  
AC AAY88413;  
XX  
DT 31-JUL-2000 (first entry)  
XX  
DE Human heat shock protein SHSP70 amino acid sequence.  
XX  
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
OS Homo sapiens.  
XX  
PN JP2000069999-A.  
XX  
PD 07-MAR-2000.  
XX  
PF 01-JUN-1995; 99JP-0257146.  
XX  
PR 01-JUN-1995; 95JP-0158581.  
XX  
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX  
DR WPI; 2000-264458/23.  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
PT  
PS Disclosure; Fig 6; 11pp; Japanese.  
XX  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
SQ Sequence 554 AA;

Query Match 87.0%; Score 40; DB 21; Length 554;

Best Local Similarity 88.9%; Pred. No. 4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEEGIDAY 9  
DB 200 slifegidfy 208

RESULT 10  
AAB23252  
ID AAB23252 standard; Protein; 624 AA.  
XX  
AC AAB23252;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human Hsp72 (heat shock protein 72).  
XX  
KW Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX  
OS Homo sapiens.  
XX  
PN WO200054814-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US07350.  
XX  
PR 18-MAR-1999; 99US-0125046.  
XX  
PA (PHYL-) PHYLOGENY INC.  
XX  
PI Volloch Vz, Sherman M;  
XX  
DR WPI: 2000-647056/62.  
DR N-PSDB; AAA97541.  
XX  
XX Identifying compounds that inhibit proliferation of cells and capable  
PT of modulating the expression of heat shock protein 72 gene and/or  
PT activity of Hsp72 useful for treating cancers such as leukemia,  
PT lymphoma  
XX  
PS Examples; Fig 16B; 77pp; English.  
XX  
XX The invention relates to a novel method of identifying compounds that  
CC inhibit proliferation of cells comprising contacting a test compound with  
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
CC if the test compound inhibits activity or expression of Hsp72.  
CC Optionally, Hsp72 is contacted with the test compound under optimum  
CC conditions to allow the two components to interact and bind, forming a  
CC complex which is detected. The invention also relates to a method of  
CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
CC activation, comprising contacting a test compound with a cell which  
CC expresses Hsp72, exposing the cell to a heat induced stress and  
CC determining if the compound inhibits JNK phosphatase activity. The  
CC invention additionally encompasses compositions comprising an inhibitor  
CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
CC inhibiting the proliferation of cells. Modulation of the activity of the  
CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
CC as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and  
CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
CC Hsp72 activity can also be administered to treat premalignant conditions  
CC and to prevent progression to a neoplastic or malignant state. The  
CC compounds that inhibit Hsp72 function are administered to a patient  
CC having a disease or disorder mediated by an increase of Hsp72 expression  
CC or activity relative to normal levels. The present sequence represents  
CC human Hsp72 used in the exemplifications of the invention.  
XX  
XX Sequence 624 AA;



Query Match 87.0%; Score 40; DB 21; Length 624;  
 Best Local Similarity 88.9%; Pred. No. 4.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 11  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.  
 XX  
 AC AAR03930;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Gallus gallus HSP (chkhsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Gallus gallus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 634 /note= "residue given as "O" in specification"  
 FT

XX W09002564-A.  
 XX  
 XX 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 XX (CODO-) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has  
 635 amino acid residues, the sequence itself has only 634,  
 including "O" (?) at position 634.  
 XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 of organisms: 1. M.hypneumoniae (Mhysp70 - AAR03922);  
 2. Bacillus megaterium (Bmehsp70 - AAR03923);  
 3. E. coli (dnaK - AAR03924);  
 4. T. cruzi (tc70kd - AAR03925);  
 5. T. cruzi (AAR03926);  
 6. Rat rattus (rathsp70 - AAR03927);  
 7. Xenopus laevis (xl70 - AAR03928);  
 8. Homo sapiens (humhsp70 - AAR03929);  
 9. Gallus gallus (chkhsp70 - AAR03930);  
 10. Zea mays (mzhsp70 - AAR03931);  
 11. Serratia marcescens (smahsp70 - AAR03932).  
 XX The proteins having homology to hsp's of T. cruzi can be used in  
 vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 Mycobacteria species.

XX Sequence 634 AA;

Query Match 87.0%; Score 40; DB 11; Length 634;  
 Best Local Similarity 88.9%; Pred. No. 4.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 289 slfegidfy 297

RESULT 12  
 AAR03929  
 ID AAR03929 standard; Protein; 640 AA.  
 XX  
 AC AAR03929;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Homo sapiens HSP (humhsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 640 /note= "residue given as "O" in specification"  
 FT

XX W09002564-A.  
 XX  
 XX 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 XX (CODO-) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has  
 641 amino acid residues, the sequence itself has only 640,  
 including "O" (?) at position 640.  
 XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 of organisms: 1. M.hypneumoniae (Mhysp70 - AAR03922);  
 2. Bacillus megaterium (Bmehsp70 - AAR03923);  
 3. E. coli (dnaK - AAR03924);  
 4. T. cruzi (tc70kd - AAR03925);  
 5. T. cruzi (AAR03926);  
 6. Rat rattus (rathsp70 - AAR03927);  
 7. Xenopus laevis (xl70 - AAR03928);  
 8. Homo sapiens (humhsp70 - AAR03929);  
 9. Gallus gallus (chkhsp70 - AAR03930);  
 10. Zea mays (mzhsp70 - AAR03931);  
 11. Serratia marcescens (smahsp70 - AAR03932).  
 XX The proteins having homology to hsp's of T. cruzi can be used in  
 vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 Mycobacteria species.

XX Sequence 640 AA;

Query Match 87.0%; Score 40; DB 11; Length 640;  
 Best Local Similarity 88.9%; Pred. No. 4.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 286 slfegidfy 294



```

RESULT 13
AAW10065
ID AAW10065 standard; Protein; 640 AA.
XX
AC AAW10065;
XX
DT 24-OCT-1997 (first entry)
XX
DE Human heat shock protein 70.
XX
KW Human; heat shock protein 70; HSP70; primer; probe; detection;
KW intracellular; abnormal transcription; acute; chronic; sustained;
KW stress.
XX
OS Homo sapiens.
XX
PN JP08322577-A.
XX
PD 10-DEC-1996.
XX
PF 01-JUN-1995; 95JP-0158581.
XX
PR 01-JUN-1995; 95JP-0158581.
XX
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
DR WPI: 1997-081088/08.
XX
DR N-PSDB; AAW58086.
XX
PT Detection of abnormal transcription of HSP70 mRNA - using HSP70
PT specific primer or probe, used in detection of human acute and
PT chronic sustained stress load
XX
PS Claim 1; Fig 1; 13pp; Japanese.
XX
CC The cDNA encoding the present sequence, human heat shock protein 70
CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24
CC and 21. Primers and probes based on the HSP70 cDNA coding
CC sequence can be used to detect the abnormal transcription of
CC intracellular HSP70 mRNA in human acute and chronic sustained
CC stress load.
XX
SQ Sequence 640 AA;

Query Match 87.0%; Score 40; DB 18; Length 640;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
DB 286 slfegidfy 294

RESULT 14
AAB23653
ID AAB23653 standard; protein; 640 AA.
XX
AC AAB23653;
XX
DT 05-JAN-2001 (first entry)
XX
DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
XX
KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytostatic; immunostimulant; cellular immune response inducer;
KW protozoacide; leukaemia; cancer.
XX
OS Homo sapiens.
XX
PN WO200049041-A1.

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XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP00941.
XX
PR 19-FEB-1999; 99JP-0041535.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
PI Shinbara N, Udono H, Yui K;
XX
DR WPI: 2000-543748/49.
XX
PT Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer
XX
PS Claim 3; Page 49-52; 72pp; Japanese.
XX
CC The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a specifically claimed heat shock
CC protein for use in a fused protein of the present invention.
XX
SQ Sequence 640 AA;

Query Match 87.0%; Score 40; DB 21; Length 640;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
DB 286 slfegidfy 294

RESULT 15
AAAY88408
ID AAY88408 standard; Protein; 640 AA.
XX
AC AAY88408;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human heat shock protein HSP70 amino acid sequence.
XX
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW depression; nephrotic syndrome.
XX
OS Homo sapiens.
XX
PN JP2000069999-A.
XX
PD 07-MAR-2000.
XX
PF 01-JUN-1995; 99JP-0257146.
XX
PR 01-JUN-1995; 95JP-0158581.
XX
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
DR WPI: 2000-264458/23.
DR N-PSDB; AAA15620.

```



XX  
PT  
PT  
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PS  
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XX  
CC  
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CC  
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CC  
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XX  
SQ

Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application

Claim 2; Fig 1; 11pp; Japanese.

This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatism, schizophrenia, depression and nephrotic syndrome.

Sequence 640 AA;

Query Match 87.0%; Score 40; DB 21; Length 640;  
Best Local Similarity 88.9%; Pred. No. 4.7;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAY 9  
| | | | | | | |  
Db 286 slfegidfy 294

Search completed: December 6, 2001, 08:04:02  
Job time: 610 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:26 ; Search time 88.19 Seconds  
(without alignments)  
7.774 Million cell updates/sec

Title: PEPI-MOD8A  
Perfect score: 46  
Sequence: 1 SLFEGIDAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_58:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	87.0	208	B44261	dnak-type molecule
2	40	87.0	209	A44261	dnak-type molecule
3	40	87.0	278	I51344	dnak-type molecule
4	40	87.0	372	P00138	dnak-type molecule
5	40	87.0	420	A26283	dnak-type molecule
6	40	87.0	467	T45477	heat-shock protein
7	40	87.0	467	T45479	heat-shock protein
8	40	87.0	468	T45476	heat-shock protein
9	40	87.0	469	T45478	heat-shock protein
10	40	87.0	617	H96605	probable heat shock
11	40	87.0	632	T45471	dnak-type molecule
12	40	87.0	634	A25646	dnak-type molecule
13	40	87.0	636	A48872	dnak-type molecule
14	40	87.0	638	S31766	dnak-type molecule
15	40	87.0	639	JC1391	dnak-type molecule
16	40	87.0	639	S20139	dnak-type molecule
17	40	87.0	640	1 HKW7A	dnak-type molecule
18	40	87.0	640	A29160	dnak-type molecule
19	40	87.0	640	S37394	dnak-type molecule
20	40	87.0	640	T21394	dnak-type molecule
21	40	87.0	640	T43724	hypothetical prote
22	40	87.0	641	S53357	dnak-type molecule
23	40	87.0	641	S35718	dnak-type molecule
24	40	87.0	641	I54542	dnak-type molecule
25	40	87.0	641	A45871	dnak-type molecule
26	40	87.0	642	1 HHYAL	dnak-type molecule
27	40	87.0	642	2 JH0095	dnak-type molecule
28	40	87.0	642	2 B36590	dnak-type molecule
29	40	87.0	644	2 A45635	dnak-type molecule

30	40	87.0	645	2 I51129	dnak-type molecule
31	40	87.0	646	2 T46650	heat shock protein
32	40	87.0	647	1 HHXL70	dnak-type molecule
33	40	87.0	647	2 S44168	dnak-type molecule
34	40	87.0	647	2 T41121	heat shock protein
35	40	87.0	650	2 JC7088	heat shock protein
36	39	84.8	214	2 A03309	dnak-type molecule
37	39	84.8	379	2 I46588	dnak-type molecule
38	39	84.8	467	2 T45473	heat-shock protein
39	39	84.8	467	2 T45474	heat-shock protein
40	39	84.8	641	2 JN0668	dnak-type molecule
41	39	84.8	641	2 PC7036	heat shock protein
42	39	84.8	643	2 S25585	dnak-type molecule
43	39	84.8	643	2 S09036	dnak-type molecule
44	39	84.8	651	2 T45517	heat shock protein
45	39	84.8	651	2 JC7132	heat shock protein

## ALIGNMENTS

### RESULT 1

B44261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KU>

A>Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

A:Gene: HSC70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 87.0%; Score 40; DB 2; Length 208;  
Best Local Similarity 88.9%; Pred. No. 0.72;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9

Db 132 SLFEGIDFY 140

### RESULT 2

A44261

dnak-type molecular chaperone HSP70a - California sea hare (fragment)

N:Alternate names: heat shock protein 70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: A44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: A44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-209 <KU>

A>Note: sequence extracted from NCBI backbone (NCBIP:118951)

C:Genetics:

A:Gene: HSP70a

C:Function:



A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 87.0%; Score 40; DB 2; Length 209;

Best Local Similarity 88.9%; Pred. No. 0.72;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9

|||||||

Db 133 SLFEGIDYY 141

RESULT 3

I51344

dnak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)

N:Alternate names: 70K heat shock protein

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999

C:Accession: I51344

R:Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of d

A:Reference number: I51344; MUID:85036330

A:Accession: I51344

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-278 <KOT>

A:Cross-references: GB:R02549; NID:g213803; PIDN:AAA49562.1; PID:g213804

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match

Best Local Similarity 87.0%; Score 40; DB 2; Length 278;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9

|||||||

Db 156 SLFEGIDFY 164

RESULT 4

PQ0138

dnak-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)

N:Alternate names: heat shock protein 70

C:Species: Paracentrotus lividus (common urchin)

C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 20-Aug-1999

C:Accession: PQ0138

R:Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.

Gene 96, 295-300, 1990

A:Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.

A:Reference number: PQ0138; MUID:91099690

A:Accession: PQ0138

A:Molecule type: DNA

A:Residues: 1-372 <ROS>

A:Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001

C:Genetics:

A:Gene: hsp70 II

A:Introns: 68/1; 137/1; 188/3; 281/3

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match

Best Local Similarity 87.0%; Score 40; DB 2; Length 372;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9

|||||||

Db 286 SLFEGIDYY 294

RESULT 5

A26283

dnak-type molecular chaperone - mouse (fragment)

N:Alternate names: heat shock protein 68

C:Species: Mus musculus (house mouse)

C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999

C:Accession: A26283

R:Lowe, D.G.; Moran, L.A.

J. Biol. Chem. 261, 2102-2112, 1986

A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000

A:Reference number: A26283; MUID:86111900

A:Accession: A26283

A:Molecule type: mRNA

A:Residues: 1-420 <LOW>

A:Cross-references: GB:M12571; NID:gl94014; PIDN:AAA57234.1; PID:g387208

A>Note: the authors translated the codon CTG for residue 173 as Val and CGC for resid

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match

Best Local Similarity 87.0%; Score 40; DB 2; Length 420;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9

|||||||

Db 65 SLFEGIDFY 73

RESULT 6

T45477

heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

C:Species: Chondrosia reniformis

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45477

R:Borchellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45477

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match

Best Local Similarity 87.0%; Score 40; DB 2; Length 467;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9

|||||||

Db 252 SLFEGIDFY 260

RESULT 7

T45479

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C:Species: Eunicella cavolini

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45479

R:Borchellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983



A:Accession: T45479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 87.0%; Score 40; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 1; Indels

Qy	1	SLFEGIDAY	9
			1
Db	252	SLFEGIDFY	260

RESULT 8  
T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
C:Species: Funiculina quadrangularis  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45476  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45476  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-468 <BOR>  
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 87.0%; Score 40; DB 2; Length 468;  
Best Local Similarity 88.9%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 1; Indels

QY	1	SLFEGIDAY	9
			1
Db	253	SLFEGIDFY	261

RESULT 9  
T45478  
heat-shock protein 70 [imported] - Euniceella cavolini (fragment)  
C:Species: Euniceella cavolini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45478  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45478  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-469 <BOR>  
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 87.0%; Score 40; DB 2; Length 469;  
Best Local Similarity 88.9%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 1; Indels

QY	1	SLFEGIDAY	9
			1
DB	254	SLFEGIDFY	262

RESULT	10
--------	----

REF ID: A96605

probable meat snock protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: H96605  
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizlar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719

Query Match	87.0%	Score 40;	DB 2;	Length 617;
Best Local Similarity	88.9%	Pred. No. 2.4;		
Matches	8;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY 1 SLFEGIDAY 9  
 Db 292 SLFEGIDFY 300

RESULT 11  
T45471  
dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostellium discoideum  
N;Alternate names: heat shock cognate protein 70  
C;Species: Dictyostellium discoideum  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
C;Accession: T45471  
R;Boves, H.; Minter, U.; Dittlich, W.; Faix, J.; Gerisch, G.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z22980  
A;Accession: T45471  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-632 <BOV>  
A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
A;Experimental source: strain AX3  
C;Genetics:  
A;Gene: hsc70  
A;Note: localized to filopodias and cortex  
C;Superfamily: heat shock protein 70

Query Match	87.0%	Score 40;	DB 2;	Length 632;
Best Local Similarity	88.9%	Pred. No. 2.5;		
Matches	8;	Conservative	0;	Mismatches
			1;	Indels
			0;	Gaps

QY 1 SLFEGIDAY 9  
Db 285 SLFEGIDFY 293

RESULT 12  
A25646  
dnaK-type molecular chaperone - chicken



N;Alternate names: heat shock protein 70  
 C;Species: Gallus gallus (chicken)  
 C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
 C;Accession: A25646  
 R;Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
 J. Biol. Chem. 261, 12692-12699, 1986  
 A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.  
 A;Reference number: A25646; MUID:86304452  
 A;Accession: A25646  
 A;Molecule type: DNA  
 A;Residues: 1-634 <MOR>  
 A;Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941  
 A;Note: the authors translated the codon TCG for residue 583 as Trp  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein comp  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 87.0%; Score 40; DB 2; Length 634;  
 Best Local Similarity 88.9%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 289 SLFEGIDFY 297

## RESULT 13

A48872  
 dnak-type molecular chaperone hspB - slime mold (Dictyostellium discoideum) (fragment)  
 N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein ag  
 C;Species: Dictyostellium discoideum  
 C;Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
 C;Accession: A48872  
 R;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
 J. Biol. Chem. 268, 23267-23274, 1993  
 A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an  
 A;Reference number: A48872; MUID:94043116  
 A;Accession: A48872  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-636 <EDD>  
 A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180  
 A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein comp  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 87.0%; Score 40; DB 2; Length 636;  
 Best Local Similarity 88.9%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 280 SLFEGIDFY 288

## RESULT 14

S31766  
 dnak-type molecular chaperone hsp70 - green monkey  
 N;Alternate names: heat shock protein 70  
 C;Species: Cercopithecus aethiops (green monkey, grivet)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
 C;Accession: S31766; I36927  
 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 submitted to the EMBL Data Library, January 1993  
 A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
 A;Reference number: S31766  
 A;Accession: S31766  
 A;Molecule type: mRNA

A;Residues: 1-638 <SAI>  
 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FEBS Lett. 355, 282-286, 1994  
 A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible  
 A;Reference number: I36927; MUID:95080396  
 A;Accession: I36927  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 1-638 <RES>  
 A;Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
 A;Experimental source: kidney; cell line COS-1  
 C;Genetics:  
 A;Gene: hsp70  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein co  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 87.0%; Score 40; DB 2; Length 638;  
 Best Local Similarity 88.9%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 284 SLFEGIDFY 292

## RESULT 15

JC1391  
 dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
 N;Alternate names: heat shock protein 70IV; hsp70IV protein  
 C;Species: Paracentrotus lividus (common urchin)  
 C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C;Accession: JC1391  
 R;Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp  
 A;Reference number: JC1391; MUID:93077053  
 A;Accession: JC1391  
 A;Molecule type: DNA  
 A;Residues: 1-639 <SCO>  
 A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
 C;Genetics:  
 A;Gene: hsp70IV  
 A;Introns: 61/2  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein co  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 87.0%; Score 40; DB 2; Length 639;  
 Best Local Similarity 88.9%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 |||||  
 Db 286 SLFEGIDFY 294

Search completed: December 6, 2001, 07:58:26  
 Job time: 274 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:27 ; Search time 88.19 Seconds  
(without alignments)  
7.774 Million cell updates/sec

Title: PEPL-MOD8F  
Perfect score: 48  
Sequence: 1 SLFEGIDFY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	208	2 B44261	dnak-type molecule
2	48	100.0	278	2 IS1344	dnak-type molecule
3	48	100.0	420	2 A26283	dnak-type molecule
4	48	100.0	467	2 T45477	heat-shock protein
5	48	100.0	467	2 T45479	heat-shock protein
6	48	100.0	468	2 T45476	heat-shock protein
7	48	100.0	469	2 T45478	heat-shock protein
8	48	100.0	617	2 H96605	probable heat shock
9	48	100.0	632	2 T45471	dnak-type molecule
10	48	100.0	634	2 A25646	dnak-type molecule
11	48	100.0	636	2 A48872	dnak-type molecule
12	48	100.0	638	2 S31766	dnak-type molecule
13	48	100.0	639	2 JCI391	dnak-type molecule
14	48	100.0	639	2 S20139	dnak-type molecule
15	48	100.0	640	1 HHKW7A	dnak-type molecule
16	48	100.0	640	2 A29160	dnak-type molecule
17	48	100.0	640	2 S37394	dnak-type molecule
18	48	100.0	640	2 T21394	hypothetical prote
19	48	100.0	640	2 T43724	dnak-type molecule
20	48	100.0	641	2 S53357	dnak-type molecule
21	48	100.0	641	2 S35718	dnak-type molecule
22	48	100.0	641	2 IS4542	dnak-type molecule
23	48	100.0	641	2 A45871	dnak-type molecule
24	48	100.0	642	1 HHBYA1	dnak-type molecule
25	48	100.0	642	2 JH0095	dnak-type molecule
26	48	100.0	642	2 B36590	dnak-type molecule
27	48	100.0	644	2 A45635	dnak-type molecule
28	48	100.0	645	2 IS1129	dnak-type molecule
29	48	100.0	646	2 T46650	heat shock protein

30	48	100.0	647	1 HHXL70	dnak-type molecule
31	48	100.0	647	2 S44168	dnak-type molecule
32	48	100.0	647	2 T41121	heat shock protein
33	48	100.0	650	2 JC7088	dnak-type molecule
34	47	97.9	214	2 A03309	dnak-type molecule
35	47	97.9	379	2 I46588	dnak-type molecule
36	47	97.9	467	2 T45473	heat-shock protein
37	47	97.9	467	2 T45474	heat-shock protein
38	47	97.9	641	2 JN0668	dnak-type molecule
39	47	97.9	641	2 PC7036	heat shock protein
40	47	97.9	643	2 S25585	dnak-type molecule
41	47	97.9	643	2 S09036	dnak-type molecule
42	47	97.9	651	2 T45517	heat shock protein
43	47	97.9	651	2 JC7132	heat shock protein
44	45	93.8	209	2 S48024	dnak-type molecule
45	45	93.8	209	2 S48025	dnak-type molecule

ALIGNMENTS

RESULT 1

B44261  
dnak-type molecular chaperone HSC70 - California sea hare (fragment)  
N:Alternate names: heat shock protein 70 homolog HSC70  
C:Species: Aplysia californica (California sea hare)  
C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999  
C:Accession: B44261  
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.  
J. Cell Biol. 119, 1069-1076, 1992  
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr  
A:Reference number: A44261; MUID:93077669  
A:Accession: B44261  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-208 <KU>  
A>Note: sequence extracted from NCBI backbone (NCBIP:118950)  
C:Genetics:  
A:Gene: HSC70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
DB 132 SLFEGIDFY 140

RESULT 2

IS1344  
dnak-type molecular chaperone (clone pHS70.7) - rainbow trout (fragment)  
N:Alternate names: 70K heat shock protein  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999  
C:Accession: IS1344  
R:Kothary, R.K.; Jones, D.; Candido, E.P.M.  
Mol. Cell. Biol. 4, 1785-1791, 1984  
A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o  
A:Reference number: IS1344; MUID:85036330  
A:Accession: IS1344  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-278 <KOT>  
A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70



C;Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 278;

Best Local Similarity 100.0%; Pred. No. 0.039; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

Db 156 SLFEGIDFY 164

#### RESULT 3

A26283 dnak-type molecular chaperone - mouse (fragment)

N;Alternate names: heat shock protein 68

C;Species: Mus musculus (house mouse)

C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999

C;Accession: A26283

R;Lowe, D.G.; Moran, L.A.

J. Biol. Chem. 261, 2102-2112, 1986

A;Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he

A;Reference number: A26283; MUID:86111900

A;Accession: A26283

A;Molecule type: mRNA

A;Residues: 1-420 <LOW>

A;Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208

A;Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue

C;Function:

A;Description: Involved in protein folding and assembling/disassembling of protein comp

C;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 420;

Best Local Similarity 100.0%; Pred. No. 0.061; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

Db 65 SLFEGIDFY 73

#### RESULT 4

T45477

heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

C;Species: Chondrosia reniformis

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45477

R;Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: 222983

A;Accession: T45477

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-467 <BOR>

A;Cross-references: EMBL:AF026517; PIDN:AAC05362.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match 100.0%; Score 48; DB 2; Length 467;

Best Local Similarity 100.0%; Pred. No. 0.068; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

Db 252 SLFEGIDFY 260

#### RESULT 5

T45479

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C;Species: Eunicella cavolini

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45479

R;Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: 222983

A;Accession: T45479

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-467 <BOR>

A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match 100.0%; Score 48; DB 2; Length 467;

Best Local Similarity 100.0%; Pred. No. 0.068; Mismatches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

Db 252 SLFEGIDFY 260

#### RESULT 6

T45476

heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)

C;Species: Funiculina quadrangularis

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45476

R;Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: 222983

A;Accession: T45476

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-468 <BOR>

A;Cross-references: EMBL:AF026516; PIDN:AAC05361.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 468;

Mismatches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

Db 253 SLFEGIDFY 261

#### RESULT 7

T45478

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C;Species: Eunicella cavolini

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45478

R;Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: 222983

A;Accession: T45478

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-469 <BOR>

A;Cross-references: EMBL:AF026518; PIDN:AAC05363.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70



Query Match 100.0%; Score 48; DB 2; Length 469;  
Best Local Similarity 100.0%; Pred. No. 0.069;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

DB 254 SLFEGIDFY 262

RESULT 8  
H96605  
Probable heat shock protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: H96605  
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
ansen, N.F.; Hughes, B.; Hulzar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
A:Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96605  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-617 <STO>  
A:Cross-references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F13N6.9  
A:Map position: 1  
C:Superfamily: heat shock protein 70

Query Match 100.0%; Score 48; DB 2; Length 617;  
Best Local Similarity 100.0%; Pred. No. 0.093;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
|||||

DB 292 SLFEGIDFY 300

RESULT 9  
T45471  
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostelium discoideum  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T45471  
R:Boves, H.; Mintert, U.; Dittlich, W.; Faix, J.; Gerisch, G.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22980  
A:Accession: T45471  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-632 <BOV>  
A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
A:Experimental source: strain AX3  
C:Genetics:  
A:Gene: hsc70  
A:Note: localized to filopodias and cortex  
C:Superfamily: heat shock protein 70

Query Match 100.0%; Score 48; DB 2; Length 632;  
Best Local Similarity 100.0%; Pred. No. 0.095;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9

DB 285 SLFEGIDFY 293  
|||||

RESULT 10  
A25646

dnak-type molecular chaperone - chicken  
N:Alternate names: heat shock protein 70  
C:Species: Gallus gallus (chicken)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25646  
R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
J. Biol. Chem. 261, 12692-12699, 1986  
A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge  
A:Reference number: A25646; MUID:86304452  
A:Accession: A25646  
A:Molecule type: DNA  
A:Residues: 1-634 <MOR>  
A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941  
A:Note: the authors translated the codon TCG for residue 583 as Trp  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 634;  
Best Local Similarity 100.0%; Pred. No. 0.095;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9

DB 289 SLFEGIDFY 297

RESULT 11  
A48872

dnak-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)  
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein  
C:Species: Dictyostelium discoideum  
C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
C:Accession: A48872  
R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
J. Biol. Chem. 268, 23267-23274, 1993  
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with  
A:Reference number: A48872; MUID:94043116  
A:Accession: A48872  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-636 <EDD>  
A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180  
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 636;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9

DB 280 SLFEGIDFY 288

RESULT 12  
S31766

dnak-type molecular chaperone hsp70 - green monkey  
N:Alternate names: heat shock protein 70  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999



C;Accession: S31766; I36927  
 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 submitted to the EMBL Data Library, January 1993  
 A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
 A;Reference number: S31766  
 A;Accession: S31766  
 A;Molecule type: mRNA  
 A;Residues: 1-638 <SAI>  
 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FEBS Lett. 355, 282-286, 1994  
 A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me  
 A;Reference number: I36927; MUID:95080396  
 A;Accession: I36927  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-638 <RES>  
 A;Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
 A;Experimental source: kidney; cell line COS-1  
 C;Genetics:  
 A;Gene: hsp70  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein comp  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
 |||||  
 Db 284 SLFEGIDFY 292

RESULT 13  
 JC1391  
 dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
 N;Alternate names: heat shock protein 70IV; hsp70IV protein  
 C;Species: Paracentrotus lividus (common urchin)  
 C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C;Accession: JC1391  
 R;Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
 A;Reference number: JC1391; MUID:93077053  
 A;Accession: JC1391  
 A;Molecule type: DNA  
 A;Residues: 1-639 <SCO>  
 A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
 C;Genetics:  
 A;Gene: hsp70IV  
 A;Introns: 61/2  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein comp  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 100.0%; Score 48; DB 2; Length 639;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
 |||||  
 Db 286 SLFEGIDFY 294

RESULT 14  
 S20139  
 dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: heat shock protein YG102; protein I0971; protein YLL024c  
 C;Species: Saccharomyces cerevisiae

C;Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C;Accession: S20139; S64772; S64775; S69383  
 R;Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A;Reference number: S20139; MUID:89128457  
 A;Accession: S20139  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-639 <SLA>  
 A;Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
 R;Goffeau, A.; Purnelle, B.  
 submitted to the Protein Sequence Database, May 1996  
 A;Reference number: S64761  
 A;Accession: S64772  
 A;Molecule type: DNA  
 A;Residues: 1-639 <GOF>  
 A;Cross-references: EMBL:Z73129; NID:gl360201; PIDN:CAA97472.1; PID:gl360202; MIPS:YL  
 A;Experimental source: strain S288C  
 R;Purnelle, B.; Goffeau, A.  
 submitted to the EMBL Data Library, April 1996  
 A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals  
 mily and a new ABC transporter homologous to the human multidrug resistance protein.  
 A;Reference number: S69380  
 A;Accession: S69383  
 A;Molecule type: DNA  
 A;Residues: 1-639 <PUR>  
 A;Cross-references: EMBL:X97560; NID:gl297003; PIDN:CAA66167.1; PID:gl297007  
 C;Genetics:  
 A;Gene: SGD:SSA2  
 A;Cross-references: MIPS:YLL024c; SGB:S0003947  
 A;Map position: 12L  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein co  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 48; DB 2; Length 639;  
 Best Local Similarity 100.0%; Pred. No. 0.096;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
 |||||  
 Db 283 SLFEGIDFY 291

RESULT 15  
 HHKW7A  
 dnaK-type molecular chaperone hsp70A - Caenorhabditis elegans  
 N;Alternate names: heat shock protein 70 A  
 C;Species: Caenorhabditis elegans  
 C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
 C;Accession: JT0285  
 R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
 Gene 64, 241-255, 1988  
 A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri  
 A;Reference number: JT0285; MUID:88297155  
 A;Accession: JT0285  
 A;Molecule type: DNA; mRNA  
 A;Residues: 1-640 <SNU>  
 A;Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352  
 A;Note: genomic clones representing six distinct members of the hsp70 gene family wer  
 A;Note: transcripts of hsp70A are abundant in control worms and also increase two- to  
 A;Note: one of the three introns in hsp70A is in a position similar to an intron in D



C:Genetics:  
A:Gene: hsp70A  
A:Map position: IV  
A:Introns: 69/1; 331/3; 558/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 100.0%; Score 48; DB 1; Length 640;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
Db 287 SLFEGIDFY 295

Search completed: December 6, 2001, 07:58:27  
Job time: 275 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:03 ; Search time 184.09 Seconds  
(without alignments)  
3.621 Million cell updates/sec

Title: PEPL-MOD8F  
Perfect score: 48  
Sequence: 1 SLFEGIDFY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues  
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	10	22	Heat shock protein
2	48	100.0	554	21	Human heat shock p
3	48	100.0	554	21	Human heat shock p
4	48	100.0	554	21	Human heat shock p
5	48	100.0	554	21	Human heat shock p
6	48	100.0	624	21	Human Hsp72 (heat
7	48	100.0	634	11	Gallus gallus Hsp
8	48	100.0	640	11	Homo sapiens HSP (
9	48	100.0	640	18	Human heat shock p
10	48	100.0	640	21	Human heat shock p
11	48	100.0	640	21	Human heat shock p

12	48	100.0	640	21	AA198411	Human heat shock p
13	48	100.0	641	14	AA198404	Mature mouse sperm
14	48	100.0	641	19	AA198439	Human heat shock p
15	48	100.0	641	21	AA198432	Human heat shock p
16	48	100.0	641	22	AA198434	Human heat shock p
17	48	100.0	642	21	AA198435	Rat heat shock pro
18	48	100.0	642	21	AA198436	Xenopus laevis HSP
19	47	97.9	643	11	AA198437	Marmoset intracell
20	47	97.9	665	21	AA198438	Lung cancer associ
21	45	93.8	91	21	AA198439	Human secreted pro
22	45	93.8	253	21	AA198440	Arabidopsis thalia
23	45	93.8	279	21	AA198441	Arabidopsis thalia
24	45	93.8	342	21	AA198442	Arabidopsis thalia
25	45	93.8	646	11	AA198443	Rat HSP (rathsp70)
26	45	93.8	646	19	AA198444	Heat shock cognate
27	45	93.8	646	20	AA198445	Human heat shock c
28	45	93.8	646	20	AA198446	Mouse heat shock c
29	45	93.8	646	21	AA198447	Mouse heat shock p
30	45	93.8	646	21	AA198448	Human heat shock p
31	45	93.8	646	22	AA198449	Human heat shock p
32	45	93.8	656	18	AA198450	Candida albicans h
33	45	93.8	890	21	AA198451	GFP-HSC70 fusion p
34	44	91.7	633	14	AA198452	Mouse SLIP1 homolo
35	42	87.5	9	21	AA198453	Heat shock protein
36	42	87.5	9	22	AA198454	Heat shock protein
37	42	87.5	10	21	AA198455	Heat shock protein
38	42	87.5	10	22	AA198456	Heat shock protein
39	41	85.4	421	21	AA198457	Arabidopsis thalia
40	41	85.4	542	21	AA198458	Arabidopsis thalia
41	41	85.4	623	21	AA198459	Arabidopsis thalia
42	41	85.4	646	11	AA198460	Zea mays HSP (mzeh
43	41	85.4	646	21	AA198461	Arabidopsis thalia
44	38	79.2	647	20	AA198462	T. gondii antigen
45	38	79.2	647	22	AA198463	Toxoplasma gondii

## ALIGNMENTS

### RESULT 1

AA198463  
ID AAB97603 standard; peptide: 10 AA.

AC AAB97603;

DT 30-JUL-2001 (first entry)

DE Heat shock protein 70 (HSP70) peptidic fragment 3.

KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.

OS Homo sapiens.

PN WO200129190-A1.

PD 26-APR-2001.

PF 29-SEP-2000; 2000WO-EP09530.

PR 15-OCT-1999; 99EP-0120484.

PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

DR WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -



PS Claim 8; Page 15; 2lpp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
CC human heat shock protein 70 (HSP70) is given. The new invention relates  
CC to lymphocytes which recognise cells of a patient in which overexpression  
CC of HSP has been induced. Overexpression of HSP leads to a substantial  
CC increase in the numbers of HSPs and HSP epitopes presented on the  
CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
CC response which kills the target cells. As a further embodiment of the  
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells, (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumour or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

XX Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
| | | | | | | |  
Db 1 slfegidfy 9

RESULT 2

AAV88409  
ID AAY88409 standard; Protein; 554 AA.

XX AAY88409;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB; AAA15621.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX Examples; Fig 2; 1lpp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 100.0%; Score 48; DB 21; Length 554;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
| | | | | | | |  
Db 200 slfegidfy 208

RESULT 3

AAV88410  
ID AAY88410 standard; Protein; 554 AA.

XX AAY88410;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB; AAA15622.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX Disclosure; Fig 3; 1lpp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 100.0%; Score 48; DB 21; Length 554;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
| | | | | | | |  
Db 200 slfegidfy 208

RESULT 4

AAV88412  
ID AAY88412 standard; Protein; 554 AA.

XX AAY88412;



```
XX 31-JUL-2000 (first entry)
XX Human heat shock protein SHSP70 amino acid sequence.
XX
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX depression; nephrotic syndrome; SHSP70.
XX
XX Homo sapiens.
XX
XX JP2000069999-A.
XX
XX 07-MAR-2000.
XX
XX 01-JUN-1995; 99JP-0257146.
XX
XX 01-JUN-1995; 95JP-0158581.
XX
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI; 2000-264458/23.
XX
XX Abnormal transcription of intracellular HSP70mRNA under acute and
XX chronic continuous load of stress in a human being and its application
XX -
XX
XX Disclosure; Fig 5; 11pp; Japanese.
XX
XX This sequence represents the human heat shock protein SHSP70 amino acid
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX and 14q22-24. The invention relates to the abnormal transcription of
XX intracellular HSP70mRNA under acute and chronic stress load in a human.
XX The abnormal transcription of HSP70 can be used in the improvement of
XX stress and response and diagnosis of stress diseases including
XX rheumatism, schizophrenia, depression and nephrotic syndrome.
XX
XX Sequence 554 AA;
XX
XX Query Match 100.0%; Score 48; DB 21; Length 554;
XX Best Local Similarity 100.0%; Pred. No. 0.11;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDFY 9
XX Db 200 slfegidfy 208
XX
XX RESULT 5
XX AAY88413
XX ID AAY88413 standard; Protein; 554 AA.
XX
XX AC AAY88413;
XX
XX 31-JUL-2000 (first entry)
XX
XX Human heat shock protein SHSP70 amino acid sequence.
XX
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX depression; nephrotic syndrome; SHSP70.
XX
XX Homo sapiens.
XX
XX JP2000069999-A.
XX
XX 07-MAR-2000.
XX
XX 01-JUN-1995; 99JP-0257146.
XX
XX 01-JUN-1995; 95JP-0158581.
XX
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI; 2000-264458/23.
XX
XX Abnormal transcription of intracellular HSP70mRNA under acute and
XX chronic continuous load of stress in a human being and its application
XX -
XX
XX Disclosure; Fig 5; 11pp; Japanese.
XX
XX This sequence represents the human heat shock protein SHSP70 amino acid
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX and 14q22-24. The invention relates to the abnormal transcription of
XX intracellular HSP70mRNA under acute and chronic stress load in a human.
XX The abnormal transcription of HSP70 can be used in the improvement of
XX stress and response and diagnosis of stress diseases including
XX rheumatism, schizophrenia, depression and nephrotic syndrome.
XX
XX Sequence 554 AA;
XX
XX Query Match 100.0%; Score 48; DB 21; Length 554;
XX Best Local Similarity 100.0%; Pred. No. 0.11;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDFY 9
XX Db 200 slfegidfy 208
XX
XX RESULT 6
XX AAB23252
XX ID AAB23252 standard; Protein; 624 AA.
XX
XX AC AAB23252;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human Hsp72 (heat shock protein 72).
XX
XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
XX expression modulator; JNK phosphatase inhibitor; antiproliferative;
XX drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;
XX carcinoma; breast cancer; prostate cancer; premalignant condition.
XX
XX Homo sapiens.
XX
XX WO200054814-A1.
XX
XX 21-SEP-2000.
XX
XX 17-MAR-2000; 2000WO-US07350.
XX
XX 18-MAR-1999; 99US-0125046.
XX
XX (PHYL-) PHYLOGENY INC.
XX
XX Volloch VZ, Sherman M;
XX
XX WPI; 2000-647056/62.
XX
XX N-PSDB; AAA97541.
XX
XX Identifying compounds that inhibit proliferation of cells and capable
XX of modulating the expression of heat shock protein 72 gene and/or
XX activity of Hsp72 useful for treating cancers such as leukemia,
XX lymphoma -
XX
XX Examples; Fig 16B; 77pp; English.
XX
XX The invention relates to a novel method of identifying compounds that
XX inhibit proliferation of cells comprising contacting a test compound with
XX a cell which overexpresses Hsp72 (heat shock protein 72), and determining
XX if the test compound inhibits activity or expression of Hsp72.
XX
```



CC Optionally, Hsp72 is contacted with the test compound under optimum  
 CC conditions to allow the two components to interact and bind, forming a  
 CC complex which is detected. The invention also relates to a method of  
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
 CC activation, comprising contacting a test compound with a cell which  
 CC expresses Hsp72, exposing the cell to a heat induced stress and  
 CC determining if the compound inhibits JNK phosphatase activity. The  
 CC invention additionally encompasses compositions comprising an inhibitor  
 CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
 CC inhibiting the proliferation of cells. Modulation of the activity of the  
 CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.

XX SQ Sequence 624 AA;

Query Match 100.0%; Score 48; DB 21; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 |||||

Db 286 slfegidfy 294

RESULT 7  
 AAR03930  
 ID AAR03930 standard; Protein: 634 AA.

XX AC AAR03930;

DT 30-AUG-1990 (first entry)

XX Gallus gallus HSP (chkhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Gallus gallus.

XX Key Location/Qualifiers

FT Misc-difference 634 /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has  
 CC 635 amino acid residues, the sequence itself has only 634,  
 CC including "O" (?) at position 634.

CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bmeahsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);  
 CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. Xenopus laevis (xl70 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).

CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.

XX SQ Sequence 634 AA;

Query Match 100.0%; Score 48; DB 11; Length 634;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 |||||

Db 289 slfegidfy 297

RESULT 8  
 AAR03929  
 ID AAR03929 standard; Protein: 640 AA.

XX AC AAR03929;

DT 30-AUG-1990 (first entry)

XX Homo sapiens HSP (humhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 640 /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has  
 CC 641 amino acid residues, the sequence itself has only 640,  
 CC including "O" (?) at position 640.

XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bmeahsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);



CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. xenopus laevis (xl70 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 640 AA;

Query Match 100.0%; Score 48; DB 11; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0;

QY 1 SLFEGIDFY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 9  
 AAW10065  
 ID AAW10065 standard; Protein; 640 AA.  
 XX  
 AC AAW10065;  
 XX  
 DT 24-OCT-1997 (first entry)  
 XX  
 DE Human heat shock protein 70.  
 XX  
 KW Human; heat shock protein 70; HSP70; primer; probe; detection;  
 KW Intracellular; abnormal transcription; acute; chronic; sustained;  
 KW stress.  
 XX  
 OS Homo sapiens.  
 OS  
 PN JP08322577-A.  
 XX

PD 10-DEC-1996.  
 XX  
 PF 01-JUN-1995; 95JP-0158581.  
 XX  
 PR 01-JUN-1995; 95JP-0158581.  
 XX  
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 DR WPI: 1997-081088/08.  
 DR N-PSDB; AAT58086.  
 XX  
 PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
 PT specific primer or probe, used in detection of human acute and  
 PT chronic sustained stress load  
 XX  
 PS Claim 1: Fig 1; 13pp; Japanese.  
 XX

CC The cDNA encoding the present sequence, human heat shock protein 70  
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
 CC and 21. Primers and probes based on the HSP70 cDNA coding  
 CC sequence can be used to detect the abnormal transcription of  
 CC intracellular HSP70 mRNA in human acute and chronic sustained  
 CC stress load.  
 CC  
 XX  
 SQ Sequence 640 AA;

Query Match 100.0%; Score 48; DB 18; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0;

QY 1 SLFEGIDFY 9

Db 286 slfegidfy 294  
 |||||  
 RESULT 10  
 AAB23653  
 ID AAB23653 standard; Protein; 640 AA.  
 XX  
 AC AAB23653;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW Immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytototoxic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200049041-A1.  
 XX

PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX

PA (SUME) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX  
 DR WPI: 2000-543748/49.

PT Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer -  
 XX

PS Claim 3; Page 49-52; 72pp; Japanese.

CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX

SQ Sequence 640 AA;

Query Match 100.0%; Score 48; DB 21; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 11  
 AAY88408  
 ID AAY88408 standard; Protein; 640 AA.  
 XX  
 AC AAY88408;  
 XX



DT 31-JUL-2000 (first entry)  
 XX Human heat shock protein HSP70 amino acid sequence.  
 DE  
 XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2000069999-A.  
 PN  
 XX 07-MAR-2000.  
 PD  
 XX 01-JUN-1995; 99JP-0257146.  
 PF  
 XX 01-JUN-1995; 95JP-0158581.  
 PR  
 XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 XX WPI: 2000-264458/23.  
 DR N-PSDB; AAA15620.  
 XX  
 XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application  
 PT  
 PT  
 XX Claim 2; Fig 1; 11pp; Japanese.  
 PS  
 XX This sequence represents the human heat shock protein HSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 XX  
 XX Sequence 640 AA;  
 SQ

Query Match 100.0%; Score 48; DB 21; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 12  
 AAY88411  
 ID AAY88411 standard; Protein; 640 AA.  
 XX  
 AC AAY88411;  
 XX  
 XX 31-JUL-2000 (first entry)  
 DT  
 XX Human heat shock protein LHPSP70 amino acid sequence.  
 DE  
 XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; LHPSP70.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2000069999-A.  
 PN  
 XX 07-MAR-2000.  
 PD  
 XX 01-JUN-1995; 99JP-0257146.  
 PF  
 XX 01-JUN-1995; 95JP-0158581.  
 PR  
 XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 XX WPI: 2000-264458/23.  
 DR N-PSDB; AAA15620.  
 XX  
 XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application  
 PT  
 PT  
 XX Claim 2; Fig 1; 11pp; Japanese.  
 PS  
 XX This sequence represents the human heat shock protein HSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 XX  
 XX Sequence 640 AA;  
 SQ

Query Match 100.0%; Score 48; DB 21; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 13  
 AAR43004  
 ID AAR43004 standard; protein; 641 AA.  
 XX  
 AC AAR43004;  
 XX  
 XX 20-MAY-1994 (first entry)  
 DT  
 XX Mature mouse sperm 70kd heat shock protein.  
 DE  
 XX Sulphoglycolipid immobilising protein 1; sperm plasma membrane;  
 KW HSC70B; mammalian; infertility; mycoplasma; HSP70.  
 KW  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..385  
 FT Region  
 FT /label= 44kd.Atpase\_fragment  
 FT /note= "peptides comprising an intact domain from  
 FT the Atpase fragment of hsp70 are claimed;  
 FT the peptides are homologous to sequences  
 FT conserved between SLIP1 and 74.5kd  
 FT mycoplasma protein"  
 FT  
 FT Domain 1..39  
 FT /label= IA  
 FT /note= "part"  
 FT 40..115  
 FT Domain /label= IB  
 FT 116..188  
 FT Domain /label= IA  
 FT /note= "part"  
 FT 189..228  
 FT Domain /label= IIA  
 FT /note= "part"  
 FT 229..306  
 FT Domain /label= IIB  
 FT 307..385  
 FT Domain /label= IIA  
 FT /note= "part"  
 FT  
 XX WO9321954-A.  
 PN  
 XX 11-NOV-1993.  
 PD



XX 22-APR-1993; 93WO-US03816.  
 XX  
 PR 24-APR-1992; 92US-0873961.  
 XX  
 PA (BERL-) BERLEX LAB INC.  
 PA (OTTA-) OTTAWA CIVIC HOSPITAL.  
 XX  
 PI Faulds DH, Lingwood CA, Tanphaichitr N;  
 XX  
 DR WPI; 1993-368422/46.  
 XX  
 PT Mammalian fertilisation decrease for detecting and treating  
 PT infertility - using sulpho glyco lipid immobilising protein  
 PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
 PT infection treatment  
 XX  
 PS Claim 2 and Claim 17; Page 60-62; 77pp; English.  
 XX  
 CC The likelihood of mammalian fertilisation is decreased by contacting  
 CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIPI)/  
 CC sulphated glyco-moiety interfering composition. The interfering  
 CC compsn. is e.g. the heat shock 70kd protein, SLIPI (or analogues  
 CC such as the mouse SLIPI analogue "HSC70B" comprising the amino acid  
 CC sequence AAR43002) or the 74.5kd mycoplasma protein (AAR43003).  
 XX  
 XX Sequence 641 AA;  
 SQ  
 Query Match 100.0%; Score 48; DB 14; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLFEGIDFY 9  
 Db |||||||  
 286 slfegidfy 294  
 RESULT 14  
 AAW54349  
 ID AAW54349 standard; protein; 641 AA.  
 XX  
 AC AAW54349;  
 XX  
 DT 14-AUG-1998 (first entry)  
 XX  
 DE Human heat shock 70 kd protein 1.  
 XX  
 KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
 KW 2D gel electrophoresis; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9810291-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 05-SEP-1997; 97WO-GB02394.  
 XX  
 PR 08-APR-1997; 97GB-0007132.  
 PR 06-SEP-1996; 96GB-0018600.  
 XX  
 PA (CLIN-) CENT CLINICAL & BASIC RES.  
 XX  
 PI Byrjalsen I, Fey SJ, Larsen P;  
 XX  
 DR WPI; 1998-207057/18.  
 XX  
 PT Biochemical markers of human endometrium - useful for, e.g.  
 PT diagnosis of hyperplasia and adenocarcinoma  
 XX  
 PS Disclosure; Page 19; 77pp; English.  
 XX

CC Proteins AAW54349-W54364 are examples of proteins produced in the  
 CC endometrium during the hyperplasia, adenocarcinoma or proliferative  
 CC phase of the endometrium. The presence and quantities of these proteins  
 CC can be detected using 2D gel electrophoresis comparison of cell lysates.  
 CC The proteins can be used as biochemical markers to detect the phase of  
 CC the endometrium and can be measured in body fluids, obviating the need  
 CC for endometrial biopsies.  
 XX  
 SQ Sequence 641 AA;  
 Query Match 100.0%; Score 48; DB 19; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLFEGIDFY 9  
 Db |||||||  
 286 slfegidfy 294  
 RESULT 15  
 AAB23652  
 ID AAB23652 standard; protein; 641 AA.  
 XX  
 AC AAB23652;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytostatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX  
 PA (SUME ) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Uono H, Yui K;  
 XX  
 DR WPI; 2000-543748/49.  
 XX  
 PT Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer -  
 XX  
 PS Claim 3; Page 46-48; 72pp; Japanese.  
 XX  
 CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX  
 SQ Sequence 641 AA;



Tue Dec 11 08:45:44 2001

Query Match 100.0%; Score 48; DB 21; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDFY 9  
| | | | | | | | | |  
Db 286 slfegidfy 294

Search completed: December 6, 2001, 08:04:03  
Job time: 611 sec

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OM protein - protein search, using sw model  
Run on: December 6, 2001, 08:00:51 ; Search time 50.21 seconds  
(without alignments)  
6.572 Million cell updates/sec

Title: PEPL-MOD8F  
Perfect score: 48  
Sequence: 1 SLFEGIDFY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	48	100.0	322	1 HS70_ONCVO	P11503 onchocerca
2	48	100.0	420	1 HS73_MOUSE	Q61696 mus musculus
3	48	100.0	503	1 HS70_PENCI	Q92260 penicillium
4	48	100.0	634	1 HS70_CHICK	P08106 gallus galli
5	48	100.0	638	1 HS71_CERAE	Q28222 cercopithec
6	48	100.0	638	1 HS72_YEAST	P10592 saccharomyc
7	48	100.0	639	1 HS74_PARLI	Q06248 paracentrot
8	48	100.0	640	1 HS7A_CAEEL	P09446 caenorhabdi
9	48	100.0	640	1 HS7C_DICDI	P36415 dictyosteli
10	48	100.0	641	1 HS71_BOVIN	Q27975 bos taurus
11	48	100.0	641	1 HS71_HUMAN	P08107 homo sapien
12	48	100.0	641	1 HS71_MOUSE	P17879 mus musculus
13	48	100.0	641	1 HS71_PIG	P34930 sus scrofa
14	48	100.0	641	1 HS71_RAT	Q07439 rattus norv
15	48	100.0	641	1 HS71_YEAST	P10591 saccharomyc
16	48	100.0	641	1 HS72_BOVIN	Q27965 bos taurus
17	48	100.0	641	1 HS74_YEAST	P22202 saccharomyc
18	48	100.0	644	1 HS70_BRUMA	P27541 brugia mala
19	48	100.0	644	1 HS70_ONCTS	Q91233 oncorhynch
20	48	100.0	645	1 HS70_PLEWA	Q91291 pleurodeles
21	48	100.0	646	1 HS70_NEUCR	Q01233 neurospora
22	48	100.0	647	1 HS70_XENLA	P02827 xenopus lae
23	48	100.0	649	1 HS70_BLAEM	P48720 blastoclad
24	48	100.0	652	1 HS7D_MANSE	Q96639 manduca sex
25	47	97.9	214	1 HS7A_DRORI	P02826 drosophila
26	47	97.9	379	1 HS7X_PIG	P34934 sus scrofa
27	47	97.9	641	1 HS7A_DROME	P29843 drosophila
28	47	97.9	643	1 HS76_HUMAN	P17066 homo sapien
29	47	97.9	643	1 HS76_PIG	Q04967 sus scrofa
30	47	97.9	648	1 HS71_PUCGR	Q01877 puccinia gr
31	45	93.8	372	1 HS72_PARLI	P22623 paracentrot
32	45	93.8	641	1 HS73_RAT	P50633 rattus norv
33	45	93.8	641	1 HS7H_HUMAN	P34931 homo sapien

34	45	93.8	641	1 HS7T_MOUSE	P16627 mus musculus
35	45	93.8	642	1 HS72_PICAN	P53623 pichia angu
36	45	93.8	643	1 HS71_SCHPO	Q10265 schizosacch
37	45	93.8	644	1 HS71_PICAN	P53421 pichia angu
38	45	93.8	644	1 HS72_LYCES	P27322 lycopersico
39	45	93.8	645	1 HS70_SOYBN	P26413 glycine max
40	45	93.8	646	1 HS7C_CRIGR	P19378 cricetulus
41	45	93.8	646	1 HS7C_HUMAN	P11142 homo sapien
42	45	93.8	646	1 HS7C_MOUSE	P08109 mus musculus
43	45	93.8	649	1 HS70_PARRR	P87047 paracoccidi
44	45	93.8	649	1 HS73_ARATH	O65719 arabidopsis
45	45	93.8	649	1 HS73_YEAST	P09435 saccharomyc

ALIGNMENTS

RESULT 1  
HS70\_ONCVO STANDARD; PRT; 322 AA.  
AC P11503;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89201313; PubMed=2704388;  
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;  
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in  
macrofilaremic individuals from a filariasis-endemic area.";  
RL Mol. Biochem. Parasitol. 33:229-236(1989).  
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A  
MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
-----  
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the European Bioinformatics Institute. There are no restrictions on its  
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-----  
CC EMBL; J04006; AAA29417.1; -.  
DR HSSP; P19120; IATP.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock.  
FT NON\_TER 1  
FT NON\_TER 322 322  
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
Db 43 SLFEGIDFY 51

RESULT 2  
HS73\_MOUSE STANDARD; PRT; 420 AA.  
ID HS73\_MOUSE



AC Q61696; Q61697;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).  
GN HSP70-3 OR HSP70A1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86111900; PubMed=2868009;  
RA Lowe D.G., Moran L.A.;  
RT "Molecular cloning and analysis of DNA complementary to three mouse  
RT Mr = 68,000 heat shock protein mRNAs.";  
RL J. Biol. Chem. 261:2102-2112(1986).  
RN [2]  
RP SEQUENCE OF 155-420 FROM N.A.  
RX MEDLINE=94357449; PubMed=8076831;  
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
RT "Structure and expression of an inducible HSP70-encoding gene from  
RT Mus musculus.";  
RL Gene 146:273-278(1994).  
CC -|- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
CC -|- INDUCTION: BY HEAT SHOCK.  
CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC  
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CC  
CC EMBL; M12571; AAA57234.1; -  
CC EMBL; M12572; AAA57235.1; -  
CC HSP; P19120; 1A7R.  
CC MGD; MGI:96244; Hsp70-3.  
CC InterPro: IPR001023; HSP70.  
CC Pfam; PF00012; HSP70; 1.  
CC PROSITE; PS00297; HSP70\_1; PARTIAL.  
CC PROSITE; PS00329; HSP70\_2; PARTIAL.  
CC PROSITE; PS01036; HSP70\_3; 1.  
CC ATP-binding; Chaperone; Heat shock; Multigene family.  
KW NON\_TER 1  
FT VARIANT 188 188 V -> G.  
FT SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;  
  
Query Match 100.0%; Score 48; DB 1; Length 420;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDFY 9  
Db 65 SLFEGIDFY 73  
|||||  
  
RESULT 3  
ID HS70\_PENCI STANDARD; PRT; 503 AA.  
AC Q92260;  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
GN HSP70;  
OS Penicillium citrinum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
OX NCBI\_TaxID=5077;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;  
RT "Molecular cloning and expression of a Penicillium citrinum  
RT allergen with sequence homology and antigenic cross-reactivity to  
RT a hsp70 human heat shock protein.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC  
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CC  
CC EMBL; U64207; AAB06397.1; -  
CC HSP; P19120; 3HSC.  
CC InterPro: IPR001023; HSP70.  
CC Pfam; PF00012; HSP70; 1.  
CC PRINTS; PR00301; HEATSHOCK70.  
CC PROSITE; PS00329; HSP70\_2; 1.  
CC PROSITE; PS01036; HSP70\_3; 1.  
CC ATP-binding; Chaperone; Heat shock; Allergen.  
KW NON\_TER 1  
FT SEQUENCE 503 AA; 55125 MW; B7433C11FAE1320 CRC64;  
  
Query Match 100.0%; Score 48; DB 1; Length 503;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDFY 9  
Db 154 SLFEGIDFY 162  
|||||  
  
RESULT 4  
ID HS70\_CHICK STANDARD; PRT; 634 AA.  
AC P08106;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86304452; PubMed=3017985;  
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
RT "Organization, nucleotide sequence, and transcription of the chicken  
RT HSP70 gene.";  
RL J. Biol. Chem. 261:12692-12699(1986).  
CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC  
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CC -----
DR EMBL: J02579; AAA48825.1; -.
DR PIR: A25646; A25646.
DR HSSP: P19120; IATR.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 100.0%; Score 48; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLFEGIDFY 9
   |||||
Db 289 SLFEGIDFY 297

RESULT 5
ID HS71_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X70684; CAA50019.1; -.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.

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DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLFEGIDFY 9
   |||||
Db 284 SLFEGIDFY 292

RESULT 6
ID HS72_YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YLL024C OR L0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Purnelle B., Goffeau A.;
RN [3]
RP Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RA Duesterhoft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RN Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

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CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; X12927; CAA31394.1; -.
CC EMBL; Z73129; CAA97472.1; -.
CC EMBL; X97560; CAA66167.1; -.
CC PIR; S20139; S20139.
CC HSP; P19120; INGJ.
CC SWISS-2DPAGE; P10592; YEAST.
CC YEPD; 9800; -.
CC SGD; S0003947; SSA2.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70_1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 282 SLFEGIDFY 290
|||||

RESULT 7
HS74_PARLI STANDARD; PRT; 639 AA.
AC O06248;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
GN HSP70IV.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
RL lividus hsp70 gene family and its expression."
RL Gene 121:353-358(1992).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; X61379; CAA43653.1; -.

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DR PIR; JCI391; JCI391.
DR HSP; P19120; INGJ.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 100.0%; Score 48; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 286 SLFEGIDFY 294
|||||

RESULT 8
HS7A_CAEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
RT characterization."
RL Gene 64:241-255(1988).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL; M18540; AAA28078.1; -.
DR PIR; JI0285; HHKW7A.
DR HSP; P19120; INGJ.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 287 SLFEGIDFY 295
|||||

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RESULT 9
HS7C_DICDI          STANDARD;          PRT;          640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Eukaryota; Metazoa; Dictyostelida; Dictyostelium.
OC Eukaryota; Metazoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44669;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008983; PubMed=8404847;
RA Naegel A.A., Schleicher M.;
RA Haug U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RT *The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RT cap32/34.*;
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RX STRAIN=AX3;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT *Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an hsc70 in Dictyostelium.*;
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; X75263; CAA53039.1; -.
DR EMBL; L22736; AAA33219.1; -.
DR PIR; S37394; S37394.
DR HSP; P19120; INGT.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDB; D001078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; 266BDC2D896A9F5D CRC64;
KW CONFLICT 1 29
FT FT
FT IHHHNGNATWVESGYPVSEVLSFN (IN REF. 2).
FT N -> T (IN REF. 2).
FT V -> A (IN REF. 2).
FT R -> A (IN REF. 2).
FT S -> A (IN REF. 2).
FT V -> A (IN REF. 2).
FT I -> L (IN REF. 2).
FT F -> P (IN REF. 2).
FT SEQUENCE 640 AA; 70499 MW; 266BDC2D896A9F5D CRC64;
Query Match 100.0%; Score 48; DB 1; Length 640;
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Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
DB 284 SLFEGIDFY 292

RESULT 10
HS7L_BOVIN
ID HS7L_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Gueriero V.;
RT *Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.*;
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RX STRAIN=ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT *An AluI polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus.*;
RL Anim. Genet. 25:196-196(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U09861; AAA73914.1; -.
DR EMBL; U02891; AAA03450.1; -.
DR HSP; P19120; INGC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
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Query Match 100.0%; Score 48; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 286 SLFEGIDFY 294

RESULT 11
HS71_HUMAN STANDARD; PRT; 641 AA.
ID HS71_MOUSE STANDARD; PRT; 641 AA.
AC P17990; Q9UQO0; Q9UQO1;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RN MEDLINE=91055806; PubMed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
[2]
SEQUENCE FROM N.A.
RN MEDLINE=86016721; PubMed=3931075;
RA Hunt C., Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
[3]
SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RN MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
[5]
SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RN MEDLINE=87066768; PubMed=3786141;
RA Drabant B., Genthe A., Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
[6]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RN MEDLINE=99234376; PubMed=10216320;
RA Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
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RX MEDLINE-94368874; PubMed-8086479;
RA Lisowska K., Krawczyk Z., Widlak W., Wolniczék P., Wisniewski J.;
RT "Cloning, nucleotide sequence and expression of rat heat inducible
RL hsp70 gene.";
CC Biochim. Biophys. Acta 1219:64-72(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; L16764; AAA17441.1; -
CC EMBL; X77208; CAA54423.1; -
CC EMBL; X77207; CAA54422.1; -
CC EMBL; X74271; CAA52328.1; -
CC HSP; P19120; INGC.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 71 72 KR -> NG (IN REF. 3).
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).
FT CONFLICT 408 408 G -> A (IN REF. 3).
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C968583 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9
Db 286 SLFEGIDFY 294

RESULT 15
ID HS71_YEAST STANDARD; PRT; 641 AA.
AC P10591;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSAL (HEAT SHOCK PROTEIN YG100).
GN SSAL OR YAL005C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE-89128457; PubMed-2644626;
RA Slater M.R., Craig E.A.;
RT "The SSAL and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN-S288C / AB972;
RX MEDLINE-95028152; PubMed-7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SP07-CENI-CDCL5 region.";
RL Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 590-641 FROM N.A.
RX MEDLINE-85087943; PubMed=6096826;
RA Ogden R.C., Lee M.-C., Knapp G.;
RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
RT substrates.";
RL Nucleic Acids Res. 12:9367-9382(1984).
RN [4]
RP REVISIONS TO 207; 417 AND 421.
RA Slater M.R.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN-S288C;
RX MEDLINE-95203288; PubMed-7895733;
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [6]
RP SEQUENCE OF 186-195.
RC STRAIN-ATPC 38331 / Y41;
RX MEDLINE-97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [7]
RP ACETYLATION.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: SSAL MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSAL AND SSA2 PROTEINS IS EXPECTED. SSAL CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X12926; CAA31393.1; -
CC EMBL; L22015; AAC04952.1; ALT_SEQ.
CC PIR; S25438; HHBYAL.
CC PIR; S42164; S42164.
CC HSP; P19120; IATR.
CC SWISS-2DPAGE; P10591; YEAST.
CC YEPD; 9788; -.
CC SGD; S0000004; SSAL.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation.
FT INIT_MET 0 0 1
FT MOD_RES 1 1 1 ACETYLATION.

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SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 641;

Best Local Similarity 100.0%; Pred. No. 0.046;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9

|||||

Db 282 SLFEGIDFY 290

Search completed: December 6, 2001, 08:00:51

Job time: 419 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:02 ; Search time 184.09 seconds  
(without alignments)  
3.621 Million cell updates/sec

Title: PEPL-MOD8G

Perfect score: 48

Sequence: 1 SLFEGIDCY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	81.2	10	22	Heat shock protein
2	39	81.2	554	21	Human heat shock p
3	39	81.2	554	21	Human heat shock p
4	39	81.2	554	21	Human heat shock p
5	39	81.2	554	21	Human heat shock p
6	39	81.2	624	21	Human Hsp72 (heat
7	39	81.2	634	11	Gallus gallus HSP
8	39	81.2	640	11	Homo sapiens HSP
9	39	81.2	640	18	Human heat shock p
10	39	81.2	640	21	Human heat shock p
11	39	81.2	640	21	Human heat shock p

12	39	81.2	640	21	AA198411	Human heat shock p
13	39	81.2	641	14	AA198404	Mature mouse sperm
14	39	81.2	641	19	AA198439	Human heat shock 7
15	39	81.2	641	21	AA198452	Human heat shock p
16	39	81.2	641	22	AA198453	Human heat shock p
17	39	81.2	642	21	AA198454	Rat heat shock pro
18	39	81.2	647	11	AA198455	Xenopus laevis HSP
19	38	79.2	9	21	AA198456	Heat shock protein
20	38	79.2	9	22	AA198457	Heat shock protein
21	38	79.2	10	21	AA198458	Heat shock protein
22	38	79.2	10	22	AA198459	Heat shock protein
23	38	79.2	303	18	AA198460	Pyrobaculum aerop
24	38	79.2	643	18	AA198461	Marimset intracell
25	38	79.2	665	21	AA198462	Lung cancer associ
26	36	75.0	83	21	AA198463	Arabidopsis thalia
27	36	75.0	91	21	AA198464	Human secreted pro
28	36	75.0	160	22	AA198465	C glutamicum prote
29	36	75.0	160	22	AA198466	Corynebacterium gl
30	36	75.0	200	21	AA198467	Arabidopsis thalia
31	36	75.0	225	21	AA198468	Arabidopsis thalia
32	36	75.0	229	21	AA198469	Arabidopsis thalia
33	36	75.0	253	21	AA198470	Arabidopsis thalia
34	36	75.0	279	21	AA198471	Arabidopsis thalia
35	36	75.0	342	21	AA198472	Arabidopsis thalia
36	36	75.0	646	11	AA198473	Rat HSP (rathsp70)
37	36	75.0	646	19	AA198474	Heat shock cognate
38	36	75.0	646	20	AA198475	Human heat shock c
39	36	75.0	646	20	AA198476	Mouse heat shock c
40	36	75.0	646	21	AA198477	Mouse heat shock p
41	36	75.0	646	21	AA198478	Human heat shock p
42	36	75.0	646	22	AA198479	Human heat shock p
43	36	75.0	656	18	AA198480	Candida albicans h
44	36	75.0	890	21	AA198481	GFP-HSC70 fusion p
45	35	72.9	180	18	AA198482	H. pylori cytoplas

#### ALIGNMENTS

RESULT 1  
AAB97603  
ID : AAB97603 standard; peptide; 10 AA.  
XX  
AC AAB97603;  
XX  
DT 30-JUL-2001 (first entry)  
XX  
DE Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX Homo sapiens.

XX WO200129190-A1.

PD 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
PT transformed human cells with induced and increased membrane expression  
PT of heat shock protein -



PS Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
CC human heat shock protein 70 (HSP70) is given. The new invention relates  
CC to lymphocytes which recognise cells of a patient in which overexpression  
CC of HSP has been induced. Overexpression of HSP leads to a substantial  
CC increase in the numbers of HSPs and HSP epitopes presented on the  
CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
CC response which kills the target cells. As a further embodiment of the  
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells, (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumour or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

XX Sequence 10 AA;

Query Match 81.2%; Score 39; DB 22; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.24;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
| | | | | | | |  
Db 1 slfegidfy 9

RESULT 2

AY88409  
ID AAY88409 standard; Protein; 554 AA.

XX AAY88409;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB; AAA15621.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX Examples; Fig 2; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 81.2%; Score 39; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
| | | | | | | |  
Db 200 slfegidfy 208

RESULT 3

AY88410  
ID AAY88410 standard; Protein; 554 AA.

XX AAY88410;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX N-PSDB; AAA15622.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX Disclosure; Fig 3; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 81.2%; Score 39; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
| | | | | | | |  
Db 200 slfegidfy 208

RESULT 4

AY88412  
ID AAY88412 standard; Protein; 554 AA.

XX AAY88412;



:T0C9CT0-4NCC,'CEET-NOC-T0

the invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.



CC Optionally, Hsp72 is contacted with the test compound under optimum  
 CC conditions to allow the two components to interact and bind, forming a  
 CC complex which is detected. The invention also relates to a method of  
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
 CC activation, comprising contacting a test compound with a cell which  
 CC expresses Hsp72, exposing the cell to a heat induced stress and  
 CC determining if the compound inhibits JNK phosphatase activity. The  
 CC invention additionally encompasses compositions comprising an inhibitor  
 CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
 CC inhibiting the proliferation of cells. Modulation of the activity of the  
 CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.

XX SQ Sequence 624 AA;

Query Match 81.2%; Score 39; DB 21; Length 624;  
 Best Local Similarity 88.9%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFEGIDGY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 7  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.

XX AC AAR03930;

DT 30-AUG-1990 (first entry)

DE Gallus gallus HSP (chkhsp70).

KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX OS Gallus gallus.

FH Key Location/Qualifiers

FT Misc-difference 634 /note= "residue given as "O" in specification"

XX PN WO9002564-A.

XX PD 22-MAR-1990.

XX PF 12-SEP-1989; 89WO-0003955.

XX PR 12-SEP-1988; 88US-0243474.

XX PA (CODO-) CODON.

XX PI Dragon E, Faulds D, Sias S;

XX DR WPI; 1990-115820/15.

XX PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX PS Disclosure; Fig 2.1-2.14; 86pp; English.

XX CC According to the legend of Fig 2, the G. gallus HSP sequence has  
 635 amino acid residues, the sequence itself has only 634,  
 including "O" (?) at position 634.

CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 2. Bacillus megaterium (Bmeahsp70 - AAR03923);  
 3. E. coli (dnaK - AAR03924);  
 4. T. cruzi (tc70kd - AAR03925);

CC 5. T. cruzi (AAR03926);

CC 6. Rat rattus (rathsp70 - AAR03927);

CC 7. Xenopus laevis (xl70 - AAR03928);

CC 8. Homo sapiens (humhsp70 - AAR03929);

CC 9. Gallus gallus (chkhsp70 - AAR03930);

CC 10. Zea mays (mzehsp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).

CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.

XX SQ Sequence 634 AA;

Query Match 81.2%; Score 39; DB 11; Length 634;  
 Best Local Similarity 88.9%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFEGIDGY 9  
 |||||  
 Db 289 slfegidfy 297

RESULT 8

AAR03929  
 ID AAR03929 standard; Protein; 640 AA.

XX AC AAR03929;

DT 30-AUG-1990 (first entry)

DE Homo sapiens HSP (humhsp70).

KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 640 /note= "residue given as "O" in specification"

XX PN WO9002564-A.

XX PD 22-MAR-1990.

XX PF 12-SEP-1989; 89WO-0003955.

XX PR 12-SEP-1988; 88US-0243474.

XX PA (CODO-) CODON.

XX PI Dragon E, Faulds D, Sias S;

XX DR WPI; 1990-115820/15.

XX PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX PS Disclosure; Fig 2.1-2.14; 86pp; English.

XX CC According to the legend of Fig 2, the H. sapiens HSP sequence has  
 641 amino acid residues, the sequence itself has only 640,  
 including "O" (?) at position 640.

XX CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 2. Bacillus megaterium (Bmeahsp70 - AAR03923);

XX CC 3. E. coli (dnaK - AAR03924);

XX CC 4. T. cruzi (tc70kd - AAR03925);



CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. Xenopus laevis (xl70 - AAR03928);  
 CC 8. Homo sapiens (humsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 640 AA;

Query Match 81.2%; Score 39; DB 11; Length 640;  
 Best Local Similarity 88.9%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 9  
 AAW10065  
 ID AAW10065 standard; Protein; 640 AA.  
 XX  
 AC AAW10065;  
 XX  
 DT 24-OCT-1997 (first entry)  
 XX  
 DE Human heat shock protein 70.  
 XX  
 KW Human; heat shock protein 70; HSP70; primer; probe; detection;  
 KW intracellular; abnormal transcription; acute; chronic; sustained;  
 KW stress.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP08322577-A.  
 XX  
 PD 10-DEC-1996.  
 XX  
 PF 01-JUN-1995; 95JP-0158581.  
 XX  
 PR 01-JUN-1995; 95JP-0158581.  
 XX  
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 DR WPI: 1997-081088/08.  
 DR N-PSDB; AAT58086.  
 XX  
 PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
 PT specific primer or probe, used in detection of human acute and  
 PT chronic sustained stress load  
 XX  
 PS Claim 1; Fig 1; 13pp; Japanese.  
 XX

CC The cDNA encoding the present sequence, human heat shock protein 70  
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
 CC and 21. Primers and probes based on the HSP70 cDNA coding  
 CC sequence can be used to detect the abnormal transcription of  
 CC intracellular HSP70 mRNA in human acute and chronic sustained  
 CC stress load.  
 XX  
 SQ Sequence 640 AA;

Query Match 81.2%; Score 39; DB 18; Length 640;  
 Best Local Similarity 88.9%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGY 9

Db 286 slfegidfy 294  
 |||||  
 RESULT 10  
 AAB23653  
 ID AAB23653 standard; protein; 640 AA.  
 XX  
 AC AAB23653;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytosatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX  
 PA (SUNE) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX  
 DR WPI: 2000-543748/49.  
 XX  
 PT Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer -  
 XX  
 PS Claim 3; Page 49-52; 72pp; Japanese.  
 XX  
 CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (1)  
 CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX  
 SQ Sequence 640 AA;

Query Match 81.2%; Score 39; DB 21; Length 640;  
 Best Local Similarity 88.9%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGY 9  
 |||||  
 Db 286 slfegidfy 294

RESULT 11  
 AAY88408  
 ID AAY88408 standard; Protein; 640 AA.  
 XX  
 AC AAY88408;  
 XX







XX 22-APR-1993; 93WO-0503816.  
XX  
XX 24-APR-1992; 92US-0873961.  
XX  
XX (BERL-) BERLEX LAB INC.  
XX (OTTA-) OTTAWA CIVIC HOSPITAL.  
XX  
XX Faulds DH, Lingwood CA, Tanphaichitr N;  
XX WPI; 1993-368422/46.  
XX  
XX Mammalian fertilisation decrease for detecting and treating  
XX PT infertility - using sulpho glyco lipid immobilising protein  
XX PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
XX PT infection treatment  
XX  
XX Claim 2 and Claim 17; Page 60-62; 77pp; English.  
XX  
XX The likelihood of mammalian fertilisation is decreased by contacting  
XX CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIPI)/  
XX CC sulphated glyco-moiety interfering composition. The interfering  
XX CC compsn. is e.g. the heat shock 70KD protein, SLIPI (or analogues  
XX CC such as the mouse SLIPI analogue "HSC70B" comprising the amino acid  
XX CC sequence AAR43002) or the 74.5KD mycoplasma protein (AAR43003).  
XX  
XX Sequence 641 AA;  
XX  
XX Query Match 81.2%; Score 39; DB 14; Length 641;  
XX Best Local Similarity 88.9%; Pred. No. 22;  
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1 SLFEGIDGY 9  
XX | | | | | | | |  
XX Db 286 slfegidgy 294  
XX  
XX RESULT 14  
XX AAW54349  
XX ID AAW54349 standard; protein; 641 AA.  
XX AC AAW54349;  
XX  
XX 14-AUG-1998 (first entry)  
XX  
XX Human heat shock 70 kD protein 1.  
XX  
XX Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
XX 2D gel electrophoresis; detection.  
XX  
XX Homo sapiens.  
XX  
XX WO9810291-A1.  
XX  
XX 12-MAR-1998.  
XX  
XX 05-SEP-1997; 97WO-GB02394.  
XX  
XX 08-APR-1997; 97GB-0007132.  
XX 06-SEP-1996; 96GB-0018600.  
XX  
XX (CLIN-) CENT CLINICAL & BASIC RES.  
XX  
XX Byrjalsen I, Fey SJ, Larsen P;  
XX WPI; 1998-207057/18.  
XX  
XX Biochemical markers of human endometrium - useful for, e.g.  
XX PT diagnosis of hyperplasia and adenocarcinoma  
XX  
XX Disclosure; Page 19; 77pp; English.  
XX

CC Proteins AAW54349-W54364 are examples of proteins produced in the  
CC endometrium during the hyperplasia, adenocarcinoma or proliferative  
CC phase of the endometrium. The presence and quantities of these proteins  
CC can be detected using 2D gel electrophoresis comparison of cell lysates.  
CC The proteins can be used as biochemical markers to detect the phase of  
CC the endometrium and can be measured in body fluids, obviating the need  
CC for endometrial biopsies.  
XX  
XX SQ Sequence 641 AA;  
XX  
XX Query Match 81.2%; Score 39; DB 19; Length 641;  
XX Best Local Similarity 88.9%; Pred. No. 22;  
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1 SLFEGIDGY 9  
XX | | | | | | | |  
XX Db 286 slfegidgy 294  
XX  
XX RESULT 15  
XX AAB23652  
XX ID AAB23652 standard; protein; 641 AA.  
XX AC AAB23652;  
XX  
XX 05-JAN-2001 (first entry)  
XX  
XX Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.  
XX  
XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
XX KW immune response; infectious disease; malaria; cytotoxic T cell;  
XX KW cytosolic; immunostimulant; cellular immune response inducer;  
XX KW protozoacide; leukaemia; cancer.  
XX  
XX Homo sapiens.  
XX  
XX WO2000049041-A1.  
XX  
XX 24-AUG-2000.  
XX  
XX 18-FEB-2000; 2000WO-JP00941.  
XX  
XX 19-FEB-1999; 99JP-0041535.  
XX  
XX (SUME ) SUMITOMO ELECTRIC IND CO.  
XX  
XX Shinbara N, Udono H, Yui K;  
XX WPI; 2000-543748/49.  
XX  
XX Fused protein capable of inducing cellular immune response, useful as  
XX PT active ingredient for drug compositions in preventing and/or treating  
XX PT infectious diseases such as malaria or cancer -  
XX  
XX Claim 3; Page 46-48; 72pp; Japanese.  
XX  
XX The present invention describes a fused protein (I) prepared from a  
XX CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
XX CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
XX CC shock protein. Also described are: (1) a drug composition containing (I)  
XX CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
XX CC containing the DNA of (2); and (4) a transformant which can retain the  
XX CC expression vector of (3). (I) has cytostatic, immunostimulant and  
XX CC protozoacide activities, and can be used as a cellular immune response  
XX CC inducer. The protein is useful as an active ingredient for drug  
XX CC compositions in preventing and/or treating infectious diseases such as  
XX CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
XX CC The present sequence represents a specifically claimed heat shock  
XX CC protein for use in a fused protein of the present invention.  
XX  
XX SQ Sequence 641 AA;



Query Match 81.2%; Score 39; DB 21; Length 641;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLEPIDGY 9  
DB 286 slfegidfy 294

Search completed: December 6, 2001, 08:04:03  
Job time: 611 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:01 : Search time 184.09 seconds  
(without alignments)  
3.621 Million cell updates/sec

Title: PEPL-MOD81

Perfect score: 46

Sequence: 1 SLFEGIDLY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	95.7	9	21	AAV44199
2	44	95.7	9	22	AB97601
3	44	95.7	10	22	AAV44200
4	44	95.7	10	22	AB97602
5	42	91.3	10	22	AAV97603
6	42	91.3	554	21	AAV88409
7	42	91.3	554	21	AAV88410
8	42	91.3	554	21	AAV88412
9	42	91.3	554	21	AAV88413
10	42	91.3	624	21	AAV23252
11	42	91.3	634	11	AAV03930

12	42	91.3	640	11	AAV03929	Homo sapiens HSP (
13	42	91.3	640	18	AAV10065	Human heat shock p
14	42	91.3	640	21	AAV23653	Human heat shock p
15	42	91.3	640	21	AAV88408	Human heat shock p
16	42	91.3	640	21	AAV88411	Human heat shock p
17	42	91.3	641	14	AAV43004	Mature mouse sperm
18	42	91.3	641	19	AAV54349	Human heat shock 7
19	42	91.3	641	21	AAV23652	Human heat shock p
20	42	91.3	641	22	AAV82534	Human heat shock p
21	42	91.3	642	21	AAV23850	Rat heat shock pro
22	42	91.3	647	11	AAV03928	Xenopus laevis HSP
23	41	89.1	643	18	AAV22895	Marmoset intracell
24	41	89.1	665	21	AAV58386	Lung cancer associ
25	39	84.8	91	21	AAV02174	Human secreted pro
26	39	84.8	253	21	AAV24333	Arabidopsis thalia
27	39	84.8	279	21	AAV24332	Arabidopsis thalia
28	39	84.8	342	21	AAV24331	Arabidopsis thalia
29	39	84.8	646	11	AAV03927	Rat HSP (rathsp70)
30	39	84.8	646	19	AAV54364	Heat shock cognate
31	39	84.8	646	20	AAV17407	Human heat shock c
32	39	84.8	646	20	AAV17408	Mouse heat shock c
33	39	84.8	646	21	AAV23649	Human heat shock p
34	39	84.8	646	22	AAV23651	Human heat shock p
35	39	84.8	646	22	AAV82535	Human heat shock p
36	39	84.8	656	18	AAV01638	Candida albicans h
37	39	84.8	890	21	AAV22938	GFP-HSC70 fusion p
38	38	82.6	412	22	AAV61974	S. avermitilis ORF
39	38	82.6	633	14	AAV43002	Mouse SLIPI homolo
40	36	78.3	134	22	AAV72082	Human olfactory re
41	36	78.3	134	22	AAV72333	Human OR-like poly
42	35	76.1	188	21	AAV40410	Human ORF ORF174
43	35	76.1	421	21	AAV27768	Arabidopsis thalia
44	35	76.1	515	21	AAV41383	Arabidopsis thalia
45	35	76.1	542	21	AAV53606	Arabidopsis thalia

#### ALIGNMENTS

#### RESULT 1

AAV44199  
ID AAV44199 standard; peptide; 9 AA.

XX  
AC AAV44199;

XX  
DT 15-FEB-2000 (first entry)

DE Heat shock protein 70 amino acid residues 286-294.

XX Human; heat shock protein 70; hsp70; identification; tumour; mutation;  
KW T cell response; amplification; vector; bacterium; cancer; allele;  
KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;  
KW Immune defence; immunogenicity; specificity; human leucocyte antigen.

XX Homo sapiens.

XX OS

XX PN WO954464-A1.

XX PD 28-OCT-1999.

XX PF 22-APR-1999; 99WO-FR00957.

XX PR 22-APR-1998; 98FR-0005033.

XX PA (INSR ) INST ROUSSY GUSTAVE.

XX PI Triebel F, Gaudin C;

XX PX WPI; 2000-013251/01.

XX PT Identifying mutant peptides from heat-shock protein 70, for treatment  
of cancer -

XX



PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-294 of the human

CC heat shock protein 70 (hsp70). The invention relates to a method of

CC identifying peptides, derived from hsp70 that stimulate a tumour-specific

CC T cell response. Identification of the hsp70 peptides that have at least

CC one mutation or alteration compared with the native sequence, and induce

CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70

CC encoding DNA from one or more tumours; (ii) cloning the amplified

CC sequences into a vector that can be replicated in bacteria;

CC (iii) sequencing fragments in each cultured bacterial colony to identify

CC any hsp70 mutations, and (iv) determining the immunogenicity of the

CC mutant peptides identified. The peptides, optionally formulated with an

CC agent that induces cellular stress, are used for treatment of cancer,

CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,

CC cancers of head and neck, particularly kidney cancer). The peptides may

CC also be used to increase the proportion of tumour-specific cytotoxic

CC T lymphocytes in a cell culture and/or induce these cells to secrete

CC cytotoxic factors (specifically interleukin-2, interferon-gamma and

CC tumour necrosis factor), particularly where the cells are used to

CC stimulate immune defences. The method identifies peptides with high

CC immunogenicity and high specificity for particular HLA (human leucocyte

XX antigen) alleles.

SQ Sequence 9 AA;

Query Match 95.7%; Score 44; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 4.3e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9

DB 1 slfegidly 9

RESULT 2

ID AAB97601 standard; peptide; 9 AA.

AC AAB97601;

XX

DT 30-JUL-2001 (first entry)

DE

DE Heat shock protein 70 (HSP70) peptidic fragment 1.

XX

KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;

KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

XX cytotoxic response; epitope; antigen presenting cell; fragment 1.

OS Homo sapiens.

XX

PN WO200129190-A1.

XX

PD 26-APR-2001.

XX

PF 29-SEP-2000; 2000WO-EP09530.

XX

PR 15-OCT-1999; 99EP-0120484.

XX

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PA

PI Abastado JP, Bartholeyns J;

XX

XX WPI; 2001-290909/30.

DR

XX Lymphocytes useful for treating cancer, recognizes specifically

PT transformed human cells with induced and increased membrane expression

PT of heat shock protein -

XX

XX Claim 8; Page 15; 21pp; English.

XX

XX The amino acid sequence of fragment 1 relating to position 286-294 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates

CC to lymphocytes which recognise cells of a patient in which overexpression

CC of HSP has been induced. Overexpression of HSP leads to a substantial

CC increase in the numbers of HSPs and HSP epitopes presented on the

CC pericellular membrane. Recognition of increased numbers of HSP epitopes

CC on cell pericellular membranes by lymphocytes elicits a cytotoxic

CC response which kills the target cells. As a further embodiment of the

CC invention, HSP70 epitopes are mutated prior to being loaded into antigen

CC presenting cells. This has the effect of increasing the immune response

CC to HSP and helps direct the immune response to specific cells, (e.g.

CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to

CC the tumour or to the virus associated HSP is broken using an immunogenic

CC mutated form of HSP and induction of a stress on the target tumoural or

CC intracellular infected cells.

XX

SQ Sequence 9 AA;

Query Match 95.7%; Score 44; DB 22; Length 9;

Best Local Similarity 88.9%; Pred. No. 4.3e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9

DB 1 slfegidly 9

RESULT 3

AY44200

ID AAY44200 standard; peptide; 10 AA.

XX

AC AAY44200;

XX

DT 15-FEB-2000 (first entry)

XX

DE Heat shock protein 70 amino acid residues 286-295.

XX

KW Human; heat shock protein 70; hsp70; identification; tumour; mutation;

KW T cell response; amplification; vector; bacterium; cancer; allele;

KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;

XX immune defence; immunogenicity; specificity; human leucocyte antigen.

OS Homo sapiens.

XX

PN WO954464-A1.

XX

PD 28-OCT-1999.

XX

PF 22-APR-1999; 99WO-FR00957.

XX

PR 22-APR-1998; 98FR-0005033.

XX

PA (INSR) INST ROUSSY GUSTAVE.

XX

PI Triebel F, Gaudin C;

XX

DR WPI; 2000-013251/01.

XX

PT Identifying mutant peptides from heat-shock protein 70, for treatment

PT of cancer -

XX

XX Claim 10; Page 6; 56pp; French.

XX

CC This peptide corresponds to amino acid residues 286-295 of the human

CC heat shock protein 70 (hsp70). The invention relates to a method of

CC identifying peptides, derived from hsp70 that stimulate a tumour-specific

CC T cell response. Identification of the hsp70 peptides that have at least

CC one mutation or alteration compared with the native sequence, and induce

CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70

CC encoding DNA from one or more tumours; (ii) cloning the amplified

CC sequences into a vector that can be replicated in bacteria;

CC (iii) sequencing fragments in each cultured bacterial colony to identify



CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
 CC mutant peptides identified. The peptides, optionally formulated with an  
 CC agent that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic  
 CC T lymphocytes in a cell culture and/or induce these cells to secrete  
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
 CC tumour necrosis factor), particularly where the cells are used to  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles.  
 XX  
 SQ Sequence 10 AA;

Query Match 95.7%; Score 44; DB 21; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.013;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 Db 1 slfegidly 9

## RESULT 4

AAB97602  
 ID AAB97602 standard; peptide; 10 AA.

XX AAB97602;

DT 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 2.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 2.

OS Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -

PS Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 2 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.  
 XX  
 SQ Sequence 10 AA;

Query Match 95.7%; Score 44; DB 22; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.013;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 Db 1 slfegidly 9

## RESULT 5

AAB97603  
 ID AAB97603 standard; peptide; 10 AA.

XX AAB97603;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

OS Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -

PS Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX Sequence 10 AA;



Query Match 91.3%; Score 42; DB 22; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.032;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 DB 1 slfegidfy 9

## RESULT 6

AAV88409  
 ID AAY88409 standard; Protein; 554 AA.

XX AC AAY88409;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI: 2000-264458/23.

XX DR N-PSDB; AAA15621.

XX PT Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

XX PS Examples; Fig 2; l1pp; Japanese.

XX CC This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 91.3%; Score 42; DB 21; Length 554;  
 Best Local Similarity 88.9%; Pred. No. 2.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDLY 9  
 Db 200 slfegidfy 208

## RESULT 7

AAV88410  
 ID AAY88410 standard; Protein; 554 AA.

XX AC AAY88410;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI: 2000-264458/23.

XX DR N-PSDB; AAA15622.

XX PT Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

XX PS Disclosure; Fig 3; l1pp; Japanese.

XX CC This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 91.3%; Score 42; DB 21; Length 554;  
 Best Local Similarity 88.9%; Pred. No. 2.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 DB 200 slfegidfy 208

## RESULT 8

AAV88412  
 ID AAY88412 standard; Protein; 554 AA.

XX AC AAY88412;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI: 2000-264458/23.



XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
XX Disclosure; Fig 5; 11pp; Japanese.  
XX  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;  
SQ

Query Match 91.3%; Score 42; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDLY 9  
DB 200 slifegidfy 208  
XXXXXXXXXX

RESULT 9  
AAY88413  
XX ID AAY88413 standard; Protein; 554 AA.  
XX AC AAY88413;  
XX DT 31-JUL-2000 (first entry)  
XX DE Human heat shock protein SHSP70 amino acid sequence.  
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
XX OS Homo sapiens.  
XX PN JP2000069999-A.  
XX PD 07-MAR-2000.  
XX PF 01-JUN-1995; 99JP-0257146.  
XX PR 01-JUN-1995; 95JP-0158581.  
XX PA (HOKE-) HOKEN KAGAKU KENYUSHO KK.  
XX DR WPI; 2000-264458/23.  
XX AB Normal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
XX Disclosure; Fig 6; 11pp; Japanese.  
XX  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;  
SQ

Query Match 91.3%; Score 42; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDLY 9  
DB 200 slifegidfy 208  
XXXXXXXXXX

Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDLY 9  
DB 200 slifegidfy 208  
XXXXXXXXXX

RESULT 10  
AAB23252  
XX ID AAB23252 standard; Protein; 624 AA.  
XX AC AAB23252;  
XX DT 29-JAN-2001 (first entry)  
XX DE Human Hsp72 (heat shock protein 72).  
XX KW Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX OS Homo sapiens.  
XX PN WO200054814-A1.  
XX PD 21-SEP-2000.  
XX PF 17-MAR-2000; 2000WO-US07350.  
XX PR 18-MAR-1999; 99US-0125046.  
XX PA (PHYL-) PHYLOGENY INC.  
XX PI Volloch VZ, Sherman M;  
XX DR WPI; 2000-647056/62.  
XX DR N-PSDB; AAA97541.  
XX PT Identifying compounds that inhibit proliferation of cells and capable  
PT of modulating the expression of heat shock protein 72 gene and/or  
PT activity of Hsp72 useful for treating cancers such as leukemia,  
PT lymphoma  
XX  
XX Examples; Fig 16B; 77pp; English.  
XX  
XX The invention relates to a novel method of identifying compounds that  
CC inhibit proliferation of cells comprising contacting a test compound with  
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
CC if the test compound inhibits activity or expression of Hsp72.  
CC Optionally, Hsp72 is contacted with the test compound under optimum  
CC conditions to allow the two components to interact and bind, forming a  
CC complex which is detected. The invention also relates to a method of  
CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
CC activation, comprising contacting a test compound with a cell which  
CC expresses Hsp72, exposing the cell to a heat induced stress and  
CC determining if the compound inhibits JNK phosphatase activity. The  
CC invention additionally encompasses compositions comprising an inhibitor  
CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
CC inhibiting the proliferation of cells. Modulation of the activity of the  
CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
CC as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and  
CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
CC Hsp72 activity can also be administered to treat premalignant conditions  
CC and to prevent progression to a neoplastic or malignant state. The  
CC compounds that inhibit Hsp72 function are administered to a patient  
CC having a disease or disorder mediated by an increase of Hsp72 expression  
CC or activity relative to normal levels. The present sequence represents  
CC human Hsp72 used in the exemplifications of the invention.  
XX  
XX Sequence 624 AA;  
SQ



Query Match 91.3%; Score 42; DB 21; Length 624;  
 Best Local Similarity 88.9%; Pred. No. 2.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 DB 286 slfegidfy 294

RESULT 11  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.  
 AC AAR03930;  
 XX  
 DT 30-AUG-1990 (first entry)  
 DE Gallus gallus HSP (chkhsp70).  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Gallus gallus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 634  
 FT /note= "residue given as "O" in specification"  
 XX  
 PN W09002564-A.  
 XX  
 PD 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 PA (CODO-) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.  
 XX  
 PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.  
 XX  
 CC According to the legend of Fig 2, the G. gallus HSP sequence has  
 CC 635 amino acid residues, the sequence itself has only 634,  
 CC including "O" (?) at position 634.  
 CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03923);  
 CC 2. Bacillus megaterium (Bmeahsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);  
 CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. Xenopus laevis (xl70 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 634 AA;

Query Match 91.3%; Score 42; DB 11; Length 634;  
 Best Local Similarity 88.9%; Pred. No. 2.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 DB 286 slfegidfy 294

RESULT 12  
 AAR03929  
 ID AAR03929 standard; Protein; 640 AA.  
 AC AAR03929;  
 XX  
 DT 30-AUG-1990 (first entry)  
 DE Homo sapiens HSP (humhsp70).  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 640  
 FT /note= "residue given as "O" in specification"  
 XX  
 PN W09002564-A.  
 XX  
 PD 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 PA (CODO-) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.  
 XX  
 PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.  
 XX  
 CC According to the legend of Fig 2, the H. sapiens HSP sequence has  
 CC 641 amino acid residues, the sequence itself has only 640,  
 CC including "O" (?) at position 640.  
 CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bmeahsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);  
 CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. Xenopus laevis (xl70 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 640 AA;

Query Match 91.3%; Score 42; DB 11; Length 640;  
 Best Local Similarity 88.9%; Pred. No. 2.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 DB 286 slfegidfy 294



```

RESULT 13
AAW10065
ID AAW10065 standard; Protein; 640 AA.
XX
XX AAW10065;
XX
XX 24-OCT-1997 (first entry)
XX
XX Human heat shock protein 70.
XX
XX Human; heat shock protein 70; HSP70; primer; probe; detection;
KW intracellular; abnormal transcription; acute; chronic; sustained;
KW stress.
XX
XX Homo sapiens.
XX
XX JP08322577-A.
XX
XX 10-DEC-1996.
XX
XX 01-JUN-1995; 95JP-0158581.
XX
XX 01-JUN-1995; 95JP-0158581.
XX
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI; 1997-081088/08.
XX
XX N-PSDB; AAT58086.
XX
XX Detection of abnormal transcription of HSP70 mRNA - using HSP70
PT specific primer or probe, used in detection of human acute and
PT chronic sustained stress load
XX
XX Claim 1; Fig 1; 13pp; Japanese.
XX
XX The cDNA encoding the present sequence, human heat shock protein 70
CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24
CC and 21. Primers and probes based on the HSP70 cDNA coding
CC sequence can be used to detect the abnormal transcription of
CC intracellular HSP70 mRNA in human acute and chronic sustained
CC stress load.
XX
XX Sequence 640 AA;

Query Match 91.3%; Score 42; DB 18; Length 640;
Best Local Similarity 88.9%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db |||||
Db 286 slfegidfy 294

RESULT 14
AAB23653
ID AAB23653 standard; protein; 640 AA.
XX
XX AAB23653;
XX
XX 05-JAN-2001 (first entry)
XX
XX Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.
XX
XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytostatic; immunostimulant; cellular immune response inducer;
KW protozoacide; leukaemia; cancer.
XX
XX Homo sapiens.
XX
XX WO200049041-A1.

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XX
XX PD 24-AUG-2000.
XX
XX PF 18-FEB-2000; 2000WO-JP00941.
XX
XX PR 19-FEB-1999; 99JP-0041535.
XX
XX PA (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX PI Shinbara N, Uono H, Yui K;
XX
XX WPI; 2000-543748/49.
XX
XX Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer
XX
XX Claim 3; Page 49-52; 72pp; Japanese.
XX
XX The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the Appase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoacide activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC The present sequence represents a specifically claimed heat shock
CC protein for use in a fused protein of the present invention.
XX
XX Sequence 640 AA;

Query Match 91.3%; Score 42; DB 21; Length 640;
Best Local Similarity 88.9%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db |||||
Db 286 slfegidfy 294

RESULT 15
AAY88408
ID AAY88408 standard; Protein; 640 AA.
XX
XX AAY88408;
XX
XX 31-JUL-2000 (first entry)
XX
XX Human heat shock protein HSP70 amino acid sequence.
XX
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW depression; nephrotic syndrome.
XX
XX Homo sapiens.
XX
XX JP2000069999-A.
XX
XX 07-MAR-2000.
XX
XX 01-JUN-1995; 99JP-0257146.
XX
XX 01-JUN-1995; 95JP-0158581.
XX
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI; 2000-264458/23.
XX
XX N-PSDB; AAA15620.

```



XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
PS Claim 2; Fig 1; 1lpp; Japanese.  
XX This sequence represents the human heat shock protein 'HSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
SQ Sequence 640 AA;  
  
Query Match 91.3%; Score 42; DB 21; Length 640;  
Best Local Similarity 88.9%; Pred. NO. 2.7;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDL 9  
Db 286 slfegidfy 294  
  
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GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: December 6, 2001, 08:04:02 ; Search time 184.09 Seconds  
(without alignments)  
3.621 Million cell updates/sec  
Title: PEPI-MOD8V  
Perfect score: 46  
Sequence: 1 SLFEGIDVY 9  
Scoring table: BLOSUM62  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	45	97.8		9	21	AAV44199	Heat shock protein
2	45	97.8		9	22	AAV97601	Heat shock protein
3	45	97.8		10	21	AAV44200	Heat shock protein
4	45	97.8		10	22	AAV97602	Heat shock protein
5	41	89.1		10	22	AAV97603	Heat shock protein
6	41	89.1		554	21	AAV88409	Human heat shock
7	41	89.1		554	21	AAV88410	Human heat shock
8	41	89.1		554	21	AAV88412	Human heat shock
9	41	89.1		554	21	AAV88413	Human heat shock
10	41	89.1		624	21	AAV23252	Human Hsp72 (heat
11	41	89.1		634	11	AAV03930	Gallus gallus HSP

12	41	89.1	640	11	AAV88410	Homo sapiens HSP (			
13	41	89.1	640	18	AAV10065	Human heat shock p			
14	41	89.1	640	21	AAV23653	Human heat shock p			
15	41	89.1	640	21	AAV88408	Human heat shock p			
16	41	89.1	640	21	AAV88411	Human heat shock p			
17	41	89.1	641	14	AAV43004	Mature mouse sperm			
18	41	89.1	641	19	AAV54349	Human heat shock 7			
19	41	89.1	641	21	AAV23652	Human heat shock p			
20	41	89.1	641	22	AAV82534	Rat heat shock pro			
21	41	89.1	642	21	AAV23650	Xenopus laevis HSP			
22	41	89.1	647	11	AAV03928	Marimastat intracell			
23	40	87.0	643	18	AAV22895	Lung cancer associ			
24	40	87.0	665	21	AAV58386	Human secreted pro			
25	38	82.6	91	21	AAV02174	Arabidopsis thalia			
26	38	82.6	253	21	AAV24333	Arabidopsis thalia			
27	38	82.6	279	21	AAV24332	Arabidopsis thalia			
28	38	82.6	342	21	AAV24331	Rat HSP (rathsp70)			
29	38	82.6	646	11	AAV03927	Heat shock cognate			
30	38	82.6	646	19	AAV54364	Human heat shock c			
31	38	82.6	646	20	AAV17407	Mouse heat shock c			
32	38	82.6	646	20	AAV17408	Mouse heat shock p			
33	38	82.6	646	21	AAV23649	Human heat shock p			
34	38	82.6	646	21	AAV23651	Human heat shock p			
35	38	82.6	646	22	AAV82535	Human heat shock p			
36	38	82.6	656	18	AAV01638	Candida albicans h			
37	38	82.6	890	21	AAV22938	GFP-HSC70 fusion p			
38	37	80.4	214	19	AAV5808	S. pneumoniae deri			
39	37	80.4	221	19	AAV80645	S. pneumoniae prot			
40	37	80.4	412	22	AAV61974	S. avermitilis ORF			
41	37	80.4	633	14	AAV43002	Mouse SLIP1 homolo			
42	35	76.1	646	11	AAV03931	Zea mays HSP (mzeh			
43	35	76.1	647	20	AAV31380	T. gondii antigen			
44	35	76.1	647	22	AAV49099	Toxoplasma gondii			
45	34	73.9	421	21	AAV27768	Arabidopsis thalia			

ALIGNMENTS

RESULT 1  
AAV44199  
ID AAV44199 standard; peptide; 9 AA.  
AC AAV44199;  
XX  
XX  
DT 15-FEB-2000 (first entry)  
XX  
XX Heat shock protein 70 amino acid residues 286-294.  
DE  
DE Human; heat shock protein 70; hsp70; identification; tumour; mutation;  
KW T cell response; amplification; vector; bacterium; cancer; allele;  
KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;  
KW immune defence; immunogenicity; specificity; human leucocyte antigen.  
XX  
XX Homo sapiens.  
XX  
XX W09954464-A1.  
XX  
XX 28-OCT-1999.  
XX  
XX 22-APR-1999; 99WO-FR00957.  
XX  
XX 22-APR-1998; 98FR-0005033.  
XX  
XX (INSR ) INST ROUSSY GUSTAVE.  
XX  
XX Triebel F, Gaudin C;  
XX  
XX WPI; 2000-013251/01.  
XX  
XX Identifying mutant peptides from heat-shock protein 70, for treatment  
XX of cancer -  
XX



PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T lymphocytes in a cell culture and/or induce these cells to secrete cytotoxic factors (specifically interleukin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte antigen) alleles.

XX Sequence 9 AA;

Query Match 97.8%; Score 45; DB 21; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFEGIDVY 9  
Db |||||:|  
1 slifegidly 9

RESULT 2

AA97601  
ID AAB97601 standard; peptide; 9 AA.

XX AAB97601;

AC AAB97601;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 1.

DE HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1.

XX Homo sapiens.

OS WO200129190-A1.

PN 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PA Abastado JP, Bartholeyns J;  
PI WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of heat shock protein -

PS Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 1 relating to position 286-294 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). Hsp70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.

XX Sequence 9 AA;

Query Match 97.8%; Score 45; DB 22; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFEGIDVY 9  
Db |||||:|  
1 slifegidly 9

RESULT 3

AA44200  
ID AAY44200 standard; peptide; 10 AA.

XX AAY44200;

AC AAY44200;

XX 15-FEB-2000 (first entry)

DE Heat shock protein 70 amino acid residues 286-295.

XX Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.

XX Homo sapiens.

OS WO9954464-A1.

PN 28-OCT-1999.

XX 22-APR-1999; 99WO-FR00957.

XX 22-APR-1998; 98FR-0005033.

XX (INSR) INST ROUSSY GUSTAVE.

XX Triebel F, Gaudin C;  
PI WPI; 2000-013251/01.

XX Identifying mutant peptides from heat-shock protein 70, for treatment of cancer -

PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify



CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
 CC mutant peptides identified. The peptides, optionally formulated with an  
 CC agent that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic  
 CC T lymphocytes in a cell culture and/or induce these cells to secrete  
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
 CC tumour necrosis factor), particularly where the cells are used to  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles.  
 XX  
 SQ Sequence 10 AA;

Query Match 97.8%; Score 45; DB 21; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.0046;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
 Db |||||:|  
 1 slfegidiy 9

RESULT 4  
 AAB97602  
 ID AAB97602 standard; peptide; 10 AA.

XX AAB97602;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 2.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 2.

OS Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -

XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 2 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX Sequence 10 AA;

Query Match 97.8%; Score 45; DB 22; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 0.0046;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
 Db |||||:|  
 1 slfegidiy 9

RESULT 5  
 AAB97603  
 ID AAB97603 standard; peptide; 10 AA.

XX AAB97603;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

OS Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -

XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX Sequence 10 AA;



Query Match 89.1%; Score 41; DB 22; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.031;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
| | | | | | | |  
DB 1 slfegidfy 9

## RESULT 6

AA188409  
ID AAY88409 standard; Protein; 554 AA.

XX AC AAY88409;

DT 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

PD 07-MAR-2000.

PF 01-JUN-1995; 99JP-0257146.

PR 01-JUN-1995; 95JP-0158581.

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

DR N-PSDB; AAA15621.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX Examples; Fig 2; 1lpp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 89.1%; Score 41; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
| | | | | | | |  
DB 200 slfegidfy 208

## RESULT 7

AA188410  
ID AAY88410 standard; Protein; 554 AA.

XX AC AAY88410;

DT 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

XX DR N-PSDB; AAA15622.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX Disclosure; Fig 3; 1lpp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 89.1%; Score 41; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
| | | | | | | |  
DB 200 slfegidfy 208

## RESULT 8

AA188412  
ID AAY88412 standard; Protein; 554 AA.

XX AC AAY88412;

XX DT 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.



XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
PT  
XX  
PS Disclosure: Fig 5; 1lpp; Japanese.  
XX  
CC This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;

Query Match 89.1%; Score 41; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
Db 200 sifegidfy 208  
|||||||

RESULT 9  
AY88413  
ID AAY88413 standard; Protein; 554 AA.  
AC AAY88413;  
DT 31-JUL-2000 (first entry)  
XX  
XX Human heat shock protein SHSP70 amino acid sequence.  
XX  
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
OS Homo sapiens.  
XX  
PN JP2000069999-A.  
XX  
XX 07-MAR-2000.  
PD  
XX  
XX 01-JUN-1995; 99JP-0257146.  
XX  
XX 01-JUN-1995; 95JP-0158581.  
XX  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
PA  
XX  
XX WPI; 2000-264458/23.  
DR  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
PT  
XX  
XX Disclosure: Fig 6; 1lpp; Japanese.  
PS  
CC This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;

Query Match 89.1%; Score 41; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
Db 200 sifegidfy 208  
|||||||

RESULT 9  
AY88413  
ID AAY88413 standard; Protein; 554 AA.  
AC AAY88413;  
DT 31-JUL-2000 (first entry)  
XX  
XX Human heat shock protein SHSP70 amino acid sequence.  
XX  
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
OS Homo sapiens.  
XX  
PN JP2000069999-A.  
XX  
XX 07-MAR-2000.  
PD  
XX  
XX 01-JUN-1995; 99JP-0257146.  
XX  
XX 01-JUN-1995; 95JP-0158581.  
XX  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
PA  
XX  
XX WPI; 2000-264458/23.  
DR  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
PT  
XX  
XX Disclosure: Fig 6; 1lpp; Japanese.  
PS  
CC This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatisms, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;

Query Match 89.1%; Score 41; DB 21; Length 554;  
Best Local Similarity 88.9%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
Db 200 sifegidfy 208  
|||||||

RESULT 10  
AAB23252  
ID AAB23252 standard; Protein; 624 AA.  
XX  
AC AAB23252;  
DT 29-JAN-2001 (first entry)  
XX  
XX Human Hsp72 (heat shock protein 72).  
DE  
XX  
XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX  
OS Homo sapiens.  
XX  
PN WO200054814-A1.  
XX  
XX 21-SEP-2000.  
PD  
XX  
XX 17-MAR-2000; 2000WO-US07350.  
PF  
XX  
XX 18-MAR-1999; 99US-0125046.  
PR  
XX  
XX (PHYL-) PHYLOGENY INC.  
PA  
XX  
XX Volloch Vz, Sherman M;  
PI  
XX  
XX WPI; 2000-647056/62.  
DR  
XX  
XX N-PSDB; AA97541.  
DR  
XX  
XX Identifying compounds that inhibit proliferation of cells and capable  
PT of modulating the expression of heat shock protein 72 gene and/or  
PT activity of Hsp72 useful for treating cancers such as leukemia,  
PT lymphoma  
PT  
XX  
XX Examples; Fig 16B; 77pp; English.  
PS  
XX  
XX The invention relates to a novel method of identifying compounds that  
CC inhibit proliferation of cells comprising contacting a test compound with  
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
CC if the test compound inhibits activity or expression of Hsp72.  
CC Optionally, Hsp72 is contacted with the test compound under optimum  
CC conditions to allow the two components to interact and bind, forming a  
CC complex which is detected. The invention also relates to a method of  
CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
CC activation, comprising contacting a test compound with a cell which  
CC expresses Hsp72, exposing the cell to a heat induced stress and  
CC determining if the compound inhibits JNK phosphatase activity. The  
CC invention additionally encompasses compositions comprising an inhibitor  
CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
CC inhibiting the proliferation of cells. Modulation of the activity of the  
CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
CC as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and  
CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
CC Hsp72 activity can also be administered to treat premalignant conditions  
CC and to prevent progression to a neoplastic or malignant state. The  
CC compounds that inhibit Hsp72 function are administered to a patient  
CC having a disease or disorder mediated by an increase of Hsp72 expression  
CC or activity relative to normal levels. The present sequence represents  
CC human Hsp72 used in the exemplifications of the invention.  
XX  
XX Sequence 624 AA;



Query Match 89.1%; Score 41; DB 21; Length 624;  
 Best Local Similarity 88.9%; Pred. No. 2,9;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
 |||||  
 Db 286 slfigidfy 294

## RESULT 11

AAR03930  
 ID AAR03930 standard; Protein; 634 AA.

AC AAR03930;

DT 30-AUG-1990 (first entry)

XX Homo sapiens HSP (chkhsp70).

DE Gallus gallus HSP (chkhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Gallus gallus.

XX Key Location/Qualifiers

FT Misc-difference 634 /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634.

XX Fig. 2 provides an alignment of heat shock proteins from a variety of organisms:

1. M.hyponeumoniae (Mhyhsp70 - AAR03922);

2. Bacillus megaterium (Bmebsp70 - AAR03923);

3. E. coli (dnaK - AAR03924);

4. T. cruzi (tc70kd - AAR03925);

5. T. cruzi (AAR03926);

6. Rat rattus (rathsp70 - AAR03927);

7. Xenopus laevis (xl70 - AAR03928);

8. Homo sapiens (humhsp70 - AAR03929);

9. Gallus gallus (chkhsp70 - AAR03930);

10. Zea mays (mzhsp70 - AAR03931);

11. Serratia marcescens (smahsp70 - AAR03932).

XX The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and Mycobacteria species.

XX Sequence 634 AA;

## Query Match

Best Local Similarity 89.1%; Score 41; DB 11; Length 634;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9

|||||  
 Db 289 slfigidfy 297

## RESULT 12

AAR03929  
 ID AAR03929 standard; Protein; 640 AA.

XX AAR03929;

XX 30-AUG-1990 (first entry)

XX Homo sapiens HSP (humhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 640

XX /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has 641 amino acid residues, the sequence itself has only 640, including "O" (?) at position 640.

XX Fig. 2 provides an alignment of heat shock proteins from a variety of organisms:

1. M.hyponeumoniae (Mhyhsp70 - AAR03922);

2. Bacillus megaterium (Bmebsp70 - AAR03923);

3. E. coli (dnaK - AAR03924);

4. T. cruzi (tc70kd - AAR03925);

5. T. cruzi (AAR03926);

6. Rat rattus (rathsp70 - AAR03927);

7. Xenopus laevis (xl70 - AAR03928);

8. Homo sapiens (humhsp70 - AAR03929);

9. Gallus gallus (chkhsp70 - AAR03930);

10. Zea mays (mzhsp70 - AAR03931);

11. Serratia marcescens (smahsp70 - AAR03932).

XX The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and Mycobacteria species.

XX Sequence 640 AA;

Query Match 89.1%; Score 41; DB 11; Length 640;

Best Local Similarity 88.9%; Pred. No. 3;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9

|||||  
 Db 286 slfigidfy 294



RESULT 13  
AAW10065  
ID AAW10065 standard; Protein; 640 AA.  
XX  
XX  
AC AAW10065;  
XX  
DT 24-OCT-1997 (first entry)  
XX  
XX Human heat shock protein 70.  
DE  
XX  
XX Human; heat shock protein 70; HSP70; primer; probe; detection;  
KW intracellular; abnormal transcription; acute; chronic; sustained;  
KW stress.  
XX  
XX Homo sapiens.  
OS  
XX JP08322577-A.  
PN  
XX  
PD 10-DEC-1996.  
XX  
PF 01-JUN-1995; 95JP-0158581.  
XX  
PR 01-JUN-1995; 95JP-0158581.  
XX  
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX  
DR WPI; 1997-081088/08.  
XX N-PSDB; AAT58086.  
XX  
PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
PT specific primer or probe, used in detection of human acute and  
PT chronic sustained stress load  
XX  
XX Claim 1; Fig 1; 13pp; Japanese.  
XX  
CC The cDNA encoding the present sequence, human heat shock protein 70  
CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
CC and 21. Primers and probes based on the HSP70 cDNA coding  
CC sequence can be used to detect the abnormal transcription of  
CC intracellular HSP70 mRNA in human acute and chronic sustained  
CC stress load.  
XX  
SQ Sequence 640 AA;

Query Match 89.1%; Score 41; DB 18; Length 640;  
Best Local Similarity 88.9%; Pred. No. 3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVY 9  
DB 286 slfegidfy 294

RESULT 14  
AAB23653  
ID AAB23653 standard; protein; 640 AA.  
XX  
XX AAB23653;  
AC  
XX  
DT 05-JAN-2001 (first entry)  
XX  
XX Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.  
DE  
XX  
XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
KW immune response; infectious disease; malaria; cytotoxic T cell;  
KW cytosolic; immunostimulant; cellular immune response inducer;  
KW protozoacide; leukaemia; cancer.  
XX  
XX Homo sapiens.  
OS  
XX WO200049041-A1.  
PN

XX  
PD 24-AUG-2000.  
XX  
PF 18-FEB-2000; 2000WO-JP00941.  
XX  
PR 19-FEB-1999; 99JP-0041535.  
XX  
PA (SUME) SUMITOMO ELECTRIC IND CO.  
XX  
XX Shinbara N, Uono H, Yui K;  
XX WPI; 2000-543748/49.  
DR  
XX Fused protein capable of inducing cellular immune response, useful as  
PT active ingredient for drug compositions in preventing and/or treating  
PT infectious diseases such as malaria or cancer -  
XX  
XX Claim 3; Page 49-52; 72pp; Japanese.  
XX  
XX The present invention describes a fused protein (I) prepared from a  
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
CC shock protein. Also described are: (1) a drug composition containing (I)  
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
CC containing the DNA of (2); and (4) a transformant which can retain the  
CC expression vector of (3). (I) has cytostatic, immunostimulant and  
CC protozoacide activities, and can be used as a cellular immune response  
CC inducer. The protein is useful as an active ingredient for drug  
CC compositions in preventing and/or treating infectious diseases such as  
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
CC The present sequence represents a specifically claimed heat shock  
CC protein for use in a fused protein of the present invention.  
XX  
SQ Sequence 640 AA;

Query Match 89.1%; Score 41; DB 21; Length 640;  
Best Local Similarity 88.9%; Pred. No. 3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVY 9  
DB 286 slfegidfy 294

RESULT 15  
AAY88408  
ID AAY88408 standard; Protein; 640 AA.  
XX  
XX AAY88408;  
AC  
XX  
DT 31-JUL-2000 (first entry)  
XX  
XX Human heat shock protein HSP70 amino acid sequence.  
DE  
XX  
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome.  
XX  
XX Homo sapiens.  
OS  
XX JP2000069999-A.  
PN  
XX  
PD 07-MAR-2000.  
XX  
PF 01-JUN-1995; 99JP-0257146.  
XX  
PR 01-JUN-1995; 95JP-0158581.  
XX  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
PA  
XX WPI; 2000-264458/23.  
DR N-PSDB; AAA15620.



XX  
PT Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
XX  
PS Claim 2; Fig 1; 1lpp; Japanese.  
XX  
CC This sequence represents the human heat shock protein HSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 9p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
SQ Sequence 640 AA;

Query Match 89.1%; Score 41; DB 21; Length 640;  
Best Local Similarity 88.9%; Pred. No. 3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVY 9  
Db 286 slfegidfy 294  
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Job time: 610 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:04 ; Search time 184.09 Seconds  
(without alignments)  
4.024 Million cell updates/sec

Title: PEP2-MOD8A

Perfect score: 51

Sequence: 1 SLFEGIDAVT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	90.2	10	21 AAY44200	Heat shock protein
2	46	90.2	10	22 AAB37602	Heat shock protein
3	45	88.2	10	22 AAB37603	Heat shock protein
4	45	88.2	554	21 AAY88409	Human heat shock p
5	45	88.2	554	21 AAY88410	Human heat shock p
6	45	88.2	554	21 AAY88412	Human heat shock p
7	45	88.2	554	21 AAY88413	Human heat shock p
8	45	88.2	624	21 AAB32352	Human Hsp72 (heat
9	45	88.2	634	11 AAR03930	Gallus gallus HSP
10	45	88.2	640	11 AAR03929	Homo sapiens HSP (
11	45	88.2	640	18 AAW10065	Human heat shock p

12	45	88.2	640	21	AAB23653	Human heat shock p
13	45	88.2	640	21	AAY88408	Human heat shock p
14	45	88.2	640	21	AAY88411	Human heat shock p
15	45	88.2	641	14	AAR43004	Mature mouse sperm
16	45	88.2	641	19	AAW54349	Human heat shock 7
17	45	88.2	641	21	AAB23652	Human heat shock p
18	45	88.2	641	22	AAB82534	Human heat shock p
19	45	88.2	642	21	AAB23650	Rat heat shock pro
20	45	88.2	647	11	AAR03928	Xenopus laevis HSP
21	44	86.3	643	18	AAR22895	Marmoset intracell
22	44	86.3	665	21	AAB38386	Lung cancer associ
23	42	82.4	91	21	AAG02174	Human secreted pro
24	42	82.4	646	11	AAR03927	Rat HSP (rathsp70)
25	42	82.4	646	19	AAW54364	Heat shock cognate
26	42	82.4	646	20	AAW17407	Human heat shock c
27	42	82.4	646	20	AAW17408	Mouse heat shock c
28	42	82.4	646	21	AAB23649	Mouse heat shock p
29	42	82.4	646	21	AAB23651	Human heat shock p
30	42	82.4	646	22	AAB82535	Human heat shock p
31	42	82.4	656	18	AAW01638	Candida albicans h
32	42	82.4	890	21	AAB22938	GFP-HSC70 fusion p
33	41	80.4	9	21	AAY44199	Heat shock protein
34	41	80.4	9	22	AAB97601	Heat shock protein
35	41	80.4	633	14	AAW43002	Mouse S1P1 homolo
36	38	74.5	214	19	AAY85808	S. pneumoniae deri
37	38	74.5	221	19	AAW80645	S. pneumoniae prot
38	38	74.5	253	21	AAG24333	Arabidopsis thalia
39	38	74.5	279	21	AAG24332	Arabidopsis thalia
40	38	74.5	342	21	AAG24331	Arabidopsis thalia
41	36	70.6	495	18	AAW31629	Aspergillus oryzae
42	36	70.6	533	14	AAW44433	Subtilisin-like se
43	35	68.6	412	22	AAB61974	S. avermitilis ORF
44	35	68.6	558	22	AAU01251	B. subtilis dihydr
45	35	68.6	646	11	AAR03931	Zea mays HSP (mzeh

#### ALIGNMENTS

RESULT 1

AAW44200  
ID AAY44200 standard; peptide: 10 AA.  
XX  
AC AAY44200;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Heat shock protein 70 amino acid residues 286-295.  
XX  
KW Human; heat shock protein 70; hsp70; identification; tumour; mutation;  
KW T cell response; amplification; vector; bacterium; cancer; allele;  
KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;  
KW immune defence; immunogenicity; specificity; human leucocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO9954464-A1.  
XX  
PD 28-OCT-1999.  
XX  
PF 22-APR-1999; 99WO-FR00957.  
XX  
PR 22-APR-1998; 98FR-0005033.  
XX  
PA (INSR ) INST ROUSSY GUSTAVE.  
XX  
PI Triebel F, Gaudin C;  
XX  
DR WPI; 2000-013251/01.  
XX  
PT Identifying mutant peptides from heat-shock protein 70, for treatment  
PT of cancer -  
XX



PS Claim 10; Page 6; 56pp; French.

CC This peptide corresponds to amino acid residues 286-295 of the human  
 CC heat shock protein 70 (hsp70). The invention relates to a method of  
 CC identifying peptides, derived from hsp70 that stimulate a tumour-specific  
 CC T cell response. Identification of the hsp70 peptides that have at least  
 CC one mutation or alteration compared with the native sequence, and induce  
 CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70  
 CC encoding DNA from one or more tumours; (ii) cloning the amplified  
 CC sequences into a vector that can be replicated in bacteria;  
 CC (iii) sequencing fragments in each cultured bacterial colony to identify  
 CC any hsp70 mutations; and (iv) determining the immunogenicity of the  
 CC mutant peptides identified. The peptides, optionally formulated with an  
 CC agent that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic  
 CC cytotoxic factors in a cell culture and/or induce these cells to secrete  
 CC tumour necrosis factor), particularly interleukin-2, interferon-gamma and  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles.

XX SQ Sequence 10 AA;

Query Match 90.2%; Score 46; DB 21; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.0031;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 Db 1 slfegidiyt 10  
 |||||

RESULT 2  
 AAB97602  
 ID AAB97602 standard; peptide; 10 AA.  
 AC AAB97602;  
 DT 30-JUL-2001 (first entry)  
 DE Heat shock protein 70 (HSP70) peptidic fragment 2.  
 KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 2.  
 XX Homo sapiens.  
 OS  
 PN WO200129190-A1.  
 PD 26-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-EP09530.  
 XX  
 PR 15-OCT-1999; 99EP-0120484.  
 XX  
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.  
 PI Abastado JP, Bartholeyns J;  
 XX WPI; 2001-290909/30.  
 DR  
 XX  
 XX Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -  
 XX  
 PS Claim 8; Page 15; 21pp; English.  
 CC The amino acid sequence of fragment 2 relating to position 286-295 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX SQ Sequence 10 AA;

Query Match 90.2%; Score 46; DB 22; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.0031;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 Db 1 slfegidiyt 10  
 |||||

RESULT 3  
 AAB97603  
 ID AAB97603 standard; peptide; 10 AA.  
 AC AAB97603;  
 XX  
 DT 30-JUL-2001 (first entry)  
 DE Heat shock protein 70 (HSP70) peptidic fragment 3.  
 KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
 KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
 KW cytotoxic response; epitope; antigen presenting cell; fragment 3.  
 XX Homo sapiens.  
 OS  
 PN WO200129190-A1.  
 PD 26-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-EP09530.  
 XX  
 PR 15-OCT-1999; 99EP-0120484.  
 XX  
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.  
 PI Abastado JP, Bartholeyns J;  
 XX WPI; 2001-290909/30.  
 DR  
 XX  
 XX Lymphocytes useful for treating cancer, recognizes specifically  
 PT transformed human cells with induced and increased membrane expression  
 PT of heat shock protein -  
 XX  
 PS Claim 8; Page 15; 21pp; English.  
 CC The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen



CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells, (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumour or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

XX  
SQ Sequence 10 AA;

Query Match 88.2%; Score 45; DB 22; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.005;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||||  
Db 1 slfegidft 10

RESULT 4

AAAY88409  
ID AAY88409 standard; Protein; 554 AA.

XX  
AC AAY88409;

XX  
DT 31-JUL-2000 (first entry)

XX  
DE Human heat shock protein SHSP70 amino acid sequence.

XX  
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX  
OS Homo sapiens.

XX  
PN JP2000069999-A.

XX  
PD 07-MAR-2000.

XX  
PF 01-JUN-1995; 99JP-0257146.

XX  
PR 01-JUN-1995; 95JP-0158581.

XX  
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX  
DR WPI; 2000-264458/23.

XX  
DR N-PSDB; AAA15621.

XX  
PT Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX  
PS Examples; Fig 2; 11pp; Japanese.

XX  
CC This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX  
SQ Sequence 554 AA;

Query Match 88.2%; Score 45; DB 21; Length 554;

Best Local Similarity 90.0%; Pred. No. 0.49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||||  
Db 200 slfegidft 209

RESULT 5

AAAY88410  
ID AAY88410 standard; Protein; 554 AA.

XX  
AC AAY88410;

XX  
DT 31-JUL-2000 (first entry)

XX  
DE Human heat shock protein SHSP70 amino acid sequence.

XX  
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX  
OS Homo sapiens.

XX  
PN JP2000069999-A.

XX  
PD 07-MAR-2000.

XX  
PF 01-JUN-1995; 99JP-0257146.

XX  
PR 01-JUN-1995; 95JP-0158581.

XX  
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX  
DR WPI; 2000-264458/23.

XX  
DR N-PSDB; AAA15622.

XX  
PT Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

XX  
PS Disclosure; Fig 3; 11pp; Japanese.

XX  
CC This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX  
SQ Sequence 554 AA;

Query Match 88.2%; Score 45; DB 21; Length 554;

Best Local Similarity 90.0%; Pred. No. 0.49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10

|||||||  
Db 200 slfegidft 209

RESULT 6

AAAY88412  
ID AAY88412 standard; Protein; 554 AA.

XX  
AC AAY88412;

XX  
DT 31-JUL-2000 (first entry)

XX  
DE Human heat shock protein SHSP70 amino acid sequence.

XX  
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX  
OS Homo sapiens.



PN JP2000069999-A.  
XX 07-MAR-2000.  
XX 01-JUN-1995; 99JP-0257146.  
XX 01-JUN-1995; 95JP-0158581.  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX WPI; 2000-264458/23.  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
XX chronic continuous load of stress in a human being and its application  
XX  
XX Disclosure; Fig 5; 11pp; Japanese.  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
XX and 14q22-24. The invention relates to the abnormal transcription of  
XX intracellular HSP70mRNA under acute and chronic stress load in a human.  
XX The abnormal transcription of HSP70 can be used in the improvement of  
XX stress and response and diagnosis of stress diseases including  
XX rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX Sequence 554 AA;  
SQ

Query Match 88.2%; Score 45; DB 21; Length 554;  
Best Local Similarity 90.0%; Pred. NO. 0.49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDAYT 10  
DB 200 sifegidft 209

RESULT 7  
AAY88413  
ID AAY88413 standard; Protein; 554 AA.  
XX  
XX AAY88413;  
XX  
XX 31-JUL-2000 (first entry)  
XX Human heat shock protein SHSP70 amino acid sequence.  
XX  
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
XX depression; nephrotic syndrome; SHSP70.  
XX Homo sapiens.  
XX JP2000069999-A.  
XX  
XX 07-MAR-2000.  
XX  
XX 01-JUN-1995; 99JP-0257146.  
XX  
XX 01-JUN-1995; 95JP-0158581.  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX WPI; 2000-264458/23.  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
XX chronic continuous load of stress in a human being and its application  
XX  
XX Disclosure; Fig 6; 11pp; Japanese.  
XX This sequence represents the human heat shock protein SHSP70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX Sequence 554 AA;  
SQ

Query Match 88.2%; Score 45; DB 21; Length 554;  
Best Local Similarity 90.0%; Pred. NO. 0.49;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDAYT 10  
DB 200 sifegidft 209

RESULT 8  
AAB23252  
ID AAB23252 standard; Protein; 624 AA.  
XX  
XX AAB23252;  
XX  
XX 29-JAN-2001 (first entry)  
XX Human Hsp72 (heat shock protein 72).  
XX  
XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
XX expression modulator; JNK phosphatase inhibitor; antiproliferative;  
XX drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
XX carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX Homo sapiens.  
XX OS  
XX WO200054814-A1.  
XX  
XX 21-SEP-2000.  
XX  
XX 17-MAR-2000; 2000WO-US07350.  
XX  
XX 18-MAR-1999; 99US-0125046.  
XX (PHYL-) PHYLOGENY INC.  
XX  
XX Volloch VZ, Sherman M;  
XX  
XX WPI; 2000-647056/62.  
XX N-PSDB; AAA97541.  
XX  
XX Identifying compounds that inhibit proliferation of cells and capable  
XX of modulating the expression of heat shock protein 72 gene and/or  
XX activity of Hsp72 useful for treating cancers such as leukemia,  
XX lymphoma  
XX  
XX Examples; Fig 16B; 77pp; English.  
XX  
XX The invention relates to a novel method of identifying compounds that  
XX inhibit proliferation of cells comprising contacting a test compound with  
XX a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
XX if the test compound inhibits activity or expression of Hsp72.  
XX Optionally, Hsp72 is contacted with the test compound under optimum  
XX conditions to allow the two components to interact and bind, forming a  
XX complex which is detected. The invention also relates to a method of  
XX identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
XX activation, comprising contacting a test compound with a cell which  
XX expresses Hsp72, exposing the cell to a heat induced stress and  
XX determining if the compound inhibits JNK phosphatase activity. The  
XX invention additionally encompasses compositions comprising an inhibitor  
XX of Hsp72 or JNK phosphatase activity. The compounds identified as  
XX inhibitors of Hsp72 or JNK phosphatase activity are useful for  
XX inhibiting the proliferation of cells. Modulation of the activity of the



CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.  
 XX  
 SQ Sequence 624 AA;

Query Match 88.2%; Score 45; DB 21; Length 624;  
 Best Local Similarity 90.0%; Pred. No. 0.56;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDAYT 10  
 ||||| ||  
 Db 286 slfegidft 295

RESULT 9  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.  
 XX  
 AC AAR03930;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Gallus gallus HSP (chkhsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Gallus gallus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 634 /note= "residue given as "O" in specification"  
 XX  
 PN WO9002564-A.  
 XX  
 PD 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 PA (CODON) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.  
 XX  
 PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.

CC According to the legend of Fig 2, the G. gallus HSP sequence has  
 CC 635 amino acid residues, the sequence itself has only 634,  
 CC including "O" (?) at position 634.  
 CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bmebsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);  
 CC 5. Rat rattus (rathsp70 - AAR03926);  
 CC 6. Xenopus laevis (xl170 - AAR03928);  
 CC 7. Homo sapiens (humbsp70 - AAR03929);  
 CC 8. Gallus gallus (chkhsp70 - AAR03930);  
 CC 9. Zea mays (mzeshp70 - AAR03931);  
 CC 10. Zea mays (mzeshp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 634 AA;

Query Match 88.2%; Score 45; DB 11; Length 634;  
 Best Local Similarity 90.0%; Pred. No. 0.57;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDAYT 10  
 ||||| ||  
 Db 289 slfegidft 298

RESULT 10  
 AAR03929  
 ID AAR03929 standard; Protein; 640 AA.  
 XX  
 AC AAR03929;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Homo sapiens HSP (humbsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 640 /note= "residue given as "O" in specification"  
 XX  
 PN WO9002564-A.  
 XX  
 PD 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 PA (CODON) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.  
 XX  
 PT Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.  
 XX  
 CC According to the legend of Fig 2, the H. sapiens HSP sequence has  
 CC 641 amino acid residues, the sequence itself has only 640,  
 CC including "O" (?) at position 640.  
 CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bmebsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);  
 CC 5. Rat rattus (rathsp70 - AAR03926);  
 CC 6. Xenopus laevis (xl170 - AAR03928);  
 CC 7. Homo sapiens (humbsp70 - AAR03929);  
 CC 8. Gallus gallus (chkhsp70 - AAR03930);  
 CC 9. Zea mays (mzeshp70 - AAR03931);  
 CC 10. Zea mays (mzeshp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.



SQ Sequence 640 AA;

Query Match 88.2%; Score 45; DB 11; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.58;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 |||||||  
 Db 286 slfegidft 295

RESULT 11  
 AAW10065  
 ID AAW10065 standard; Protein; 640 AA.  
 XX  
 AC AAW10065;  
 XX  
 DT 24-OCT-1997 (first entry)  
 XX  
 DE Human heat shock protein 70.  
 XX  
 KW Human; heat shock protein 70; HSP70; primer; probe; detection;  
 KW intracellular; abnormal transcription; acute; chronic; sustained;  
 KW stress.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP08322577-A.  
 XX  
 PD 10-DEC-1996.  
 XX  
 PF 01-JUN-1995; 95JP-0158581.  
 XX  
 PR 01-JUN-1995; 95JP-0158581.  
 XX  
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 XX WPI; 1997-081088/08.  
 DR N-PSDB; AAT58086.  
 DR  
 XX Detection of abnormal transcription of HSP70 mRNA - using HSP70  
 PT specific primer or probe, used in detection of human acute and  
 PT chronic sustained stress load  
 XX  
 PS Claim 1; Fig 1; 13pp; Japanese.  
 XX  
 CC The cDNA encoding the present sequence, human heat shock protein 70  
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
 CC and 21. Primers and probes based on the HSP70 cDNA coding  
 CC sequence can be used to detect the abnormal transcription of  
 CC intracellular HSP70 mRNA in human acute and chronic sustained  
 CC stress load.  
 XX  
 SQ Sequence 640 AA;

Query Match 88.2%; Score 45; DB 18; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.58;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 |||||||  
 Db 286 slfegidft 295

RESULT 12  
 AAB23653  
 ID AAB23653 standard; protein; 640 AA.  
 XX  
 AC AAB23653;  
 XX  
 DT 05-JAN-2001 (first entry)

XX Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.  
 DE  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytotatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX  
 PA (SUME) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX  
 XX WPI; 2000-543748/49.  
 DR  
 XX Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer -  
 XX  
 PS Claim 3; Page 49-52; 72pp; Japanese.  
 XX  
 CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (1) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX  
 SQ Sequence 640 AA;

Query Match 88.2%; Score 45; DB 21; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.58;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 |||||||  
 Db 286 slfegidft 295

RESULT 13  
 AAY88408  
 ID AAY88408 standard; Protein; 640 AA.  
 XX  
 AC AAY88408;  
 XX  
 DT 31-JUL-2000 (first entry)  
 XX  
 DE Human heat shock protein HSP70 amino acid sequence.  
 XX  
 KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2000069999-A.



```

XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-0257146.
XX PR 01-JUN-1995; 95JP-0158581.
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX WPI; 2000-264458/23.
XX DR N-PSDB; AAA15620.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and
XX PT chronic continuous load of stress in a human being and its application
XX PT -
XX PS Claim 2; Fig 1; 1lpp; Japanese.
XX CC This sequence represents the human heat shock protein HSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome.
XX SQ Sequence 640 AA;

Query Match 88.2%; Score 45; DB 21; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10
Db 286 slfegidft 295

RESULT 15
AAR43004
ID AAR43004 standard; protein; 641 AA.
XX AC AAR43004;
XX DT 20-MAY-1994 (first entry)
XX DE Mature mouse sperm 70kD heat shock protein.
XX KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
XX KW HSC70B; mammalian; infertility; mycoplasma; HSP70.
XX OS Mus musculus.
XX FH Key
XX FT Region
XX FT Location/Qualifiers
XX FT 1..385
XX FT /label= 44kD ATPase fragment
XX FT /note= "peptides comprising an intact domain from
XX FT the ATPase fragment of hsp70 are claimed;
XX FT the peptides are homologous to sequences
XX FT conserved between Slp1 and 74.5kD
XX FT mycoplasma protein"
XX FT Domain
XX FT 1..39
XX FT /label= IA
XX FT /note= "part"
XX FT Domain
XX FT 40..115
XX FT /label= IB
XX FT Domain
XX FT 116..188
XX FT /label= IA
XX FT /note= "part"
XX FT Domain
XX FT 189..228
XX FT /label= IIA
XX FT /note= "part"
XX FT Domain
XX FT 229..306
XX FT /label= IIB
XX FT Domain
XX FT 307..385
XX FT /label= IIA
XX FT /note= "part"
XX PN WO9321954-A.
XX PD 11-NOV-1993.
XX PF 22-APR-1993; 93WO-US03816.
XX PR 24-APR-1992; 92US-0873961.
XX PA (BERL-) BERLEX LAB INC.
XX PA (OTTA-) OTTAWA CIVIC HOSPITAL.
XX PI Faulds DH, Lingwood CA, Tanphaichitr N;
XX DR WPI; 1993-368422/46.

Query Match 88.2%; Score 45; DB 21; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10
Db 286 slfegidft 295

RESULT 14
AAY88411
ID AAY88411 standard; Protein; 640 AA.
XX AC AAY88411;
XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein LHSP70 amino acid sequence.
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; LHSP70.
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-0257146.
XX PR 01-JUN-1995; 95JP-0158581.
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX WPI; 2000-264458/23.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and
XX PT chronic continuous load of stress in a human being and its application
XX PT -
XX PS Disclosure; Fig 4; 1lpp; Japanese.
XX CC This sequence represents the human heat shock protein LHSP70 amino acid

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```

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
CC and 14q22-24. The invention relates to the abnormal transcription of
CC intracellular HSP70mRNA under acute and chronic stress load in a human.
CC The abnormal transcription of HSP70 can be used in the improvement of
CC stress and response and diagnosis of stress diseases including
CC rheumatism, schizophrenia, depression and nephrotic syndrome.
XX SQ Sequence 640 AA;

```

```

Query Match 88.2%; Score 45; DB 21; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Qy 1 SLFEGIDAYT 10
Db 286 slfegidft 295

```

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RESULT 15
AAR43004
ID AAR43004 standard; protein; 641 AA.

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XX AC AAR43004;

```

```

XX DT 20-MAY-1994 (first entry)

```

```

XX DE Mature mouse sperm 70kD heat shock protein.

```

```

XX KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
XX KW HSC70B; mammalian; infertility; mycoplasma; HSP70.

```

```

XX OS Mus musculus.

```

```

XX FH Key
XX FT Region
XX FT Location/Qualifiers

```

```

XX FT 1..385
XX FT /label= 44kD ATPase fragment
XX FT /note= "peptides comprising an intact domain from
XX FT the ATPase fragment of hsp70 are claimed;
XX FT the peptides are homologous to sequences
XX FT conserved between Slp1 and 74.5kD
XX FT mycoplasma protein"

```

```

XX FT Domain

```

```

XX FT 1..39
XX FT /label= IA
XX FT /note= "part"

```

```

XX FT Domain

```

```

XX FT 40..115
XX FT /label= IB

```

```

XX FT Domain

```

```

XX FT 116..188
XX FT /label= IA
XX FT /note= "part"

```

```

XX FT Domain

```

```

XX FT 189..228
XX FT /label= IIA
XX FT /note= "part"

```

```

XX FT Domain

```

```

XX FT 229..306
XX FT /label= IIB

```

```

XX FT Domain

```

```

XX FT 307..385
XX FT /label= IIA
XX FT /note= "part"

```

```

XX PN WO9321954-A.

```

```

XX PD 11-NOV-1993.

```

```

XX PF 22-APR-1993; 93WO-US03816.

```

```

XX PR 24-APR-1992; 92US-0873961.

```

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XX PA (BERL-) BERLEX LAB INC.
XX PA (OTTA-) OTTAWA CIVIC HOSPITAL.

```

```

XX PI Faulds DH, Lingwood CA, Tanphaichitr N;
XX DR WPI; 1993-368422/46.

```



XX Mammalian fertilisation decrease for detecting and treating  
PT infertility - using sulpho glyco lipid immobilising protein  
PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
PT infection treatment  
XX  
PS Claim 2 and Claim 17; Page 60-62; 77pp; English.  
XX  
CC The likelihood of mammalian fertilisation is decreased by contacting  
CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIPI)/  
CC sulphated glyco-moiety interfering composition. The interfering  
CC compsn. is e.g. the heat shock 70KD protein, SLIPI (or analogues  
CC such as the mouse SLIPI analogue "HSC70B" comprising the amino acid  
CC sequence AAR43002) or the 74.5KD mycoplasma protein (AAR43003).  
XX  
SQ Sequence 641 AA;  
  
Query Match 88.2%; Score 45; DB 14; Length 641;  
Best Local Similarity 90.0%; Pred. No. 0.58;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDAYT 10  
DB 286 slfegidfy 295

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OM protein - protein search, using sw model

Run On: December 6, 2001, 08:04:05 ; Search time 184.09 Seconds  
(without alignments)  
4.024 Million cell updates/sec

Title: PEP2-MOD8F

Perfect score: 53

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	53	100.0	10	22	Heat shock protein
2	53	100.0	554	21	Human heat shock p
3	53	100.0	554	21	Human heat shock p
4	53	100.0	554	21	Human heat shock p
5	53	100.0	554	21	Human heat shock p
6	53	100.0	624	21	Human Hsp72 (heat
7	53	100.0	634	11	Gallus gallus HSP
8	53	100.0	640	11	Homo sapiens HSP
9	53	100.0	640	18	Human heat shock p
10	53	100.0	640	21	Human heat shock p
11	53	100.0	640	21	Human heat shock p

12	53	100.0	640	21	AAAY88411	Human heat shock p
13	53	100.0	641	14	AAAR43004	Mature mouse sperm
14	53	100.0	641	19	AAW54349	Human heat shock 7
15	53	100.0	641	21	AAAB23652	Human heat shock p
16	53	100.0	641	22	AAAB82534	Human heat shock p
17	53	100.0	642	21	AAAB23650	Rat heat shock pro
18	53	100.0	647	11	AAAR03928	Xenopus laevis HSP
19	52	98.1	643	18	AAW22895	Marmoset intracell
20	52	98.1	665	21	AAAB58386	Lung cancer associ
21	50	94.3	91	21	AAAG02174	Human secreted pro
22	50	94.3	646	11	AAAR03927	Rat HSP (rathsp70)
23	50	94.3	646	19	AAW54364	Heat shock cognate
24	50	94.3	646	20	AAAY17407	Human heat shock c
25	50	94.3	646	20	AAAY17408	Mouse heat shock c
26	50	94.3	646	20	AAAB23649	Mouse heat shock p
27	50	94.3	646	21	AAAB23651	Human heat shock p
28	50	94.3	646	22	AAAB82535	Human heat shock p
29	50	94.3	656	18	AAW01638	Candida albicans h
30	50	94.3	890	21	AAAB22938	GFP-HSC70 fusion p
31	49	92.5	633	14	AAAR43002	Mouse SLTP1 homolo
32	47	88.7	10	21	AAAY44200	Heat shock protein
33	47	88.7	10	22	AAAB97602	Heat shock protein
34	46	86.8	253	21	AAAG24333	Arabidopsis thalia
35	46	86.8	279	21	AAAG24332	Arabidopsis thalia
36	46	86.8	342	21	AAAG24331	Arabidopsis thalia
37	42	79.2	9	21	AAAY44199	Heat shock protein
38	42	79.2	9	22	AAAB97601	Heat shock protein
39	42	79.2	620	11	AAAR03932	Serratia marcescen
40	41	77.4	421	21	AAAG27768	Arabidopsis thalia
41	41	77.4	542	21	AAAG53606	Arabidopsis thalia
42	41	77.4	623	21	AAAG53605	Arabidopsis thalia
43	41	77.4	646	11	AAAR03931	Zea mays HSP (mzeh
44	41	77.4	646	21	AAAG53604	Arabidopsis thalia
45	39	73.6	187	21	AAAB54038	Human pancreatic c

#### ALIGNMENTS

#### RESULT 1

AAAB97603  
ID AAB97603 standard; peptide; 10 AA.

XX AAB97603;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP: HSP70; heat shock protein 70; cancer; chronic infectious disease;  
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
PT transformed human cells with induced and increased membrane expression  
PT of heat shock protein -



PS Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX Sequence 10 AA;

Query Match 100.0%; Score 53; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00031; Mismatches 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||

Db 1 slfegidfyt 10

# RESULT 2

AY88409  
 ID AAY88409 standard; Protein; 554 AA.

XX AAY88409;

31-JUL-2000 (first entry)

Human heat shock protein SHSP70 amino acid sequence.

Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 depression; nephrotic syndrome; SHSP70.

Homo sapiens.

JP2000069999-A.

07-MAR-2000.

01-JUN-1995; 99JP-0257146.

01-JUN-1995; 95JP-0158581.

(HOKU-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 2000-264458/23.

N-PSDB; AAA15621.

Abnormal transcription of intracellular HSP70mRNA under acute and  
 chronic continuous load of stress in a human being and its application

Examples; Fig 2; 11pp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid  
 sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 and 14q22-24. The invention relates to the abnormal transcription of  
 intracellular HSP70mRNA under acute and chronic stress load in a human.  
 The abnormal transcription of HSP70 can be used in the improvement of  
 stress and response and diagnosis of stress diseases including  
 -rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 100.0%; Score 53; DB 21; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||

Db 200 slfegidfyt 209

# RESULT 3

AY88410  
 ID AAY88410 standard; Protein; 554 AA.

XX AAY88410;

31-JUL-2000 (first entry)

Human; heat shock protein SHSP70 amino acid sequence.

Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 depression; nephrotic syndrome; SHSP70.

Homo sapiens.

JP2000069999-A.

07-MAR-2000.

01-JUN-1995; 99JP-0257146.

01-JUN-1995; 95JP-0158581.

(HOKU-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 2000-264458/23.

N-PSDB; AAA15622.

Abnormal transcription of intracellular HSP70mRNA under acute and  
 chronic continuous load of stress in a human being and its application

Disclosure; Fig 3; 11pp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid  
 sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 and 14q22-24. The invention relates to the abnormal transcription of  
 intracellular HSP70mRNA under acute and chronic stress load in a human.  
 The abnormal transcription of HSP70 can be used in the improvement of  
 stress and response and diagnosis of stress diseases including  
 rheumatism, schizophrenia, depression and nephrotic syndrome.

Sequence 554 AA;

Query Match 100.0%; Score 53; DB 21; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||

Db 200 slfegidfyt 209

# RESULT 4

AY88412  
 ID AAY88412 standard; Protein; 554 AA.

XX AAY88412;

AC AAY88412;



```

XX 31-JUL-2000 (first entry)
XX DT
XX DE
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX KW
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS
XX OS Homo sapiens.
XX XX
XX PN JP2000069999-A.
XX XX
XX PD 07-MAR-2000.
XX XX
XX PF 01-JUN-1995; 99JP-0257146.
XX XX
XX PR 01-JUN-1995; 95JP-0158581.
XX XX
XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX XX
XX DR WPI; 2000-264458/23.
XX XX
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and
XX PT chronic continuous load of stress in a human being and its application
XX PT
XX PS Disclosure; Fig 5; 11pp; Japanese.
XX XX
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome.
XX XX
XX SQ Sequence 554 AA;

Query Match 100.0%; Score 53; DB 21; Length 554;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 200 slfegidfy 209

RESULT 5
AAY88413
ID AAY88413 standard; Protein; 554 AA.
XX AC
XX AC AAY88413;
XX DT
XX DT 31-JUL-2000 (first entry)
XX DE
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX KW
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS
XX OS Homo sapiens.
XX XX
XX PN JP2000069999-A.
XX XX
XX PD 07-MAR-2000.
XX XX
XX PF 01-JUN-1995; 99JP-0257146.
XX XX
XX PR 01-JUN-1995; 95JP-0158581.
XX XX

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PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX DR
XX DR WPI; 2000-264458/23.
XX XX
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and
XX PT chronic continuous load of stress in a human being and its application
XX PT
XX PS Disclosure; Fig 6; 11pp; Japanese.
XX XX
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome.
XX XX
XX SQ Sequence 554 AA;

Query Match 100.0%; Score 53; DB 21; Length 554;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 200 slfegidfy 209

RESULT 6
AAB23252
ID AAB23252 standard; Protein; 624 AA.
XX AC
XX AC AAB23252;
XX DT
XX DT 29-JAN-2001 (first entry)
XX DE
XX DE Human Hsp72 (heat shock protein 72).
XX KW
XX KW Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
XX KW expression modulator; JNK phosphatase inhibitor; antiproliferative;
XX KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;
XX KW carcinoma; breast cancer; prostate cancer; premalignant condition.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200054814-A1.
XX PD
XX PD 21-SEP-2000.
XX PF
XX PF 17-MAR-2000; 2000WO-US07350.
XX PR
XX PR 18-MAR-1999; 99US-0125046.
XX XX
XX XX (PHYL-) PHYLOGENY INC.
XX XX
XX XX Volloch VZ, Sherman M;
XX XX
XX XX WPI; 2000-647056/62.
XX XX
XX XX N-PSDB; AAA97541.
XX XX
XX XX Identifying compounds that inhibit proliferation of cells and capable
XX XX of modulating the expression of heat shock protein 72 gene and/or
XX XX activity of Hsp72 useful for treating cancers such as leukemia,
XX XX lymphoma
XX XX
XX XX Examples; Fig 16B; 77pp; English.
XX XX
XX CC The invention relates to a novel method of identifying compounds that
XX CC inhibit proliferation of cells comprising contacting a test compound with
XX CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining
XX CC if the test compound inhibits activity or expression of Hsp72.
XX CC

```



CC Optionally, Hsp72 is contacted with the test compound under optimum  
 CC conditions to allow the two components to interact and bind, forming a  
 CC complex which is detected. The invention also relates to a method of  
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
 CC activation, comprising contacting a test compound with a cell which  
 CC expresses Hsp72, exposing the cell to a heat induced stress and  
 CC determining if the compound inhibits JNK phosphatase activity. The  
 CC invention additionally encompasses compositions comprising an inhibitor  
 CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
 CC inhibiting the proliferation of cells. Modulation of the activity of the  
 CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.

XX Sequence 624 AA;  
 SQ  
 Query Match 100.0%; Score 53; DB 21; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 0.027;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 DB 286 slfegidfyf 295  
 |||||

RESULT 7  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.  
 XX  
 AC AAR03930;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Gallus gallus HSP (chkhsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Gallus gallus.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 634  
 FT /note= "residue given as "O" in specification"  
 XX  
 PN WO9002564-A.  
 XX  
 PD 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 PA (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;  
 XX WPI; 1990-115820/15.  
 XX  
 XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.  
 XX  
 XX According to the legend of Fig 2, the G. gallus HSP sequence has  
 CC 635 amino acid residues, the sequence itself has only 634,  
 CC "including "O" (?) at position 634.

CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bnehsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);  
 CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. Xenopus laevis (xl170 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.

XX Sequence 634 AA;  
 SQ  
 Query Match 100.0%; Score 53; DB 11; Length 634;  
 Best Local Similarity 100.0%; Pred. No. 0.027;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 DB 289 slfegidfyf 298  
 |||||

RESULT 8  
 AAR03929  
 ID AAR03929 standard; Protein; 640 AA.  
 XX  
 AC AAR03929;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Homo sapiens HSP (humhsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 640  
 FT /note= "residue given as "O" in specification"  
 XX  
 PN WO9002564-A.  
 XX  
 PD 22-MAR-1990.  
 XX  
 PF 12-SEP-1989; 89WO-0003955.  
 XX  
 PR 12-SEP-1988; 88US-0243474.  
 XX  
 PA (CODO-) CODON.  
 XX  
 PI Dragon E, Faulds D, Sias S;  
 XX  
 DR WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 PS Disclosure; Fig 2.1-2.14; 86pp; English.  
 XX  
 XX According to the legend of Fig 2, the H. sapiens HSP sequence has  
 CC 641 amino acid residues, the sequence itself has only 640,  
 CC including "O" (?) at position 640.  
 CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypopneumoniae (Mhyhsp70 - AAR03922);  
 CC 2. Bacillus megaterium (Bnehsp70 - AAR03923);  
 CC 3. E. coli (dnaK - AAR03924);  
 CC 4. T. cruzi (tc70kd - AAR03925);



CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. Xenopus laevis (xl70 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 640 AA;

Query Match 100.0%; Score 53; DB 11; Length 640;

Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10

DB 286 slfegidfyf 295

RESULT 9

AAW10065  
 ID AAW10065 standard; Protein; 640 AA.

AC AAW10065;

DT 24-OCT-1997 (first entry)

DE Human heat shock protein 70.

KW Human; heat shock protein 70; HSP70; primer; probe; detection;

KW intracellular; abnormal transcription; acute; chronic; sustained;  
 stress.

OS Homo sapiens.

PN JP08322577-A.

PD 10-DEC-1996.

PF 01-JUN-1995; 95JP-0158581.

PR 01-JUN-1995; 95JP-0158581.

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

DR WPI; 1997-081088/08.

DR N-PSDB; AAT58086.

PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
 specific primer or probe, used in detection of human acute and  
 chronic sustained stress load

PS Claim 1; Fig 1; 13pp; Japanese.

CC The cDNA encoding the present sequence, human heat shock protein 70  
 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
 CC and 21. Primers and probes based on the HSP70 cDNA coding  
 CC sequence can be used to detect the abnormal transcription of  
 CC intracellular HSP70 mRNA in human acute and chronic sustained  
 CC stress load.

SQ Sequence 640 AA;

Query Match 100.0%; Score 53; DB 18; Length 640;

Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10

DB 286 slfegidfyf 295

RESULT 10

AAAB23653  
 ID AAB23653 standard; Protein; 640 AA.

AC AAB23653;

DT 05-JAN-2001 (first entry)

DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytosolic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.

OS Homo sapiens.

PN WO200049041-A1.

PD 24-AUG-2000.

PF 18-FEB-2000; 2000WO-JP00941.

PR 19-FEB-1999; 99JP-0041535.

PA (SUME ) SUMITOMO ELECTRIC IND CO.

PI Shinbara N, Udono H, Yui K;

DR WPI; 2000-543748/49.

PT Fused protein capable of inducing cellular immune response, useful as  
 active ingredient for drug compositions in preventing and/or treating  
 infectious diseases such as malaria or cancer

PS Claim 3; Page 49-52; 72pp; Japanese.

CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.

SQ Sequence 640 AA;

Query Match 100.0%; Score 53; DB 21; Length 640;

Best Local Similarity 100.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10

DB 286 slfegidfyf 295

RESULT 11

AAAY88408  
 ID AAY88408 standard; Protein; 640 AA.

AC AAY88408;

XX



```

DT 31-JUL-2000 (first entry)
XX Human heat shock protein HSP70 amino acid sequence.
XX
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW depression; nephrotic syndrome.
XX
XX Homo sapiens.
OS
XX JP2000069999-A.
XX
XX 07-MAR-2000.
XX
XX 01-JUN-1995; 99JP-0257146.
XX
XX 01-JUN-1995; 95JP-0158581.
XX
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI: 2000-264458/23.
XX N-PSDB: AAA15620.
XX
XX Abnormal transcription of intracellular HSP70mRNA under acute and
XX chronic continuous load of stress in a human being and its application
XX
XX Claim 2; Fig 1; 11pp; Japanese.
XX
XX This sequence represents the human heat shock protein HSP70 amino acid
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX and 14q22-24. The invention relates to the abnormal transcription of
XX intracellular HSP70mRNA under acute and chronic stress load in a human.
XX The abnormal transcription of HSP70 can be used in the improvement of
XX stress and response and diagnosis of stress diseases including
XX rheumatism, schizophrenia, depression and nephrotic syndrome.
XX
XX Sequence 640 AA;
XX
XX Query Match 100.0%; Score 53; DB 21; Length 640;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDFYT 10
XX Db 286 slfegidfy 295
XX
XX RESULT 12
XX AAY88411
XX ID AAY88411 standard; Protein; 640 AA.
XX
XX AC AAY88411;
XX
XX DT 31-JUL-2000 (first entry)
XX
XX DE Human heat shock protein LHS70 amino acid sequence.
XX
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX depression; nephrotic syndrome; LHS70.
XX
XX OS Homo sapiens.
XX
XX PN JP2000069999-A.
XX
XX PD 07-MAR-2000.
XX
XX PF 01-JUN-1995; 99JP-0257146.
XX
XX PR 01-JUN-1995; 95JP-0158581.
XX
XX PN WO9321954-A.
XX
XX PD 11-NOV-1993.

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PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI: 2000-264458/23.
XX
XX Abnormal transcription of intracellular HSP70mRNA under acute and
XX chronic continuous load of stress in a human being and its application
XX
XX Disclosure; Fig 4; 11pp; Japanese.
XX
XX This sequence represents the human heat shock protein LHS70 amino acid
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX and 14q22-24. The invention relates to the abnormal transcription of
XX intracellular HSP70mRNA under acute and chronic stress load in a human.
XX The abnormal transcription of HSP70 can be used in the improvement of
XX stress and response and diagnosis of stress diseases including
XX rheumatism, schizophrenia, depression and nephrotic syndrome.
XX
XX Sequence 640 AA;
XX
XX Query Match 100.0%; Score 53; DB 21; Length 640;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLFEGIDFYT 10
XX Db 286 slfegidfy 295
XX
XX RESULT 13
XX AAR43004
XX ID AAR43004 standard; protein; 641 AA.
XX
XX AC AAR43004;
XX
XX DT 20-MAY-1994 (first entry)
XX
XX DE Mature mouse sperm 70KD heat shock protein.
XX
XX KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
XX HSC70B; mammalian; infertility; mycoplasma; HSP70.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX Region 1..385
XX FT /label= 44KD ATPase_fragment
XX FT /note= "peptides comprising an intact domain from
XX FT the ATPase fragment of hsp70 are claimed;
XX FT the peptides are homologous to sequences
XX FT conserved between SLIPI and 74.5kD
XX FT mycoplasma protein"
XX FT Domain 1..39
XX FT /label= IA
XX FT /note= "part"
XX FT Domain 40..115
XX FT /label= IB
XX FT /label= IA
XX FT /note= "part"
XX FT Domain 189..228
XX FT /label= IIA
XX FT /note= "part"
XX FT Domain 229..306
XX FT /label= IIB
XX FT /label= IIA
XX FT /note= "part"
XX FT Domain 307..385
XX FT /label= IIA
XX FT /note= "part"
XX
XX PN WO9321954-A.
XX
XX PD 11-NOV-1993.

```



XX 22-APR-1993; 93WO-US03816.  
 XX  
 PR 24-APR-1992; 92US-0873961.  
 XX  
 PA (BERL-) BERLEX LAB INC.  
 PA (OTTA-) OTTAWA CIVIC HOSPITAL.  
 XX  
 PI Faulds DH, Lingwood CA, Tanphaichitr N;  
 XX WPI; 1993-368422/46.  
 XX  
 XX Mammalian fertilisation decrease for detecting and treating  
 PT infertility - using sulpho glyco lipid immobilising protein  
 PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
 PT infection treatment  
 XX  
 PS Claim 2 and Claim 17; Page 60-62; 77pp; English.  
 XX  
 XX The likelihood of mammalian fertilisation is decreased by contacting  
 CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIPI)/  
 CC sulphated glyco-moiety interfering composition. The interfering  
 CC compsn. is e.g. the heat shock 70kD protein, SLIPI (or analogues  
 CC such as the mouse SLIPI analogue "HSC70B" comprising the amino acid  
 CC sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).  
 XX  
 XX Sequence 641 AA;  
 SQ

Query Match 100.0%; Score 53; DB 14; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 0.027;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 0;  
 QY 1 SLFEGIDFYT 10  
 |||||||||  
 DB 286 slfegidft 295

RESULT 14  
 AAW54349  
 ID AAW54349 standard; protein; 641 AA.  
 AC AAW54349;  
 XX  
 DT 14-AUG-1998 (first entry)  
 XX  
 DE Human heat shock 70 kD protein 1.  
 XX  
 KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
 KW 2D gel electrophoresis; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9810291-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 05-SEP-1997; 97WO-GB02394.  
 XX  
 PR 08-APR-1997; 97GB-0007132.  
 PR 06-SEP-1996; 96GB-0018600.  
 XX  
 PA (CLIN-) CENT CLINICAL & BASIC RES.  
 XX  
 PI Byrjalsen I, Fey SJ, Larsen P;  
 XX WPI; 1998-207057/18.  
 DR  
 XX Biochemical markers of human endometrium - useful for, e.g.  
 PT diagnosis of hyperplasia and adenocarcinoma  
 XX  
 PS Disclosure; Page 19; 77pp; English.  
 XX

CC Proteins AAW54349-W54364 are examples of proteins produced in the  
 CC endometrium during the hyperplasia, adenocarcinoma or proliferative  
 CC phase of the endometrium. The presence and quantities of these proteins  
 CC can be detected using 2D gel electrophoresis comparison of cell lysates.  
 CC The proteins can be used as biochemical markers to detect the phase of  
 CC the endometrium and can be measured in body fluids, obviating the need  
 CC for endometrial biopsies.  
 XX  
 SQ Sequence 641 AA;  
 Query Match 100.0%; Score 53; DB 19; Length 641;  
 Best Local Similarity 100.0%; Pred. No. 0.027;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLFEGIDFYT 10  
 |||||||||  
 DB 286 slfegidft 295

RESULT 15  
 AAB23652  
 ID AAB23652 standard; protein; 641 AA.  
 XX  
 AC AAB23652;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytostatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX  
 PA (SUME ) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Uono H, Yui K;  
 XX WPI; 2000-543748/49.  
 DR  
 XX Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer  
 XX  
 PS Claim 3; Page 46-48; 72pp; Japanese.  
 XX  
 XX The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX  
 SQ Sequence 641 AA;



Query Match 100.0%; Score 53; DB 21; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0.027;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDFYT 10  
Db 286 slfegidfyt 295

Search completed: December 6, 2001, 08:04:05  
Job time: 613 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:04 ; Search time 184.09 Seconds  
(without alignments)  
4.024 Million cell updates/sec

Title: PEP2-MOD8G

Perfect score: 53

Sequence: 1 SLFEGIDGYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
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5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	83.0	10	22	Heat shock protein
2	44	83.0	554	21	Human heat shock p
3	44	83.0	554	21	Human heat shock p
4	44	83.0	554	21	Human heat shock p
5	44	83.0	554	21	Human heat shock p
6	44	83.0	624	21	Human Hsp72 (heat
7	44	83.0	634	11	Gallus gallus HSP
8	44	83.0	640	11	Homo sapiens HSP (
9	44	83.0	640	18	Human heat shock p
10	44	83.0	640	21	Human heat shock p
11	44	83.0	640	21	Human heat shock p

12	44	83.0	640	21	AA198411	Human heat shock p
13	44	83.0	641	14	AA198404	Mature mouse sperm
14	44	83.0	641	19	AA1984349	Human heat shock 7
15	44	83.0	641	21	AA1984352	Human heat shock p
16	44	83.0	641	22	AA1984354	Human heat shock p
17	44	83.0	642	21	AA1984350	Rat heat shock pro
18	44	83.0	647	11	AA1984328	Xenopus laevis HSP
19	43	81.1	10	21	AA1984200	Heat shock protein
20	43	81.1	10	22	AA1984202	Heat shock protein
21	43	81.1	643	18	AA1984285	Marmoset intracell
22	43	81.1	665	21	AA1984386	Lung cancer associ
23	41	77.4	91	21	AA19842174	Human secreted pro
24	41	77.4	646	11	AA1984327	Rat HSP (rathsp70)
25	41	77.4	646	19	AA1984364	Heat shock cognate
26	41	77.4	646	20	AA1984707	Human heat shock c
27	41	77.4	646	20	AA1984708	Mouse heat shock c
28	41	77.4	646	21	AA1984649	Mouse heat shock p
29	41	77.4	646	21	AA1984651	Human heat shock p
30	41	77.4	646	22	AA1984653	Human heat shock p
31	41	77.4	656	18	AA1984638	Candida albicans h
32	41	77.4	890	21	AA19842938	GFP-HSC70 fusion p
33	40	75.5	633	14	AA19843002	Mouse SLP1 homolo
34	38	71.7	9	21	AA19844199	Heat shock protein
35	38	71.7	9	22	AA19847601	Heat shock protein
36	38	71.7	303	18	AA1984255	Pyrobaculum aerop
37	37	69.8	117	16	AA19846617	Hepatitis C virus
38	37	69.8	117	16	AA19846622	Hepatitis C virus
39	37	69.8	117	20	AA1984616	Protein encoded by
40	37	69.8	117	20	AA1984611	Protein encoded by
41	37	69.8	117	20	AA19840585	Hepatitis C virus
42	37	69.8	205	13	AA19841081	Non-A non-B hepati
43	37	69.8	253	21	AA1984333	Arabidopsis thalia
44	37	69.8	269	14	AA19844001	JH-1 E2/NS1 protei
45	37	69.8	279	21	AA1984332	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1

AA19847603

ID AAB97603 standard; peptide; 10 AA.

XX AAB97603;

XX 30-JUL-2001 (first entry)

DE Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
PT transformed human cells with induced and increased membrane expression  
PT of heat shock protein -



PS Claim 8; Page 15; 2lpp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

SQ Sequence 10 AA;

Query Match 83.0%; Score 44; DB 22; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.043; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
 Db 1 slfegidfyt 10  
 ||||| ||

RESULT 2  
 AAY88409  
 ID AAY88409 standard; Protein; 554 AA.  
 AC AAY88409;  
 31-JUL-2000 (first entry)  
 DT Human heat shock protein SHSP70 amino acid sequence.  
 DE Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.  
 KW Homo sapiens.  
 OS JP2000069999-A.  
 PN 07-MAR-2000.  
 PD 01-JUN-1995; 99JP-0257146.  
 PF 01-JUN-1995; 95JP-0158581.  
 PR (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 PA WPI: 2000-264458/23.  
 DR N-PSDB; AAA15621.

Abnormal transcription of intracellular HSP70mRNA under acute and  
 chronic continuous load of stress in a human being and its application

Examples; Fig 2; 1lpp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid  
 sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 and 14q22-24. The invention relates to the abnormal transcription of  
 intracellular HSP70mRNA under acute and chronic stress load in a human.  
 The abnormal transcription of HSP70 can be used in the improvement of  
 stress and response and diagnosis of stress diseases including  
 rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;  
 Query Match 83.0%; Score 44; DB 21; Length 554;  
 Best Local Similarity 90.0%; Pred. No. 3.4;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
 Db 200 slfegidfyt 209  
 ||||| ||

RESULT 3  
 AAY88410  
 ID AAY88410 standard; Protein; 554 AA.  
 AC AAY88410;  
 31-JUL-2000 (first entry)  
 DT Human heat shock protein SHSP70 amino acid sequence.  
 DE Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.  
 KW Homo sapiens.  
 OS JP2000069999-A.  
 PN 07-MAR-2000.  
 PD 01-JUN-1995; 99JP-0257146.  
 PF 01-JUN-1995; 95JP-0158581.  
 PR (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 PA WPI: 2000-264458/23.  
 DR N-PSDB; AAA15622.

Abnormal transcription of intracellular HSP70mRNA under acute and  
 chronic continuous load of stress in a human being and its application

Disclosure; Fig 3; 1lpp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid  
 sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 and 14q22-24. The invention relates to the abnormal transcription of  
 intracellular HSP70mRNA under acute and chronic stress load in a human.  
 The abnormal transcription of HSP70 can be used in the improvement of  
 stress and response and diagnosis of stress diseases including  
 rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;  
 Query Match 83.0%; Score 44; DB 21; Length 554;  
 Best Local Similarity 90.0%; Pred. No. 3.4;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
 Db 200 slfegidfyt 209  
 ||||| ||

RESULT 4  
 AAY88412  
 ID AAY88412 standard; Protein; 554 AA.  
 AC AAY88412;



XX 31-JUL-2000 (first entry)  
XX  
XX Human heat shock protein SHSP70 amino acid sequence.  
DE  
XX  
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
XX  
XX Homo sapiens.  
OS  
XX JP2000069999-A.  
PN  
XX 07-MAR-2000.  
PD  
XX 01-JUN-1995; 99JP-0257146.  
PF  
XX 01-JUN-1995; 95JP-0158581.  
PR  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
PA  
XX WPI; 2000-264458/23.  
DR  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX Disclosure; Fig 5; lipp; Japanese.  
PS  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;  
XX  
XX Query Match 83.0%; Score 44; DB 21; Length 554;  
XX Best Local Similarity 90.0%; Pred. No. 3.4;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDGYT 10  
YY |||||  
DB 200 slfegidgyt 209  
XX  
XX RESULT 5  
XX AAY88413  
ID AAY88413 standard; Protein; 554 AA.  
XX  
XX AAY88413;  
AC  
XX 31-JUL-2000 (first entry)  
DT  
XX Human heat shock protein SHSP70 amino acid sequence.  
DE  
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
XX  
XX Homo sapiens.  
OS  
XX JP2000069999-A.  
PN  
XX 07-MAR-2000.  
PD  
XX 01-JUN-1995; 99JP-0257146.  
PF  
XX 01-JUN-1995; 95JP-0158581.  
PR  
XX

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX  
XX WPI; 2000-264458/23.  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX Disclosure; Fig 6; lipp; Japanese.  
PS  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;  
XX  
XX Query Match 83.0%; Score 44; DB 21; Length 554;  
XX Best Local Similarity 90.0%; Pred. No. 3.4;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDGYT 10  
YY |||||  
DB 200 slfegidgyt 209  
XX  
XX RESULT 6  
XX AAB23252  
ID AAB23252 standard; Protein; 624 AA.  
XX  
XX AAB23252;  
AC  
XX 29-JAN-2001 (first entry)  
DT  
XX Human Hsp72 (heat shock protein 72).  
DE  
XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX  
XX Homo sapiens.  
OS  
XX WO200054814-A1.  
PN  
XX 21-SEP-2000.  
PD  
XX 17-MAR-2000; 2000WO-US07350.  
PF  
XX 18-MAR-1999; 99US-0125046.  
PR  
XX (PHYL-) PHYLOGENY INC.  
PA  
XX Volloch VZ, Sherman M;  
PI  
XX WPI; 2000-647056/62.  
DR  
XX N-PSDB; AAA97541.  
DR  
XX Identifying compounds that inhibit proliferation of cells and capable  
PT of modulating the expression of heat shock protein 72 gene and/or  
PT activity of Hsp72 useful for treating cancers such as leukemia,  
PT lymphoma  
XX  
XX Examples; Fig 16B; 77pp; English.  
PS  
XX The invention relates to a novel method of identifying compounds that  
CC inhibit proliferation of cells comprising contacting a test compound with  
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
CC if the test compound inhibits activity or expression of Hsp72.  
CC



as cancers (e.g., leukemia, lymphoma, solid tumours such as breast cancer and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention.

Query Match 83.0%; Score 44; DB 21; Length 624;  
Best Local Similarity 90.0%; Pred. No. 3.8;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	SLFEGIDGYT	10
			11
Db	286	slfegidfyt	295
RESULT 7			
AAR03930			
ID	AAR03930	standard; Protein; 634	AA.
XX	XX		
AC	AAR03930;		
XX	XX		
DT	30-AUG-1990	(first entry)	
XX	XX		
DE	Gallus gallus	HSP (chkhsp70).	
XX	XX		
KW	Hsp70;	heat shock protein; Trypanosoma cruzi; vaccines; HSP.	
XX	XX		
OS	Gallus gallus.		

AA	Key	Location/Qualifiers
FH	Misc-difference	634
FT		/note= "residue given as "O" in specification"
FT		

XX	WO9002564 - A.
XX	
PN	
XX	22-MAR-1990.
XX	
PD	
XX	
PF	12-SEP-1989; 89WO-0003955.
XX	
XX	12-SEP-1988; 88US-0243474.
PR	
XX	
PA	(CODO-) CODON.

Proteins homologous to heat shock proteins from *Trypanosoma cruzi* - used in vaccines and diagnosis for species of eg *Mycoplasma* or *Mycobacteria*.

Disclosure: Fig 2.1-2.14; 86pp; English.

According to the legend of Fig 2, the *G. gallus* HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "o" (?) at position 634

Proteins homologous to heat shock proteins from *Trypanosoma cruzi* - used in vaccines and diagnosis for species of eg *Mycoplasma* or *Mycobacteria*.

Disclosure: Fig 2.1-2.14; 86pp; English.

According to the legend of Fig 2, the *G. gallus* HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "o" (?) at position 634



CC 5. T. cruzi (AAR03926);  
 CC 6. Rat rattus (rathsp70 - AAR03927);  
 CC 7. xenopus laevis (xl170 - AAR03928);  
 CC 8. Homo sapiens (humhsp70 - AAR03929);  
 CC 9. Gallus gallus (chkhsp70 - AAR03930);  
 CC 10. Zea mays (mzehsp70 - AAR03931);  
 CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 640 AA;

Query Match 83.0%; Score 44; DB 11; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGYT 10  
 |||||  
 Db 286 slfegidfyf 295

RESULT 9  
 AAW10065  
 ID AAW10065 standard; Protein; 640 AA.  
 AC AAW10065;  
 XX  
 DT 24-OCT-1997 (first entry)  
 XX  
 DE Human heat shock protein 70.  
 XX  
 KW Human; heat shock protein 70; HSP70; primer; probe; detection;  
 KW intracellular; abnormal transcription; acute; chronic; sustained;  
 KW stress.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP08322577-A.  
 XX

PD 10-DEC-1996.  
 PF 01-JUN-1995; 95JP-0158581.  
 PR 01-JUN-1995; 95JP-0158581.  
 XX  
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 DR WPI: 1997-081088/08.  
 DR N-PSDB; AAT58086.  
 XX  
 PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
 PT specific primer or probe, used in detection of human acute and  
 PT chronic sustained stress load  
 XX  
 PS Claim 1; Fig 1; 13pp; Japanese.  
 XX

CC The cDNA encoding the present sequence, human heat shock protein 70  
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
 CC and 21. Primers and probes based on the HSP70 cDNA coding  
 CC sequence can be used to detect the abnormal transcription of  
 CC intracellular HSP70 mRNA in human acute and chronic sustained  
 CC stress load.  
 XX  
 SQ Sequence 640 AA;

Query Match 83.0%; Score 44; DB 18; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGYT 10

Db 286 slfegidfyf 295  
 |||||  
 RESULT 10  
 AAB23653  
 ID AAB23653 standard; protein; 640 AA.  
 AC AAB23653;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytostatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX  
 PA (SUME ) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Uono H, Yui K;  
 XX  
 DR WPI: 2000-543748/49.

XX Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer -  
 XX  
 PS Claim 3; Page 49-52; 72pp; Japanese.  
 CC

CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (3); (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX  
 SQ Sequence 640 AA;

Query Match 83.0%; Score 44; DB 21; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGYT 10  
 |||||  
 Db 286 slfegidfyf 295

RESULT 11  
 AAY88408  
 ID AAY88408 standard; Protein; 640 AA.  
 AC AAY88408;  
 XX



DT 31-JUL-2000 (first entry)  
 XX Human heat shock protein HSP70 amino acid sequence.  
 XX  
 KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2000069999-A.  
 XX  
 PD 07-MAR-2000.  
 XX  
 PF 01-JUN-1995; 99JP-0257146.  
 XX  
 PR 01-JUN-1995; 95JP-0158581.  
 XX  
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 DR WPI; 2000-264458/23.  
 DR N-PSDB; AAI15620.  
 XX  
 XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application  
 PT  
 PS Claim 2; Fig 1; 1lpp; Japanese.  
 XX  
 CC This sequence represents the human heat shock protein HSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 XX  
 XX Sequence 640 AA;  
 SQ  
 Query Match 83.0%; Score 44; DB 21; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 SLFEGIDGYT 10  
 DB 286 slfegidfyf 295  
 RESULT 12  
 ID AAY88411 standard; Protein; 640 AA.  
 XX  
 AC AAY88411;  
 XX  
 XX 31-JUL-2000 (first entry)  
 XX  
 DE Human heat shock protein LHP70 amino acid sequence.  
 XX  
 KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; LHP70.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2000069999-A.  
 PN  
 XX 07-MAR-2000.  
 PD  
 XX 01-JUN-1995; 99JP-0257146.  
 PF  
 XX 01-JUN-1995; 95JP-0158581.  
 PR  
 XX

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX  
 DR WPI; 2000-264458/23.  
 XX  
 PT Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application  
 PT  
 XX Disclosure; Fig 4; 1lpp; Japanese.  
 XX  
 PS This sequence represents the human heat shock protein LHP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 XX  
 XX Sequence 640 AA;  
 SQ  
 Query Match 83.0%; Score 44; DB 21; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 SLFEGIDGYT 10  
 DB 286 slfegidfyf 295  
 RESULT 13.  
 ID AAR43004  
 XX AAR43004 standard; protein; 641 AA.  
 XX  
 AC AAR43004;  
 XX  
 XX 20-MAY-1994 (first entry)  
 DT  
 DE Mature mouse sperm 70kD heat shock protein.  
 XX  
 KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane;  
 KW HSC70B; mammalian; infertility; mycoplasma; HSP70.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..385  
 FT /label= 44kD ATPase fragment  
 FT /note= "peptides comprising an intact domain from  
 FT the ATPase fragment of hsp70 are claimed;  
 FT the peptides are homologous to sequences  
 FT conserved between SLIP1 and 74.5kD  
 FT mycoplasma protein"  
 FT  
 FT Domain 1..39  
 FT /label= IA  
 FT /note= "part"  
 FT Domain 40..115  
 FT /label= IB  
 FT Domain 116..188  
 FT /label= IA  
 FT /note= "part"  
 FT Domain 189..228  
 FT /label= IIA  
 FT /note= "part"  
 FT Domain 229..306  
 FT /label= IIB  
 FT Domain 307..385  
 FT /label= IIA  
 FT /note= "part"  
 XX WO9321954-A.  
 PN  
 XX 11-NOV-1993.  
 PD



XX 22-APR-1993; 93WO-US03816.  
 XX  
 PR 24-APR-1992; 92US-0873961.  
 XX  
 PA (BERL-) BERLEX LAB INC.  
 PA (OTTA-) OTTAWA CIVIC HOSPITAL.  
 XX  
 PI Faulds DH, Lingwood CA, Tanphaichitr N;  
 DR WPI; 1993-368422/46.  
 XX  
 XX Mammalian fertilisation decrease for detecting and treating  
 PT infertility - using sulpho glyco lipid immobilising protein  
 PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
 PT infection treatment  
 XX  
 PS Claim 2 and Claim 17; Page 60-62; 77pp; English.  
 XX  
 CC The likelihood of mammalian fertilisation is decreased by contacting  
 CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIPI)/  
 CC sulphated glyco-moiety interfering composition. The interfering  
 CC compsn. is e.g. the heat shock 70kD protein, SLIPI (or analogues  
 CC such as the mouse SLIPI analogue "HSC70B" comprising the amino acid  
 CC sequence AAR43002) or the 74.5kD mycoplasma protein (AAR43003).  
 XX  
 SQ Sequence 641 AA;  
 XX

Query Match 83.0%; Score 44; DB 14; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 0;  
 QY 1 SLFEGIDGYT 10  
 |||||  
 DB 286 slfegidgyt 295

RESULT 14  
 AAW54349  
 ID AAW54349 standard; protein; 641 AA.  
 XX  
 AC AAW54349;  
 XX  
 DT 14-AUG-1998 (first entry)  
 XX  
 DE Human heat shock 70 kD protein 1.  
 XX  
 KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
 KW 2D gel electrophoresis; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9810291-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 05-SEP-1997; 97WO-GB02394.  
 XX  
 PR 08-APR-1997; 97GB-0007132.  
 PR 06-SEP-1996; 96GB-0018600.  
 XX  
 PA (CLIN-) CENT CLINICAL & BASIC RES.  
 XX  
 PI Byrjalsen I, Fey SJ, Larsen P;  
 XX  
 DR WPI; 1998-207057/18.  
 XX  
 PT Biochemical markers of human endometrium - useful for, e.g.  
 PT diagnosis of hyperplasia and adenocarcinoma  
 XX  
 PS Disclosure; Page 19; 77pp; English.  
 XX

CC Proteins AAW54349-W54364 are examples of proteins produced in the  
 CC endometrium during the hyperplasia, adenocarcinoma or proliferative  
 CC phase of the endometrium. The presence and quantities of these proteins  
 CC can be detected using 2D gel electrophoresis comparison of cell lysates.  
 CC The proteins can be used as biochemical markers to detect the phase of  
 CC the endometrium and can be measured in body fluids, obviating the need  
 CC for endometrial biopsies.  
 XX  
 SQ Sequence 641 AA;  
 XX

Query Match 83.0%; Score 44; DB 19; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGYT 10  
 |||||  
 DB 286 slfegidgyt 295

RESULT 15  
 AAB23652  
 ID AAB23652 standard; protein; 641 AA.  
 XX  
 AC AAB23652;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; infectious disease; malaria; cytotoxic T cell;  
 KW cytostatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000049041-A1.  
 XX  
 PD 24-AUG-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-JP00941.  
 XX  
 PR 19-FEB-1999; 99JP-0041535.  
 XX  
 PA (SUME ) SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX  
 DR WPI; 2000-543748/49.  
 XX  
 PT Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer  
 XX  
 PS Claim 3; Page 46-48; 72pp; Japanese.  
 XX  
 CC The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytostatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed heat shock  
 CC protein for use in a fused protein of the present invention.  
 XX  
 SQ Sequence 641 AA;  
 XX



Query Match 83.0%; Score 44; DB 21; Length 641;  
Best Local Similarity 90.0%; Pred. No. 3.9;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
|||||  
Db 286 slfegidfyt 295

Search completed: December 6, 2001, 08:04:05  
Job time: 613 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:03 ; Search time 184.09 Seconds  
(without alignments)  
4.024 Million cell updates/sec

Title: PEP2-MOD8L

Perfect score: 51

Sequence: 1 SLFEGIDLVT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length, DB	ID	Description
1	49	96.1	10	21	Heat shock protein
2	49	96.1	10	22	Heat shock protein
3	47	92.2	10	22	Heat shock protein
4	47	92.2	554	21	Human heat shock p
5	47	92.2	554	21	Human heat shock p
6	47	92.2	554	21	Human heat shock p
7	47	92.2	554	21	Human heat shock p
8	47	92.2	624	21	Human Hsp72 (heat
9	47	92.2	634	11	Gallus gallus HSP
10	47	92.2	640	11	Homo sapiens HSP
11	47	92.2	640	18	Human heat shock p

12	47	92.2	640	21	AAB23653	Human heat shock p
13	47	92.2	640	21	AAV88408	Human heat shock p
14	47	92.2	640	21	AAV88411	Human heat shock p
15	47	92.2	641	14	AAV3004	Mature mouse sperm
16	47	92.2	641	19	AAV54349	Human heat shock 7
17	47	92.2	641	21	AAB23652	Human heat shock p
18	47	92.2	641	22	AAB82534	Human heat shock p
19	47	92.2	642	21	AAB23650	Rat heat shock pro
20	47	92.2	647	11	AAV03928	Xenopus laevis HSP
21	46	90.2	643	18	AAW22895	Marmoset intracell
22	46	90.2	665	21	AAB58386	Lung cancer associ
23	44	86.3	9	21	AAV44199	Heat shock protein
24	44	86.3	9	22	AAB97601	Heat shock protein
25	44	86.3	91	21	AAG02174	Human secreted pro
26	44	86.3	646	11	AAV03927	Rat HSP (rathsp70)
27	44	86.3	646	19	AAW54364	Heat shock cognate
28	44	86.3	646	20	AAV17407	Human heat shock c
29	44	86.3	646	20	AAV17408	Mouse heat shock c
30	44	86.3	646	21	AAB23649	Mouse heat shock p
31	44	86.3	646	21	AAB23651	Human heat shock p
32	44	86.3	646	22	AAB82535	Human heat shock p
33	44	86.3	656	18	AAW01638	Candida albicans h
34	44	86.3	890	21	AAB22938	GFP-HSC70 fusion p
35	43	84.3	633	14	AAV43002	Mouse SLIP1 homolo
36	40	78.4	253	21	AAG24333	Arabidopsis thalia
37	40	78.4	279	21	AAG24332	Arabidopsis thalia
38	40	78.4	342	21	AAG24331	Arabidopsis thalia
39	39	76.5	214	19	AAV85808	S. pneumoniae deri
40	38	74.5	221	19	AAW80645	S. pneumoniae prot
41	38	74.5	412	22	AAB61974	S. avermitilis ORF
42	36	70.6	134	22	AAG72082	Human olfactory re
43	36	70.6	134	22	AAG72333	Human OR-like poly
44	36	70.6	620	11	AAV03932	Serratia marcescen
45	35	66.6	187	21	AAB54038	Human pancreatic c

#### ALIGNMENTS

RESULT 1

AAV44200

ID AAV44200 standard; peptide; 10 AA.

XX AAV44200;

AC AAV44200;

XX 15-FEB-2000 (first entry)

DF 15-FEB-2000 (first entry)

XX Heat shock protein 70 amino acid residues 286-295.

DE Human; heat shock protein 70; hsp70; identification; tumour; mutation;

XX T cell response; amplification; vector; bacterium; cancer; allele;

KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;

KW immune defence; immunogenicity; specificity; human leucocyte antigen.

OS Homo sapiens.

XX WO9954464-A1.

PN 28-OCT-1999.

PD 28-OCT-1999.

XX 22-APR-1999; 99WO-FR00957.

XX 22-APR-1998; 98FR-0005033.

XX (INSR ) INST ROUSSY GUSTAVE.

XX Triebel F, Gaudin C;

XX WPI; 2000-013251/01.

XX Identifying mutant peptides from heat-shock protein 70, for treatment

XX of cancer -



PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-295 of the human

CC heat shock protein 70 (hsp70). The invention relates to a method of

CC identifying peptides, derived from hsp70 that stimulate a tumour-specific

CC T cell response. Identification of the hsp70 peptides that have at least

CC one mutation or alteration compared with the native sequence, and induce

CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70

CC encoding DNA from one or more tumours; (ii) cloning the amplified

CC sequences into a vector that can be replicated in bacteria;

CC (iii) sequencing fragments in each cultured bacterial colony to identify

CC any hsp70 mutations, and (iv) determining the immunogenicity of the

CC mutant peptides identified. The peptides, optionally formulated with an

CC agent that induces cellular stress, are used for treatment of cancer,

CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,

CC cancers of head and neck, particularly kidney cancer). The peptides may

CC also be used to increase the proportion of tumour-specific cytotoxic

CC T lymphocytes in a cell culture and/or induce these cells to secrete

CC cytotoxic factors (specifically interleukin-2, interferon-gamma and

CC tumour necrosis factor), particularly where the cells are used to

CC stimulate immune defences. The method identifies peptides with high

CC immunogenicity and high specificity for particular HLA (human leucocyte

XX antigen) alleles.

SQ Sequence 10 AA;

Query Match 96.1%; Score 49; DB 21; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.0015;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10

DB 1 slfegidiyt 10

|||||||

RESULT 2

AAB97602

ID AAB97602 standard; peptide; 10 AA.

XX

AC AAB97602;

XX

DT 30-JUL-2001 (first entry)

XX

DE Heat shock protein 70 (HSP70) peptidic fragment 2.

XX

KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;

KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

KW cytotoxic response; epitope; antigen presenting cell; fragment 2.

XX

OS Homo sapiens.

XX

PN WO200129190-A1.

XX

PD 26-APR-2001.

XX

PF 29-SEP-2000; 2000WO-EP09530.

XX

PR 15-OCT-1999; 99EP-0120484.

XX

PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX

PI Abastado JP, Bartholeyns J;

XX

DR WPI; 2001-290909/30.

XX

XX Lymphocytes useful for treating cancer, recognizes specifically

PT transformed human cells with induced and increased membrane expression

PT of heat shock protein -

XX

PS Claim 8; Page 15; 21pp; English.

XX

CC The amino acid sequence of fragment 2 relating to position 286-295 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates

CC to lymphocytes which recognise cells of a patient in which overexpression

CC of HSP has been induced. Overexpression of HSP leads to a substantial

CC increase in the numbers of HSPs and HSP epitopes presented on the

CC pericellular membrane. Recognition of increased numbers of HSP epitopes

CC on cell pericellular membranes by lymphocytes elicits a cytotoxic

CC response which kills the target cells. As a further embodiment of the

CC invention, HSP70 epitopes are mutated prior to being loaded into antigen

CC presenting cells. This has the effect of increasing the immune response

CC to HSP and helps direct the immune response to specific cells, (e.g.

CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to

CC the tumour or to the virus associated HSP is broken using an immunogenic

CC mutated form of HSP and induction of a stress on the target tumoural or

XX intracellular infected cells.

SQ Sequence 10 AA;

Query Match 96.1%; Score 49; DB 22; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.0015;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10

DB 1 slfegidiyt 10

|||||||

RESULT 3

AAB97603

ID AAB97603 standard; peptide; 10 AA.

XX

AC AAB97603;

XX

DT 30-JUL-2001 (first entry)

XX

DE Heat shock protein 70 (HSP70) peptidic fragment 3.

XX

KW HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;

KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX

OS Homo sapiens.

XX

PN WO200129190-A1.

XX

PD 26-APR-2001.

XX

PF 29-SEP-2000; 2000WO-EP09530.

XX

PR 15-OCT-1999; 99EP-0120484.

XX

PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX

PI Abastado JP, Bartholeyns J;

XX

DR WPI; 2001-290909/30.

XX

PT Lymphocytes useful for treating cancer, recognizes specifically

PT transformed human cells with induced and increased membrane expression

PT of heat shock protein -

XX

PS Claim 8; Page 15; 21pp; English.

XX

CC The amino acid sequence of fragment 3 relating to position 286-295 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates

CC to lymphocytes which recognise cells of a patient in which overexpression

CC of HSP has been induced. Overexpression of HSP leads to a substantial

CC increase in the numbers of HSPs and HSP epitopes presented on the

CC pericellular membrane. Recognition of increased numbers of HSP epitopes

CC on cell pericellular membranes by lymphocytes elicits a cytotoxic

CC response which kills the target cells. As a further embodiment of the

CC invention, HSP70 epitopes are mutated prior to being loaded into antigen



CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

XX Sequence 10 AA;

Query Match 92.2%; Score 47; DB 22; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.0038;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLTYT 10  
 |||||  
 Db 1 slfegidft 10

RESULT 4

AY88409  
 ID AAY88409 standard; Protein; 554 AA.

XX AC AAY88409;

XX 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

OS Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

DR N-PSDB; AAA15621.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

PT

XX Examples; Fig 2; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 92.2%; Score 47; DB 21; Length 554;  
 Best Local Similarity 90.0%; Pred. No. 0.29;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLTYT 10  
 |||||  
 Db 200 slfegidft 209

RESULT 5

AY88410

ID AAY88410 standard; Protein; 554 AA.

XX AC AAY88410;

XX 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

OS Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

DR N-PSDB; AAA15622.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

PT

XX Disclosure; Fig 3; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

Query Match 92.2%; Score 47; DB 21; Length 554;  
 Best Local Similarity 90.0%; Pred. No. 0.29;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLTYT 10  
 |||||  
 Db 200 slfegidft 209

RESULT 6

AY88412

ID AAY88412 standard; Protein; 554 AA.

XX AC AAY88412;

XX 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

OS Homo sapiens.



PN JP2000069999-A.  
XX 07-MAR-2000.  
XX 01-JUN-1995; 99JP-0257146.  
XX 01-JUN-1995; 95JP-0158581.  
XX (HOKU-) HOKEN KAGAKU KENKYUSHO KK.  
XX WPI; 2000-264458/23.  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
XX chronic continuous load of stress in a human being and its application  
XX Disclosure; Fig 5; 11pp; Japanese.  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
XX and 14q22-24. The invention relates to the abnormal transcription of  
XX intracellular HSP70mRNA under acute and chronic stress load in a human.  
XX The abnormal transcription of HSP70 can be used in the improvement of  
XX stress and response and diagnosis of stress diseases including  
XX rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX Sequence . 554 AA;  
XX  
XX Query Match 92.2%; Score 47; DB 21; Length 554;  
XX Best Local Similarity 90.0%; Pred. No. 0.29;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDLTYT 10  
XX ||||| ||  
XX 200 slfegidfty 209  
XX  
XX RESULT 7  
XX ID AAY88413 standard; Protein; 554 AA.  
XX AC AAY88413;  
XX DT 31-JUL-2000 (first entry)  
XX DE Human heat shock protein SHSP70 amino acid sequence.  
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
XX KW depression; nephrotic syndrome; SHSP70.  
XX OS Homo sapiens.  
XX PN JP2000069999-A.  
XX PD 07-MAR-2000.  
XX PF 01-JUN-1995; 99JP-0257146.  
XX PR 01-JUN-1995; 95JP-0158581.  
XX PA (HOKU-) HOKEN KAGAKU KENKYUSHO KK.  
XX DR WPI; 2000-264458/23.  
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and  
XX PT chronic continuous load of stress in a human being and its application  
XX Disclosure; Fig 6; 11pp; Japanese.  
XX This sequence represents the human heat shock protein SHSP70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX Sequence 554 AA;  
XX  
XX Query Match 92.2%; Score 47; DB 21; Length 554;  
XX Best Local Similarity 90.0%; Pred. No. 0.29;  
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 SLFEGIDLTYT 10  
XX ||||| ||  
XX 200 slfegidfty 209  
XX  
XX RESULT 8  
XX ID AAB23252 standard; Protein; 624 AA.  
XX AC AAB23252;  
XX DT 29-JAN-2001 (first entry)  
XX DE Human Hsp72 (heat shock protein 72).  
XX KW Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
XX KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
XX KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
XX KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX OS Homo sapiens.  
XX PN WO200054814-A1.  
XX PD 21-SEP-2000.  
XX PF 17-MAR-2000; 2000WO-US07350.  
XX PR 18-MAR-1999; 99US-0125046.  
XX PA (PHYL-) PHYLOGENY INC.  
XX PI Volloch VZ, Sherman M;  
XX DR WPI; 2000-647056/62.  
XX DR N-PSDB; AAA97541.  
XX PT Identifying compounds that inhibit proliferation of cells and capable  
XX PT of modulating the expression of heat shock protein 72 gene and/or  
XX PT activity of Hsp72 useful for treating cancers such as leukemia,  
XX PT lymphoma -  
XX PS Examples; Fig 16B; 77pp; English.  
XX  
XX The invention relates to a novel method of identifying compounds that  
XX inhibit proliferation of cells comprising contacting a test compound with  
XX a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
XX if the test compound inhibits activity or expression of Hsp72.  
XX Optionally, Hsp72 is contacted with the test compound under optimum  
XX conditions to allow the two components to interact and bind, forming a  
XX complex which is detected. The invention also relates to a method of  
XX identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
XX activation, comprising contacting a test compound with a cell which  
XX expresses Hsp72, exposing the cell to a heat induced stress and  
XX determining if the compound inhibits JNK phosphatase activity. The  
XX invention additionally encompasses compositions comprising an inhibitor  
XX of Hsp72 or JNK phosphatase activity. The compounds identified as  
XX inhibitors of Hsp72 or JNK phosphatase activity are useful for  
XX inhibiting the proliferation of cells. Modulation of the activity of the



CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.

XX Sequence 624 AA;

Query Match 92.2%; Score 47; DB 21; Length 624;

Best Local Similarity 90.0%; Pred. No. 0.33;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10

Db 286 slfegidlyt 295

RESULT 9

AAR03930

ID AAR03930 standard; Protein; 634 AA.

XX AC AAR03930;

XX DT 30-AUG-1990 (first entry)

XX DE Gallus gallus HSP (chkhsp70).

XX KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX OS Gallus gallus.

XX FH Key Location/Qualifiers

XX FT Misc-difference 634

XX FT /note= "residue given as "O" in specification"

XX PN WO9002564-A.

XX PD 22-MAR-1990.

XX PF 12-SEP-1989; 89WO-0003955.

XX PR 12-SEP-1988; 88US-0243474.

XX PA (CODON-) CODON.

XX PI Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used

XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has

XX 635 amino acid residues, the sequence itself has only 634,

XX including "O" (?) at position 634.

XX Fig. 2 provides an alignment of heat shock proteins from a variety

XX of organisms: 1. M.hypneumoniae (Mhyhsp70 - AAR03922);

XX 2. Bacillus megaterium (Bmebsp70 - AAR03923);

XX 3. E. coli (dnaK - AAR03924);

XX 4. T. cruzi (tc70kd - AAR03925);

XX 5. T. cruzi (AAR03926);

XX 6. Rat rattus (rathsp70 - AAR03927);

XX 7. Xenopus laevis (xl70 - AAR03928);

XX 8. Homo sapiens (humhsp70 - AAR03929);

XX 9. Gallus gallus (chkhsp70 - AAR03930);

XX 10. Zea mays (mzhsp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).

CC The proteins having homology to hsp's of T. cruzi can be used in

CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and

CC Mycobacteria species.

XX SQ Sequence 634 AA;

Query Match 92.2%; Score 47; DB 11; Length 634;

Best Local Similarity 90.0%; Pred. No. 0.34;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10

Db 289 slfegidlyt 298

RESULT 10

AAR03929

ID AAR03929 standard; Protein; 640 AA.

XX AC AAR03929;

XX DT 30-AUG-1990 (first entry)

XX DE Homo sapiens HSP (humhsp70).

XX KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 640

XX FT /note= "residue given as "O" in specification"

XX PN WO9002564-A.

XX PD 22-MAR-1990.

XX PF 12-SEP-1989; 89WO-0003955.

XX PR 12-SEP-1988; 88US-0243474.

XX PA (CODON-) CODON.

XX PI Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used

XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has

XX 641 amino acid residues, the sequence itself has only 640,

XX including "O" (?) at position 640.

XX Fig. 2 provides an alignment of heat shock proteins from a variety

XX of organisms: 1. M.hypneumoniae (Mhyhsp70 - AAR03922);

XX 2. Bacillus megaterium (Bmebsp70 - AAR03923);

XX 3. E. coli (dnaK - AAR03924);

XX 4. T. cruzi (tc70kd - AAR03925);

XX 5. T. cruzi (AAR03926);

XX 6. Rat rattus (rathsp70 - AAR03927);

XX 7. Xenopus laevis (xl70 - AAR03928);

XX 8. Homo sapiens (humhsp70 - AAR03929);

XX 9. Gallus gallus (chkhsp70 - AAR03930);

XX 10. Zea mays (mzhsp70 - AAR03931);

XX 11. Serratia marcescens (smahsp70 - AAR03932).

XX The proteins having homology to hsp's of T. cruzi can be used in

XX vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and

XX Mycobacteria species.



SQ Sequence 640 AA;

Query Match 92.2%; Score 47; DB 11; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLTY 10  
||||| ||  
Db 286 slfegidfty 295

RESULT 11

AAW10065  
ID AAW10065 standard; Protein; 640 AA.

XX AC AAW10065;

DT 24-OCT-1997 (first entry)

DE Human heat shock protein 70.

XX Human; heat shock protein 70; HSP70; primer; probe; detection;  
KW intracellular; abnormal transcription; acute; chronic; sustained;  
KW stress.

OS Homo sapiens.

XX JP08322577-A.

PN 10-DEC-1996.

XX 01-JUN-1995; 95JP-0158581.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 1997-081088/08.

DR N-PSDB; AAT58086.

XX Detection of abnormal transcription of HSP70 mRNA - using HSP70  
PT specific primer or probe, used in detection of human acute and  
PT chronic sustained stress load

XX Claim 1; Fig 1; 13pp; Japanese.

XX The cDNA encoding the present sequence, human heat shock protein 70  
CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
CC and 21. Primers and probes based on the HSP70 cDNA coding  
CC sequence can be used to detect the abnormal transcription of  
CC intracellular HSP70 mRNA in human acute and chronic sustained  
CC stress load.

SQ Sequence 640 AA;

Query Match 92.2%; Score 47; DB 18; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLTY 10  
||||| ||  
Db 286 slfegidfty 295

RESULT 12

AAB23653

ID AAB23653 standard; protein; 640 AA.

XX AC AAB23653;

XX 05-JAN-2001 (first entry)

DT

XX

DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

KW immune response; infectious disease; malaria; cytotoxic T cell;

KW cytostatic; immunostimulant; cellular immune response inducer;

KW protozoacide; leukaemia; cancer.

XX Homo sapiens.

XX WO200049041-A1.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000WO-JP00941.

XX 19-FEB-1999; 99JP-0041535.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Shinbara N, Uono H, Yui K;

XX WPI; 2000-543748/49.

XX Fused protein capable of inducing cellular immune response, useful as  
PT active ingredient for drug compositions in preventing and/or treating  
PT infectious diseases such as malaria or cancer -

XX Claim; 3; Page 49-52; 72pp; Japanese.

XX The present invention describes a fused protein (1) prepared from a  
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
CC cytotoxic T cells and a protein containing the ATPase domain of a heat  
CC shock protein. Also described are: (1) a drug composition containing (1)  
CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector  
CC containing the DNA of (2); and (4) a transfectant which can retain the  
CC expression vector of (3). (1) has cytostatic, immunostimulant and  
CC protozoacide activities, and can be used as a cellular immune response  
CC inducer. The protein is useful as an active ingredient for drug  
CC compositions in preventing and/or treating infectious diseases such as  
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
CC The present sequence represents a specifically claimed heat shock  
CC protein for use in a fused protein of the present invention.

XX Sequence 640 AA;

Query Match 92.2%; Score 47; DB 21; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLTY 10

||||| ||  
Db 286 slfegidfty 295

RESULT 13

AAV88408

ID AAV88408 standard; Protein; 640 AA.

XX AC AAV88408;

XX 31-JUL-2000 (first entry)

DT

XX Human heat shock protein HSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome.

XX Homo sapiens.

XX JP2000069999-A.

PN







XX Mammalian fertilisation decrease for detecting and treating  
PT infertility - using sulpho glyco lipid immobilising protein  
PT l-sulphated-glyco moiety interfering compsn., for mycoplasma  
PT infection treatment  
XX  
PS Claim 2 and Claim 17; Page 60-62; 77pp; English.  
XX  
CC The likelihood of mammalian fertilisation is decreased by contacting  
CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIPI)/  
CC sulphated glyco-moiety interfering composition. The interfering  
CC compsn. is e.g. the heat shock 70kd protein, SLIPI (or analogues  
CC such as the mouse SLIPI analogue "HSC70B" comprising the amino acid  
CC sequence AAR43002) or the 74.5kd mycoplasma protein (AAR43003).  
XX  
SQ Sequence 641 AA;  
  
Query Match 92.2%; Score 47; DB 14; Length 641;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDLYT 10  
Db ||||||| II  
286 slfegidlyt 295

Search completed: December 6, 2001, 08:04:04  
Job time: 612 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:04:04 ; Search time 184.09 seconds  
(without alignments)  
4.024 Million cell updates/sec

Title: PEP2-MOD8V

Perfect score: 51

Sequence: 1 SLFEGIDVYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	98.0	10	21	AA44200
2	50	98.0	10	22	AA97602
3	46	90.2	10	22	AA97603
4	46	90.2	554	21	AA98409
5	46	90.2	554	21	AA98410
6	46	90.2	554	21	AA98411
7	46	90.2	554	21	AA98412
8	46	90.2	554	21	AA98413
9	46	90.2	624	11	AA98414
10	46	90.2	634	11	AA98415
11	46	90.2	640	11	AA98416
12	46	90.2	640	18	AA98417

12	46	90.2	640	21	AA98418	Human heat shock p
13	46	90.2	640	21	AA98419	Human heat shock p
14	46	90.2	640	21	AA98420	Human heat shock p
15	46	90.2	641	14	AA98421	Mature mouse sperm
16	46	90.2	641	19	AA98422	Human heat shock 7
17	46	90.2	641	21	AA98423	Human heat shock p
18	46	90.2	641	22	AA98424	Human heat shock p
19	46	90.2	642	21	AA98425	Rat heat shock pro
20	46	90.2	642	21	AA98426	Xenopus laevis HSP
21	45	88.2	647	11	AA98427	Heat shock protein
22	45	88.2	9	21	AA98428	Heat shock protein
23	45	88.2	9	22	AA98429	Marmoset intracell
24	45	88.2	643	18	AA98430	Lung cancer associ
25	43	84.3	665	21	AA98431	Human secreted pro
26	43	84.3	91	21	AA98432	Human secreted pro
27	43	84.3	646	11	AA98433	Rat HSP (ratHSP70)
28	43	84.3	646	19	AA98434	Heat shock cognate
29	43	84.3	646	20	AA98435	Human heat shock c
30	43	84.3	646	20	AA98436	Mouse heat shock c
31	43	84.3	646	21	AA98437	Mouse heat shock p
32	43	84.3	646	21	AA98438	Human heat shock p
33	43	84.3	646	22	AA98439	Human heat shock p
34	43	84.3	556	18	AA98440	Candida albicans h
35	42	82.4	890	21	AA98441	GFP-HSC70 fusion p
36	42	82.4	214	19	AA98442	S. pneumoniae deri
37	42	82.4	221	19	AA98443	S. pneumoniae prot
38	39	76.5	633	14	AA98444	Mouse SLIP1 homolo
39	39	76.5	253	21	AA98445	Arabidopsis thalia
40	39	76.5	279	21	AA98446	Arabidopsis thalia
41	37	72.5	342	21	AA98447	Arabidopsis thalia
42	35	68.6	412	22	AA98448	S. avermitilis ORF
43	35	68.6	91	21	AA98449	Zea mays protein f
44	35	68.6	126	21	AA98450	Zea mays protein f
45	35	68.6	187	21	AA98451	Human pancreatic c
			620	11	AA98452	Serratia marcescen

#### ALIGNMENTS

RESULT 1

AA44200

ID AAY44200 standard; peptide; 10 AA.

XX

AC AAY44200;

XX

DT 15-FEB-2000 (first entry)

XX

DE Heat shock protein 70 amino acid residues 286-295.

XX

Human; heat shock protein 70; hsp70; identification; tumour; mutation;

T cell response; amplification; vector; bacterium; cancer; allele;

KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;

KW immune defence; immunogenicity; specificity; human leucocyte antigen.

OS Homo sapiens.

XX

PN WO954464-A1.

XX

PD 28-OCT-1999.

XX

PF 22-APR-1999; 99WO-FR00957.

XX

PR 22-APR-1998; 98FR-0005033.

XX

PA (INSR ) INST ROUSSY GUSTAVE.

XX

PI Triebel F, Gaudin C;

XX

DR WPI; 2000-013251/01.

XX

PT Identifying mutant peptides from heat-shock protein 70, for treatment

XX

of cancer -



PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-295 of the human  
CC heat shock protein 70 (hsp70). The invention relates to a method of  
CC identifying peptides, derived from hsp70 that stimulate a tumour-specific  
CC T cell response. Identification of the hsp70 peptides that have at least  
CC one mutation or alteration compared with the native sequence, and induce  
CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70  
CC encoding DNA from one or more tumours; (ii) cloning the amplified  
CC sequences into a vector that can be replicated in bacteria;  
CC (iii) sequencing fragments in each cultured bacterial colony to identify  
CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
CC mutant peptides identified. The peptides, optionally formulated with an  
CC agent that induces cellular stress, are used for treatment of cancer,  
CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
CC cancers of head and neck, particularly kidney cancer). The peptides may  
CC also be used to increase the proportion of tumour-specific cytotoxic  
CC T lymphocytes in a cell culture and/or induce these cells to secrete  
CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
CC tumour necrosis factor), particularly where the cells are used to  
CC stimulate immune defences. The method identifies peptides with high  
CC immunogenicity and high specificity for particular HLA (human leucocyte  
CC antigen) alleles.

XX Sequence 10 AA;

Query Match 98.0%; Score 50; DB 21; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.00052;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDVYT 10  
Db |||||:||  
1 slfegidiyt 10

#### RESULT 2

AAB97602  
ID AAB97602 standard; peptide; 10 AA.

XX AAB97602;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 2.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
KW cytotoxic response; epitope; antigen presenting cell; fragment 2.

XX Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
PT transformed human cells with induced and increased membrane expression  
PT of heat shock protein -

XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 2 relating to position 286-295 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates  
CC to lymphocytes which recognise cells of a patient in which overexpression  
CC of HSP has been induced. Overexpression of HSP leads to a substantial  
CC increase in the numbers of HSPs and HSP epitopes presented on the  
CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
CC response which kills the target cells. As a further embodiment of the  
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells, (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumour or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

XX Sequence 10 AA;

Query Match 98.0%; Score 50; DB 22; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.00052;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDVYT 10  
Db |||||:||  
1 slfegidiyt 10

#### RESULT 3

AAB97603  
ID AAB97603 standard; peptide; 10 AA.

XX AAB97603;

XX 30-JUL-2001 (first entry)

XX Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;  
KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;  
KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX Homo sapiens.

XX WO200129190-A1.

XX 26-APR-2001.

XX 29-SEP-2000; 2000WO-EP09530.

XX 15-OCT-1999; 99EP-0120484.

XX (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX Abastado JP, Bartholeyns J;

XX WPI; 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically  
PT transformed human cells with induced and increased membrane expression  
PT of heat shock protein -

XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
CC human heat shock protein 70 (HSP70) is given. The new invention relates  
CC to lymphocytes which recognise cells of a patient in which overexpression  
CC of HSP has been induced. Overexpression of HSP leads to a substantial  
CC increase in the numbers of HSPs and HSP epitopes presented on the  
CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
CC response which kills the target cells. As a further embodiment of the  
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen



CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells, (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumor or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

XX Sequence 10 AA;

SQ Query Match 90.2%; Score 46; DB 22; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.0035;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVYT 10

|||||||

Db 1 slfegidft 10

RESULT 4

AAAY88409  
ID AAY88409 standard; Protein; 554 AA.

XX AC AAY88409;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI; 2000-264458/23.

XX DR N-PSDB; AAA15621.

XX PT Abnormal transcription of intracellular HSP70mRNA under acute and

XX PT chronic continuous load of stress in a human being and its application

XX PT -

XX PS Examples; Fig 2; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
XX and 14q22-24. The invention relates to the abnormal transcription of  
XX intracellular HSP70mRNA under acute and chronic stress load in a human.  
XX The abnormal transcription of HSP70 can be used in the improvement of  
XX stress and response and diagnosis of stress diseases including  
XX rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 90.2%; Score 46; DB 21; Length 554;

Best Local Similarity 90.0%; Pred. No. 0.33;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVYT 10

|||||||

Db 200 slfegidft 209

RESULT 5

AAAY88410  
ID AAY88410 standard; Protein; 554 AA.

XX AC AAY88410;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.

XX PN JP2000069999-A.

XX PD 07-MAR-2000.

XX PF 01-JUN-1995; 99JP-0257146.

XX PR 01-JUN-1995; 95JP-0158581.

XX PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX DR WPI; 2000-264458/23.

XX DR N-PSDB; AAA15622.

XX PT Abnormal transcription of intracellular HSP70mRNA under acute and

XX PT chronic continuous load of stress in a human being and its application

XX PT -

XX PS Disclosure; Fig 3; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
XX and 14q22-24. The invention relates to the abnormal transcription of  
XX intracellular HSP70mRNA under acute and chronic stress load in a human.  
XX The abnormal transcription of HSP70 can be used in the improvement of  
XX stress and response and diagnosis of stress diseases including  
XX rheumatism, schizophrenia, depression and nephrotic syndrome.

XX SQ Sequence 554 AA;

Query Match 90.2%; Score 46; DB 21; Length 554;

Best Local Similarity 90.0%; Pred. No. 0.33;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVYT 10

|||||||

Db 200 slfegidft 209

RESULT 6

AAAY88412  
ID AAY88412 standard; Protein; 554 AA.

XX AC AAY88412;

XX DT 31-JUL-2000 (first entry)

XX DE Human heat shock protein SHSP70 amino acid sequence.

XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX KW depression; nephrotic syndrome; SHSP70.

XX OS Homo sapiens.



PN JP2000069999-A.  
XX 07-MAR-2000.  
XX  
XX 01-JUN-1995; 99JP-0257146.  
PF  
XX 01-JUN-1995; 95JP-0158581.  
PR  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
PA  
XX WPI; 2000-264458/23.  
DR  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
XX  
PS Disclosure; Fig 5; 11pp; Japanese.  
XX  
CC This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;  
SQ

Query Match 90.2%; Score 46; DB 21; Length 554;  
Best Local Similarity 90.0%; Pred. No. 0.33;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVYT 10  
DB 200 slfegidfyt 209  
|||||

RESULT 7  
AAY88413  
ID AAY88413 standard; Protein; 554 AA.  
XX  
AC AAY88413;  
XX  
DT 31-JUL-2000 (first entry)  
XX  
DE Human heat shock protein SHSP70 amino acid sequence.  
XX  
KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.  
XX  
OS Homo sapiens.  
XX  
PN JP2000069999-A.  
XX  
PD 07-MAR-2000.  
XX  
PF 01-JUN-1995; 99JP-0257146.  
XX  
PR 01-JUN-1995; 95JP-0158581.  
PA  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX  
DR WPI; 2000-264458/23.  
XX  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
XX  
PS Disclosure; Fig 6; 11pp; Japanese.  
XX  
CC This sequence represents the human heat shock protein SHSP70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
XX Sequence 554 AA;  
SQ

Query Match 90.2%; Score 46; DB 21; Length 554;  
Best Local Similarity 90.0%; Pred. No. 0.33;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVYT 10  
DB 200 slfegidfyt 209  
|||||

RESULT 8  
AAB23252  
ID AAB23252 standard; Protein; 624 AA.  
XX  
AC AAB23252;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human Hsp72 (heat shock protein 72).  
XX  
KW Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;  
KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
XX  
OS Homo sapiens.  
XX  
PN WO200054814-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-US07350.  
XX  
PR 18-MAR-1999; 99US-0125046.  
XX  
PA (PHYL-) PHYLOGENY INC.  
XX  
PI Volloch VZ, Sherman M;  
XX  
DR WPI; 2000-647056/62.  
DR N-PSDB; AAA97541.  
XX  
PT Identifying compounds that inhibit proliferation of cells and capable  
PT of modulating the expression of heat shock protein 72 gene and/or  
PT activity of Hsp72 useful for treating cancers such as leukemia,  
PT lymphoma  
XX  
XX Examples; Fig 16B; 77pp; English.  
XX  
XX The invention relates to a novel method of identifying compounds that  
CC inhibit proliferation of cells comprising contacting a test compound with  
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
CC if the test compound inhibits activity or expression of Hsp72.  
CC Optionally, Hsp72 is contacted with the test compound under optimum  
CC conditions to allow the two components to interact and bind, forming a  
CC complex which is detected. The invention also relates to a method of  
CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
CC activation, comprising contacting a test compound with a cell which  
CC expresses Hsp72, exposing the cell to a heat induced stress and  
CC determining if the compound inhibits JNK phosphatase activity. The  
CC invention additionally encompasses compositions comprising an inhibitor  
CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
CC inhibiting the proliferation of cells. Modulation of the activity of the



CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.  
 XX  
 SQ Sequence 624 AA;

Query Match 90.2%; Score 46; DB 21; Length 624;  
 Best Local Similarity 90.0%; Pred. No. 0.38;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
 Db 286 slfegidfyf 295  
 |||||

RESULT 9  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.  
 XX  
 AC AAR03930;

DT 30-AUG-1990 (first entry)  
 XX  
 DE Gallus gallus HSP (chkhsp70).  
 XX  
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Gallus gallus.

XX Key Location/Qualifiers  
 FH Misc-difference 634  
 FT /note= "residue given as "O" in specification"  
 FT  
 XX

PN WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has  
 CC 635 amino acid residues, the sequence itself has only 634,  
 CC including "O" (?) at position 634.

XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hyponeumoniae (Mhyhsp70 - AAR03922);

CC 2. Bacillus megaterium (Bmechsp70 - AAR03923);

CC 3. E. coli (dnaK - AAR03924);

CC 4. T. cruzi (tc70kd - AAR03925);

CC 5. T. cruzi (AAR03926);

CC 6. Rat rattus (rathsp70 - AAR03927);

CC 7. Xenopus laevis (xl70 - AAR03928);

CC 8. Homo sapiens (humhsp70 - AAR03929);

CC 9. Gallus gallus (chkhsp70 - AAR03930);

CC 10. Zea mays (mzehsp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.  
 XX  
 SQ Sequence 634 AA;

Query Match 90.2%; Score 46; DB 11; Length 634;  
 Best Local Similarity 90.0%; Pred. No. 0.39;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
 Db 289 slfegidfyf 298  
 |||||

RESULT 10  
 AAR03929  
 ID AAR03929 standard; Protein; 640 AA.  
 XX  
 AC AAR03929;

DT 30-AUG-1990 (first entry)

XX Homo sapiens HSP (humhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 640

FT /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has  
 CC 641 amino acid residues, the sequence itself has only 640,  
 CC including "O" (?) at position 640.

XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hyponeumoniae (Mhyhsp70 - AAR03922);

CC 2. Bacillus megaterium (Bmechsp70 - AAR03923);

CC 3. E. coli (dnaK - AAR03924);

CC 4. T. cruzi (tc70kd - AAR03925);

CC 5. T. cruzi (AAR03926);

CC 6. Rat rattus (rathsp70 - AAR03927);

CC 7. Xenopus laevis (xl70 - AAR03928);

CC 8. Homo sapiens (humhsp70 - AAR03929);

CC 9. Gallus gallus (chkhsp70 - AAR03930);

CC 10. Zea mays (mzehsp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).

CC The proteins having homology to hsp's of T. cruzi can be used in

CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and

CC Mycobacteria species.



SQ Sequence 640 AA;

Query Match 90.2%; Score 46; DB 11; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVYT 10  
||||| ||

Db 286 slfegidft 295

RESULT 11

AAW10065

ID AAW10065 standard; Protein; 640 AA.

XX AC AAW10065;

DT 24-OCT-1997 (first entry)

DE Human heat shock protein 70.

KW Human; heat shock protein 70; HSP70; primer; probe; detection;  
intracellular; abnormal transcription; acute; chronic; sustained;  
stress.

XX Homo sapiens.

OS JP08322577-A.

PN 10-DEC-1996.

PD 01-JUN-1995; 95JP-0158581.

PF 01-JUN-1995; 95JP-0158581.

PR (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 1997-081088/08.

DR N-PSDB; AAT58086.

PT Detection of abnormal transcription of HSP70 mRNA - using HSP70  
specific primer or probe, used in detection of human acute and  
chronic sustained stress load

PS Claim 1; Fig 1; 13pp; Japanese.

XX The cDNA encoding the present sequence, human heat shock protein 70  
(HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24  
and 21. Primers and probes based on the HSP70 cDNA coding  
sequence can be used to detect the abnormal transcription of  
intracellular HSP70 mRNA in human acute and chronic sustained  
stress load.

SQ Sequence 640 AA;

Query Match

Best Local Similarity 90.2%; Score 46; DB 18; Length 640;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVYT 10

Db 286 slfegidft 295

RESULT 12

AAB23653

ID AAB23653 standard; protein; 640 AA.

XX AC AAB23653;

XX DT 05-JAN-2001 (first entry)

XX

DE

XX

KW

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

XX

PI

XX

DR

XX

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
immune response; infectious disease; malaria; cytotoxic T cell;  
cytostatic; immunostimulant; cellular immune response inducer;  
protozoacide; leukaemia; cancer.

Homo sapiens.

WO200049041-A1.

24-AUG-2000.

18-FEB-2000; 2000WO-JP00941.

19-FEB-1999; 99JP-0041535.

(SUME) SUMITOMO ELECTRIC IND CO.

Shinbara N, Udono H, Yui K;

WPI; 2000-543748/49.

Fused protein capable of inducing cellular immune response, useful as  
active ingredient for drug compositions in preventing and/or treating  
infectious diseases such as malaria or cancer

Claim 3; Page 49-52; 72pp; Japanese.

The present invention describes a fused protein (I) prepared from a  
peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
cytotoxic T cells and a protein containing the ATPase domain of a heat  
shock protein. Also described are: (1) a drug composition containing (I)  
as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
containing the DNA of (2); and (4) a transformant which can retain the  
expression vector of (3). (I) has cytostatic, immunostimulant and  
protozoacide activities, and can be used as a cellular immune response  
inducer. The protein is useful as an active ingredient for drug  
compositions in preventing and/or treating infectious diseases such as  
malaria or cancer e.g. to provide systemic immunity against leukaemia.  
The present sequence represents a specifically claimed heat shock  
protein for use in a fused protein of the present invention.

Sequence 640 AA;

Query Match

Best Local Similarity 90.2%; Score 46; DB 21; Length 640;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVYT 10

Db 286 slfegidft 295

RESULT 13

AAV88408

ID AAV88408 standard; Protein; 640 AA.

XX AC AAV88408;

XX DT 31-JUL-2000 (first entry)

XX Human heat shock protein HSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;

XX depression; nephrotic syndrome.

XX Homo sapiens.

XX JP2000069999-A.

PN



XX 07-MAR-2000.  
PD 01-JUN-1995; 99JJP-0257146.  
PF 01-JUN-1995; 95JJP-0158581.  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX WPI; 2000-264458/23.  
DR N-PSDB; AAL15620.  
XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT -  
XX Claim 2; Fig 1; 1lpp; Japanese.  
PS This sequence represents the human heat shock protein HSP70 amino acid  
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX Sequence 640 AA;  
SQ

Query Match 90.2%; Score 46; DB 21; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVYT 10  
Db 286 slfegidfty 295

RESULT 14  
AAY88411  
ID AAY88411 standard; Protein; 640 AA.  
AC AAY88411;  
XX 31-JUL-2000 (first entry)  
DT Human heat shock protein LHP70 amino acid sequence.  
DE Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; LHP70.  
XX Homo sapiens.  
OS JP2000069999-A.  
PN 07-MAR-2000.  
PD 01-JUN-1995; 99JJP-0257146.  
XX 01-JUN-1995; 95JJP-0158581.  
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX WPI; 2000-264458/23.  
DR Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT -  
XX Disclosure; Fig 4; 1lpp; Japanese.  
PS This sequence represents the human heat shock protein LHP70 amino acid  
CC

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX Sequence 640 AA;  
SQ

Query Match 90.2%; Score 46; DB 21; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVYT 10  
Db 286 slfegidfty 295

RESULT 15  
AAR43004  
ID AAR43004 standard; protein; 641 AA.  
XX AAR43004;  
AC 20-MAY-1994 (first entry)  
DT Mature mouse sperm 70kD heat shock protein.  
DE Sulphoglycolipid immobilising protein 1; sperm plasma membrane;  
KW HSC70B; mammalian; infertility; mycoplasma; HSP70.  
XX Mus musculus.  
OS

Key Location/Qualifiers  
FH 1..385  
FT /label= 44kD\_ATPase\_fragment  
FT /note= "peptides comprising an intact domain from  
FT the ATPase fragment of hsp70 are claimed;  
FT the peptides are homologous to sequences  
FT conserved between SLIPI and 74.5kD  
FT mycoplasma protein"  
FT Domain 1..39  
FT /label= IA  
FT /note= "part"  
FT Domain 40..115  
FT /label= IB  
FT Domain 116..188  
FT /label= IA  
FT /note= "part"  
FT Domain 189..228  
FT /label= IIA  
FT /note= "part"  
FT Domain 229..306  
FT /label= IIB  
FT Domain 307..385  
FT /label= IIA  
FT /note= "part"  
XX WO9321954-A.  
PN 11-NOV-1993.  
PD 22-APR-1993; 93WO-US03816.  
XX 24-APR-1992; 92US-0873961.  
XX (BERL-) BERLEX LAB INC.  
XX (OTTA-) OTTAWA CIVIC HOSPITAL.  
XX Faulds DH, Lingwood CA, Tanphaichitr N;  
XX WPI; 1993-368422/46.  
DR



XX Mammalian fertilisation decrease for detecting and treating  
PT infertility - using sulpho glyco lipid immobilising protein  
PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
PT infection treatment  
XX  
PS Claim 2 and Claim 17; Page 60-62; 77pp; English.  
XX  
CC The likelihood of mammalian fertilisation is decreased by contacting  
CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/  
CC sulphated glyco-moiety interfering composition. The interfering  
CC compsn. is e.g. the heat shock 70kd protein, SLIP1 (or analogues  
CC such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid  
CC sequence AAR43002) or the 74.5kd mycoplasma protein (AAR43003).  
XX  
SQ Sequence 641 AA;

Query Match 90.2%; Score 46; DB 14; Length 641;  
Best Local Similarity 90.0%; Pred. NO. 0.39;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVYT 10  
| | | | | | | |  
Db 286 slfegidft 295

Search completed: December 6, 2001, 08:04:04  
Job time: 612 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:53:52 ; Search time 88.19 Seconds  
(without alignments)  
7.774 Million cell updates/sec

Title: US-09-673-795-1

Perfect score: 46

Sequence: 1 SLFEGIDY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	91.3	208	2 B44261	dnak-type molecule
2	42	91.3	278	2 I51344	dnak-type molecule
3	42	91.3	420	2 A26283	dnak-type molecule
4	42	91.3	467	2 T45477	heat-shock protein
5	42	91.3	467	2 T45479	heat-shock protein
6	42	91.3	468	2 T45476	heat-shock protein
7	42	91.3	469	2 T45478	heat-shock protein
8	42	91.3	617	2 H96605	probable heat shock
9	42	91.3	632	2 T45471	dnak-type molecule
10	42	91.3	634	2 A25646	dnak-type molecule
11	42	91.3	636	2 A48872	dnak-type molecule
12	42	91.3	638	2 S31766	dnak-type molecule
13	42	91.3	639	2 JCL391	dnak-type molecule
14	42	91.3	639	2 S20139	dnak-type molecule
15	42	91.3	640	1 HKW7A	dnak-type molecule
16	42	91.3	640	2 A29160	dnak-type molecule
17	42	91.3	640	2 S37394	dnak-type molecule
18	42	91.3	640	2 T21394	hypothetical prote
19	42	91.3	640	2 T43724	dnak-type molecule
20	42	91.3	641	2 S5357	dnak-type molecule
21	42	91.3	641	2 S35718	dnak-type molecule
22	42	91.3	641	2 I54542	dnak-type molecule
23	42	91.3	641	2 A45871	dnak-type molecule
24	42	91.3	642	1 HBYA1	dnak-type molecule
25	42	91.3	642	2 JHU095	dnak-type molecule
26	42	91.3	642	2 B36590	dnak-type molecule
27	42	91.3	644	2 A45635	dnak-type molecule
28	42	91.3	645	2 I51129	dnak-type molecule
29	42	91.3	646	2 T46650	heat shock protein

30	42	91.3	647	1 HHXL70	dnak-type molecule
31	42	91.3	647	2 S44168	dnak-type molecule
32	42	91.3	647	2 T41121	heat shock protein
33	42	91.3	650	2 JC7088	heat shock protein
34	41	89.1	209	2 A44261	dnak-type molecule
35	41	89.1	214	2 A03309	dnak-type molecule
36	41	89.1	372	2 P00138	dnak-type molecule
37	41	89.1	379	2 I46588	dnak-type molecule
38	41	89.1	467	2 T45473	heat-shock protein
39	41	89.1	467	2 T45474	heat-shock protein
40	41	89.1	641	2 JN0668	dnak-type molecule
41	41	89.1	641	2 PC7036	heat shock protein
42	41	89.1	643	2 S25585	dnak-type molecule
43	41	89.1	643	2 S09036	dnak-type molecule
44	41	89.1	651	2 T45517	heat shock protein
45	41	89.1	651	2 JC7132	heat shock protein

ALIGNMENTS

RESULT 1

B44261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KU>

A>Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

C:Gene: HSC70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 208;  
Best Local Similarity 88.9%; Pred. No. 0.42;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9

Db 132 SLFEGIDFY 140

RESULT 2

I51344

dnak-type molecular chaperone (clone pHS70.7) - rainbow trout (fragment)

N:Alternate names: 70K heat shock protein

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999

C:Accession: I51344

R:Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A:Title: 70-Kilodalton heat shock polypeptides from rainbow trout: Characterization o

A:Reference number: I51344; MUID:85036330

A:Accession: I51344

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-278 <OT>

A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70



C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 278;  
Best Local Similarity 88.9%; Pred. No. 0.58;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9  
|||||||  
Db 156 SLFEGIDFY 164

RESULT 3

A26283

dnak-type molecular chaperone - mouse (fragment)

N:Alternate names: heat shock protein 68

C:Species: Mus musculus (house mouse)

C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999

C:Accession: A26283

R:Lowe, D.G.; Moran, L.A.

J. Biol. Chem. 261, 2102-2112, 1986

A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he

A:Reference number: A26283; MUID:86111900

A:Accession: A26283

A:Molecule type: mRNA

A:Residues: 1-420 <LOW>

A:Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208

A:Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match

Best Local Similarity 91.3%; Score 42; DB 2; Length 420;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9

|||||||

Db 65 SLFEGIDFY 73

RESULT 4

T45477

heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

C:Species: Chondrosia reniformis

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45477

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45477

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match

Best Local Similarity 91.3%; Score 42; DB 2; Length 467;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9

|||||||

Db 252 SLFEGIDFY 260

RESULT 5

T45479

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C:Species: Eunicella cavolini

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45479

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45479

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match

Best Local Similarity 91.3%; Score 42; DB 2; Length 467;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9

|||||||

Db 252 SLFEGIDFY 260

RESULT 6

T45476

heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)

C:Species: Funiculina quadrangularis

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45476

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45476

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-468 <BOR>

A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match

Best Local Similarity 91.3%; Score 42; DB 2; Length 468;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9

|||||||

Db 253 SLFEGIDFY 261

RESULT 7

T45478

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C:Species: Eunicella cavolini

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45478

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45478

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-469 <BOR>

A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70



Query Match 91.3%; Score 42; DB 2; Length 469;  
 Best Local Similarity 88.9%; Pred. No. 1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9  
 |||||  
 Db 254 SLFEGIDFY 262

RESULT 8  
 H96605  
 probable heat shock protein [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
 C:Accession: H96605  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: H96605  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-617 <STO>  
 A:Cross-references: GB:AE005173; NID:g11024845; PIDN:AG26930.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: Fl3N6.9  
 A:Map position: 1  
 C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 617;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9  
 |||||  
 Db 292 SLFEGIDFY 300

RESULT 9  
 T45471  
 dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostellium discoideum)  
 N:Alternate names: heat shock cognate protein 70  
 C:Species: Dictyostellium discoideum  
 C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
 C:Accession: T45471  
 R:Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z22980  
 A:Accession: T45471  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-632 <BOV>  
 A:Cross-references: EMBL:AF025951; PIDN:AXB81865.1  
 A:Experimental source: strain AX3  
 C:Genetics:  
 A:Gene: hsc70  
 A:Note: localized to filopodias and cortex  
 C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 632;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9

Db 285 SLFEGIDFY 293  
 |||||  
 RESULT 10

A25646  
 dnaK-type molecular chaperone - chicken  
 N:Alternate names: heat shock protein 70  
 C:Species: Gallus gallus (chicken)  
 C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
 C:Accession: A25646  
 R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
 J. Biol. Chem. 261, 12692-12699, 1986  
 A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge  
 A:Reference number: A25646; MUID:86304452  
 A:Accession: A25646  
 A:Molecule type: DNA  
 A:Residues: 1-634 <MOR>  
 A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941  
 A:Note: the authors translated the codon TCG for residue 583 as Trp  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 634;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9  
 |||||  
 Db 289 SLFEGIDFY 297

RESULT 11  
 A48872  
 dnaK-type molecular chaperone hspB - slime mold (Dictyostellium discoideum) (fragment)  
 N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein  
 C:Species: Dictyostellium discoideum  
 C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
 C:Accession: A48872  
 R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
 J. Biol. Chem. 268, 23267-23274, 1993  
 A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with  
 A:Reference number: A48872; MUID:94043116  
 A:Accession: A48872  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-636 <EDD>  
 A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180  
 A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 636;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9  
 |||||  
 Db 280 SLFEGIDFY 288

RESULT 12  
 S31766  
 dnaK-type molecular chaperone hsp70 - green monkey  
 N:Alternate names: heat shock protein 70  
 C:Species: Cercopithecus aethiops (green monkey, grivet)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999



C:Accession: S31766; I36927  
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
submitted to the EMBL Data Library, January 1993  
A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
A:Reference number: S31766  
A:Accession: S31766  
A:Molecule type: mRNA  
A:Residues: 1-638 <SAI>  
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
FEBS Lett. 355, 282-286, 1994  
A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me  
A:Reference number: I36927; MUID:95080396  
A:Accession: I36927  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-638 <RES>  
A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
A:Experimental source: kidney; cell line COS-1  
C:Genetics:  
A:Gene: hsp70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein compl  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 638;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9  
|||||||  
Db 284 SLFEGIDFY 292

RESULT 13  
JC1391  
dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
N:Alternate names: heat shock protein 70IV; hsp70IV protein  
C:Species: Paracentrotus lividus (common urchin)  
C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
C:Accession: JC1391  
R:Sconzo, G.; Scardina, G.; Ferraro, M.G.  
Gene 121, 353-358, 1992  
A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
A:Reference number: JC1391; MUID:93077053  
A:Accession: JC1391  
A:Molecule type: DNA  
A:Residues: 1-639 <SCO>  
A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
C:Genetics:  
A:Gene: hsp70IV  
A:Introns: 61/2  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein compl  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 91.3%; Score 42; DB 2; Length 639;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9  
|||||||  
Db 286 SLFEGIDFY 294

RESULT 14  
S20139  
dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: heat shock protein YG102; protein L0971; protein YLL024c  
C:Species: saccharomyces cerevisiae

C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
C:Accession: S20139; S64772; S64775; S69383  
R:Slater, M.R.; Craig, E.A.  
Nucleic Acids Res. 17, 805-806, 1989  
A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
A:Reference number: S20139; MUID:89128457  
A:Accession: S20139  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-639 <SLA>  
A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
R:Goffeau, A.; Purnelle, B.  
submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64775  
A:Accession: S64775  
A:Molecule type: DNA  
A:Residues: 72-639 <DUE>  
A:Cross-references: EMBL:Z73129; MIPS:YLL024c  
A:Experimental source: strain S288C  
R:Purnelle, B.; Goffeau, A.  
submitted to the EMBL Data Library, April 1996  
A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals  
milly and a new ABC transporter homologous to the human multidrug resistance protein.  
A:Reference number: S69383  
A:Accession: S69383  
A:Molecule type: DNA  
A:Residues: 1-639 <PUR>  
A:Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007  
C:Genetics:  
A:Gene: SGD:SSA2  
A:Cross-references: MIPS:YLL024c; SGD:S0003947  
A:Map position: 12L  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 639;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9  
|||||||  
Db 283 SLFEGIDFY 291

RESULT 15  
HHKW7A  
dnak-type molecular chaperone hsp70A - Caenorhabditis elegans  
N:Alternate names: heat shock protein 70 A  
C:Species: Caenorhabditis elegans  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
C:Accession: JT0285  
R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
Gene 64, 241-255, 1988  
A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri  
A:Reference number: JT0285; MUID:88297155  
A:Accession: JT0285  
A:Molecule type: DNA; mRNA  
A:Residues: 1-640 <SNU>  
A:Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352  
A:Note: genomic clones representing six distinct members of the hsp70 gene family wer  
A:Note: transcripts of hsp70A are abundant in control worms and also increase two-to  
A:Note: one of the three introns in hsp70A is in a position similar to an intron in D



C:Genetics:  
A:Gene: hsp70A  
A:Map position: IV  
A:Introns: 69/1; 331/3; 558/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 91.3%; Score 42; DB 1; Length 640;  
Best Local Similarity 88.9%; Pred. NO. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIV 9  
|||||||  
Db 287 SLFEGIDFY 295

Search completed: December 6, 2001, 07:58:26  
Job time: 274 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:53:52 ; Search time 50.21 Seconds  
(without alignments)  
6.572 Million cell updates/sec

Title: US-09-673-795-1  
Perfect score: 46  
Sequence: 1 SLFEGIDIY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	91.3	322	1 HS70_ONCVO	P11503 onchocerca
2	42	91.3	420	1 HS73_MOUSE	Q61696 mus musculus
3	42	91.3	503	1 HS70_PENCI	Q92260 penicillium
4	42	91.3	634	1 HS70_CHICK	P08106 gallus gall
5	42	91.3	638	1 HS71_CERAE	Q28222 cercopithec
6	42	91.3	638	1 HS72_YEAST	P10592 saccharomyc
7	42	91.3	639	1 HS74_PARLI	Q06248 paracentrot
8	42	91.3	640	1 HS7A_CAEEL	P09446 caenorhabdi
9	42	91.3	640	1 HS7C_DICDI	P36415 dictyosteli
10	42	91.3	641	1 HS71_BOVIN	Q27975 bos taurus
11	42	91.3	641	1 HS71_MOUSE	P08107 homo sapien
12	42	91.3	641	1 HS71_MOUSE	P17879 mus musculu
13	42	91.3	641	1 HS71_PIG	P34930 sus scrofa
14	42	91.3	641	1 HS71_RAT	Q07439 rattus norv
15	42	91.3	641	1 HS71_YEAST	P10591 saccharomyc
16	42	91.3	641	1 HS72_BOVIN	Q27965 bos taurus
17	42	91.3	641	1 HS74_YEAST	P22202 saccharomyc
18	42	91.3	644	1 HS70_BRUMA	P27541 brugia mala
19	42	91.3	644	1 HS70_ONCTS	Q91233 oncorhynch
20	42	91.3	645	1 HS70_PLEWA	Q91291 pleurodeles
21	42	91.3	646	1 HS70_NEUCR	Q01233 neurospora
22	42	91.3	647	1 HS70_XENLA	P02827 xenopus lae
23	42	91.3	649	1 HS70_BLAEM	P48720 blastoclad
24	42	91.3	652	1 HS7D_WANSE	Q9u639 manduca sex
25	41	89.1	214	1 HS7A_DROSI	P02826 drosophila
26	41	89.1	372	1 HS72_PARLI	P22623 paracentrot
27	41	89.1	379	1 HS7X_PIG	P34934 sus scrofa
28	41	89.1	638	1 HS70_CERCA	P91902 ceratitis c
29	41	89.1	641	1 HS7A_DROME	P29843 drosophila
30	41	89.1	643	1 HS76_HUMAN	P17066 homo sapien
31	41	89.1	643	1 HS76_PIG	Q04967 sus scrofa
32	41	89.1	648	1 HS71_PUCGR	Q01877 puccinia gr
33	39	84.8	641	1 HS73_RAT	P55063 rattus norv

34	39	84.8	641	1 HS7H_HUMAN	P34931 homo sapien
35	39	84.8	641	1 HS7T_MOUSE	P16627 mus musculus
36	39	84.8	642	1 HS72_PICAN	P53623 pichia angu
37	39	84.8	643	1 HS71_SCHPO	Q10265 schizosacch
38	39	84.8	644	1 HS71_PICAN	P53421 pichia angu
39	39	84.8	644	1 HS72_LYCES	P27322 lycopersico
40	39	84.8	645	1 HS70_SOYBN	P26413 glycine max
41	39	84.8	646	1 HS7C_CRIGR	P19378 cricetulus
42	39	84.8	646	1 HS7C_HUMAN	P11142 homo sapien
43	39	84.8	646	1 HS7C_MOUSE	P08109 mus musculus
44	39	84.8	649	1 HS70_PARBR	P87047 paracoccidi
45	39	84.8	649	1 HS73_ARATH	O65719 arabidopsis

## ALIGNMENTS

RESULT 1					
HS70_ONCVO STANDARD; PRT; 322 AA.					
AC	P11503;				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).				
OS	Onchocerca volvulus.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;				
OC	Onchocercidae; Onchocerca.				
OX	NCBI_TaxID=6282;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89201313; PubMed=2704388;				
RA	Rothstein N.M., Higashi G., Yates J., Rajan T.V.;				
RT	"Onchocerca volvulus heat shock protein 70 is a major immunogen in amicrofilaremic individuals from a filariasis-endemic area.";				
RL	Mol. Biochem. Parasitol. 33:229-236(1989).				
CC	-!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.				
CC	-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; J04006; AAA29417.1; -				
DR	HSSP; P19120; IATR.				
DR	InterPro; IPR001023; HSP70.				
DR	Pfam; PF00012; HSP70; 1.				
DR	PROSITE; PS00297; HSP70.1; PARTIAL.				
DR	PROSITE; PS00329; HSP70.2; PARTIAL.				
DR	PROSITE; PS01036; HSP70.3; 1.				
KW	ATP-binding; Heat shock.				
FT	NON_TER 322 322				
FT	NON_TER 322 322				
SQ	SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;				

Query Match 91.3%; Score 42; DB 1; Length 322;  
Best Local Similarity 88.9%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9  
|||||||

DB 43 SLFEGIDFY 51

RESULT 2  
HS73\_MOUSE STANDARD; PRT; 420 AA.



Tue Dec 11 08:46:05 2001

AC Q61696; Q61697;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).  
 GN HSP70-3 OR HSP70A1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=86111900; PubMed=2868009;  
 RA Lowe D.G., Moran L.A.;  
 RT "Molecular cloning and analysis of DNA complementary to three mouse  
 RT M1 = 68,000 heat shock protein mRNAs.";  
 RL J. Biol. Chem. 261:2102-2112(1986).  
 RN [2]  
 RP SEQUENCE OF 155-420 FROM N.A.  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";  
 RL Gene 146:273-278(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC EMBL; M12571; AAA57234.1; -  
 CC HSP; P19120; 1ATR.  
 CC MGI; 96244; Hsp70-3.  
 CC InterPro; IPR001023; HSP70.  
 CC Pfam; PF00012; HSP70; 1.  
 CC PROSITE; PS00297; HSP70\_1; PARTIAL.  
 CC PROSITE; PS00329; HSP70\_2; PARTIAL.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Multigene family.  
 KW NON-TER 188 V -> G.  
 FT VARIANT 420 AA; 46292 MW; 5DAlC6155C7B16B5 CRC64;  
 SQ SEQUENCE 420 AA; 46292 MW; 5DAlC6155C7B16B5 CRC64;  
 CC  
 CC Query Match 91.3%; Score 42; DB 1; Length 420;  
 CC Best Local Similarity 88.9%; Pred. No. 0.51; Indels 0; Gaps 0;  
 CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC QY 1 SLFEGIDIV 9  
 CC |||||  
 CC DB 65 SLFEGIDFY 73  
 CC  
 CC RESULT 3  
 CC HS70\_PENCI STANDARD; PRT; 503 AA.  
 CC AC Q92260;  
 CC DT 20-AUG-2001 (Rel. 40, Created)  
 CC DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
 GN HSP70.  
 OS Penicillium citrinum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
 OX NCBI\_TaxID=5077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;  
 RT "Molecular cloning and expression of a Penicillium citrinum  
 RT allergen with sequence homology and antigenic cross-reactivity to  
 RT a hsp70 human heat shock protein.";  
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC EMBL; U64207; AAB06397.1; -  
 CC HSP; P19120; 3HSC.  
 CC InterPro; IPR001023; HSP70.  
 CC Pfam; PF00012; HSP70; 1.  
 CC PRINTS; PR00301; HEATSHOCK70.  
 CC PROSITE; PS00329; HSP70\_2; 1.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Allergen.  
 KW NON-TER 1  
 FT VARIANT 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;  
 SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;  
 CC  
 CC Query Match 91.3%; Score 42; DB 1; Length 503;  
 CC Best Local Similarity 88.9%; Pred. No. 0.62; Indels 0; Gaps 0;  
 CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC QY 1 SLFEGIDIV 9  
 CC |||||  
 CC DB 154 SLFEGIDFY 162  
 CC  
 CC RESULT 4  
 CC HS70\_CHICK STANDARD; PRT; 634 AA.  
 CC ID HS70\_CHICK  
 CC AC P08106;  
 CC DT 01-AUG-1988 (Rel. 08, Created)  
 CC DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 CC DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 CC DE HEAT SHOCK 70 KDA PROTEIN (HSP70).  
 CC OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC OX NCBI\_TaxID=9031;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=86304452; PubMed=3017985;  
 CC Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
 CC "Organization, nucleotide sequence, and transcription of the chicken  
 CC HSP70 gene.";  
 CC J. Biol. Chem. 261:12692-12699(1986).  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC -----
DR EMBL: J02579; AAA48825.1; -.
DR PIR: A25646; A25646.
DR HSSP: P19120; IATR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 91.3%; Score 42; DB 1; Length 634;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDYIY 9
Db 289 SLFEGIDFY 297

RESULT 5
HS7L_CERAE
ID HS7L_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7986960;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDiate THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES, THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL: X70684; CAA50019.1; -.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.

DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family; MHC III.
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 638;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDYIY 9
Db 284 SLFEGIDFY 292

RESULT 6
HS72_YEAST
ID HS72_YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YLL024C OR L0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Purnelle B., Goffeau A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 71-638 FROM N.A.
RA Dueterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Nordbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
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CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X12927; CAA31394.1; -.
CC EMBL: Z73129; CAA97472.1; -.
CC EMBL: X97560; CAA66167.1; -.
CC PIR: S20139; S20139.
CC HSSP: P19120; INGI.
CC SWISS-2DPAGE: P10592; YEAST.
CC YEPD: 9800; -.
CC SGD: S0003947; SSA2.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70; 1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT-MET 0 1
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 638;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYI 9
Db 282 SLFEGIDFY 290
|||||||

RESULT 7
HS74_PARLI STANDARD; PRT; 639 AA.
ID HS74_PARLI STANDARD; PRT; 639 AA.
AC Q06248;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
GN HSP70IV.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus
OC NCBI_TaxID=7656;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
RL lividus hsp70 gene family and its expression."
Gene 121:353-358(1992).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: X61379; CAA43653.1; -.
CC
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DR PIR: JC1391; JC1391.
DR HSSP: P19120; INGI.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 91.3%; Score 42; DB 1; Length 639;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYI 9
Db 286 SLFEGIDFY 294
|||||||

RESULT 8
HS7A_CAEEL STANDARD; PRT; 640 AA.
ID HS7A_CAEEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1/OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
RL characterization."
Gene 64:241-255(1988).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: M18540; AAA28078.1; -.
DR PIR: JTO285; HHKW7A.
DR HSSP: P19120; INGI.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYI 9
Db 287 SLFEGIDFY 295
|||||||
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RESULT 9
HS7C_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AX3;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RT cap32/34."
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN=AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauter R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium."
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; X75263; CAA53039.1; -
DR EMBL; L22736; AAA33219.1; -
DR PIR; S37394; S37394.
DR HSP; P19120; INGJ.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDB; DDO1078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone.
KW CONFLICT 1 29
FT FT
FT HHHHNGNATVWVESGPVSEVLSFN (IN REF. 2).
FT N -> T (IN REF. 2).
FT V -> A (IN REF. 2).
FT R -> A (IN REF. 2).
FT S -> A (IN REF. 2).
FT V -> L (IN REF. 2).
FT I -> L (IN REF. 2).
FT F -> P (IN REF. 2).
FT MSSIGIDLGTTCYSCVGMQNDREVIAND ->
FT CONFLICT 1 29
FT FT
FT CONFLICT 32 32
FT CONFLICT 64 64
FT CONFLICT 180 180
FT CONFLICT 237 237
FT CONFLICT 240 240
FT CONFLICT 341 341
FT CONFLICT 352 352
FT SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;
FT FT
FT Query Match 91.3%; Score 42; DB 1; Length 640;

Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIIY 9
DB 284 SLFEGIDIFY 292
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RESULT 10
HS7L_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerriero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RX STRAIN=ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An AluI polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus."
RL Anim. Genet. 25:196-196(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; U09861; AAA73914.1; -
DR EMBL; U02891; AAA03450.1; -
DR HSP; P19120; INGC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
SQ
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Query Match          91.3%; Score 42; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
Db 286 SLFEGIDIFY 294

RESULT 11
HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQMO; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91055806; PubMed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Hunt C., Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
[3]
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RX MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
[5]
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RX MEDLINE=87066768; PubMed=3786141;
RA Drabant B., Genthe A., Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RX MEDLINE=99234376; PubMed=10216320;
RA Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES

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CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; M59828; AAA63226.1; --
DR EMBL; M59830; AAA63227.1; --
DR EMBL; AF134726; AAD21816.1; --
DR EMBL; AF134726; AAD21815.1; --
DR EMBL; M11717; AAA52697.1; --
DR EMBL; M24743; AAA59844.1; --
DR EMBL; M24744; AAA59845.1; --
DR EMBL; X04676; CAA28381.1; --
DR EMBL; X04677; CAA28382.1; --
DR PIR; A29160; A29160.
DR PIR; A45871; A45871.
DR PIR; A25773; A25773.
DR PDB; 1HJO; 21-OCT-98.
DR SWISS-2DPAGE; P08107; HUMAN.
DR MIM; 140550; --
DR MIM; 603012; --
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
KW 3D-structure. 7 7 I -> V (IN REF. 2).
FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).
FT CONFLICT 370 370 A -> G (IN REF. 2).
FT CONFLICT 469 469 MISSING (IN REF. 2).
FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).
SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;

Query Match          91.3%; Score 42; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIIY 9
Db 286 SLFEGIDIFY 294

RESULT 12
HS71_MOUSE STANDARD; PRT; 641 AA.
AC P17879; Q61689;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN HSPAL OR HSP70A1 OR HSP70-1 OR HCP70.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169;
RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
RT expression in mouse cell lines.";

```







RX MEDLINE-94368874; PubMed-8086479;  
 RA Lisowska K., Krawczyk Z., Widiak W., Wolnicz P., Wisniewski J.;  
 RT "Cloning, nucleotide sequence and expression of rat heat inducible  
 hsp70 gene.";  
 RL Biochim. Biophys. Acta 1219:64-72(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC EMBL; LI6764; AAA17441.1; -;  
 CC EMBL; X77208; CAA54423.1; -;  
 CC EMBL; X77207; CAA54422.1; -;  
 CC EMBL; X74271; CAA52328.1; -;  
 CC HSSP; P19120; INGC.  
 CC InterPro; IPR001023; HSP70.  
 CC Pfam; PF00012; HSP70; 1.  
 CC PRINTS; PR00301; HEATSHOCK70.  
 CC PROSITE; PS00297; HSP70\_1; 1.  
 CC PROSITE; PS00329; HSP70\_2; 1.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
 CC CONFLICT 71 72 KR -> NG (IN REF. 3).  
 CC CONFLICT 227 227 D -> H (IN REF. 2 AND 3).  
 CC CONFLICT 408 408 G -> A (IN REF. 3).  
 CC SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;  
 Query Match 91.3%; Score 42; DB 1; Length 641;  
 Best Local Similarity 88.9%; Pred. No. 0.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 SLFEGIDY 9  
 Db 286 SLFEGIDY 294  
 RESULT 15  
 HS71\_YEAST  
 ID HS71\_YEAST STANDARD; PRT; 641 AA.  
 AC P10591;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE HEAT SHOCK PROTEIN SSAL (HEAT SHOCK PROTEIN YG100).  
 OS SSAL OR YAL005C.  
 GN Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C;  
 RX MEDLINE-89128457; PubMed-2644626;  
 RA Slater M.R., Craig E.A.;  
 RT "The SSAL and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
 RL Nucleic Acids Res. 17:805-806(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-S288C / AB972;  
 RX MEDLINE-95028152; PubMed-79411740;  
 RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,  
 RT Delaney S., Ouellette B.F., Barton A.B., Kaback D.B., Bussey H.;  
 RL "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of  
 the 42 kbp SP07-CENT-CDCL5 region.";  
 RT Yeast 10:535-541(1994).  
 RN [3]  
 RP SEQUENCE OF 590-641 FROM N.A.  
 RX MEDLINE-85087943; PubMed-6096826;  
 RA Ogden R.C., Lee M.-C., Knapp G.;  
 RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the  
 RT substrates.";  
 RL Nucleic Acids Res. 12:9367-9382(1984).  
 RN [4]  
 RP REVISIONS TO 207; 417 AND 421.  
 RA Slater M.R.;  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 91-97 AND 325-341.  
 RX STRAIN-S288C;  
 RL MEDLINE-95203288; PubMed-7895733;  
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RT Volpe T., Warner J.R., McLaughlin C.S.;  
 RL "Protein identifications for a Saccharomyces cerevisiae protein  
 RL database.";  
 RL Electrophoresis 15:1466-1486(1994).  
 RN [6]  
 RP SEQUENCE OF 186-195.  
 RX STRAIN-ATCC 38531 / Y41;  
 RL MEDLINE-97089742; PubMed-8935650;  
 RA Norbeck J., Blomberg A.;  
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
 RL Saccharomyces cerevisiae.";  
 RL FEMS Microbiol. Lett. 137:1-8(1996).  
 RN [7]  
 RP ACETYLATION.  
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RT Volpe T., Warner J.R., McLaughlin C.S.;  
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: SSAL MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
 CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
 CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
 CC SSAL AND SSA2 PROTEINS IS EXPECTED. SSAL CAN PARTICIPATE IN THE  
 CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 CC EMBL; X12926; CAA31393.1; -;  
 CC EMBL; L22015; AAC04952.1; ALT\_SEQ.  
 CC PIR; S25438; HHBYA1.  
 CC PIR; S42164; S42164.  
 CC HSSP; P19120; INTR.  
 CC SWISS-2DPAGE; P10591; YEAST.  
 CC YEPD; 9788; -;  
 CC SGD; S0000004; SSAL.  
 CC InterPro; IPR001023; HSP70.  
 CC Pfam; PF00012; HSP70; 1.  
 CC PRINTS; PR00301; HEATSHOCK70.  
 CC PROSITE; PS00297; HSP70\_1; 1.  
 CC PROSITE; PS00329; HSP70\_2; 1.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC Heat shock; ATP-binding; Multigene family; Acetylation.  
 KW INIT\_MET 0 0  
 FT MOD\_RES 1 1 ACETYLATION.  
 RP



SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

Query Match 91.3%; Score 42; DB 1; Length 641;  
Best Local Similarity 88.9%; Pred. No. 0.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 9  
| | | | | | |  
Db 282 SLFEGIDFY 290

Search completed: December 6, 2001, 08:00:50  
Job time: 418 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:53:52 ; Search time 170.25 Seconds  
(without alignments)  
7.732 Million cell updates/sec

Title: US-09-673-795-1  
Perfect score: 46  
Sequence: 1 SLFEGIDY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_17.\*  
1: sp.archaea.\*  
2: sp.bacteria.\*  
3: sp.fungi.\*  
4: sp.human.\*  
5: sp.invertebrate.\*  
6: sp.mammal.\*  
7: sp.mhc.\*  
8: sp.organelle.\*  
9: sp.phage.\*  
10: sp.plant.\*  
11: sp.rodent.\*  
12: sp.virus.\*  
13: sp.vertebrate.\*  
14: sp.unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42	91.3	146	5 Q9U667	Q9U667 littorina p
2	42	91.3	153	5 Q9U670	Q9U670 littorina s
3	42	91.3	155	5 Q9U669	Q9U669 littorina s
4	42	91.3	157	5 Q9U665	Q9U665 littorina p
5	42	91.3	158	5 Q9U671	Q9U671 littorina s
6	42	91.3	158	5 Q9U668	Q9U668 littorina p
7	42	91.3	158	5 Q9U666	Q9U666 littorina p
8	42	91.3	220	5 P81159	P81159 aplysia cal
9	42	91.3	278	13 Q90520	Q90520 oncorhynch
10	42	91.3	367	13 Q98899	Q98899 fugu rubrip
11	42	91.3	455	11 Q63718	Q63718 rattus norv
12	42	91.3	467	5 O44350	O44350 chondrosia
13	42	91.3	467	5 O44352	O44352 petrobiona
14	42	91.3	467	5 Q9NJ92	Q9NJ92 guancha lac
15	42	91.3	468	5 O44349	O44349 funiculina
16	42	91.3	469	5 O44351	O44351 eunicella c
17	42	91.3	526	13 Q98897	Q98897 fugu rubrip
18	42	91.3	617	10 Q9C7X7	Q9C7X7 arabidopsis
19	42	91.3	628	5 Q93147	Q93147 botryllus s

20	42	91.3	629	5 Q93146	Q93146 botryllus s
21	42	91.3	632	5 O15766	O15766 dictyosteli
22	42	91.3	639	13 Q98900	Q98900 fugu rubrip
23	42	91.3	639	13 Q918F9	Q918F9 oryzias lat
24	42	91.3	640	5 Q93601	Q93601 caenorhabdi
25	42	91.3	640	13 Q93240	Q93240 paralichthy
26	42	91.3	641	11 O63256	O63256 rattus norv
27	42	91.3	641	11 Q9QWJ5	Q9QWJ5 mus musculu
28	42	91.3	645	5 O96541	O96541 setaria dig
29	42	91.3	645	5 Q9NJB7	Q9NJB7 wuchereria
30	42	91.3	645	5 Q9NGK9	Q9NGK9 wuchereria
31	42	91.3	645	10 O48563	O48563 brassica na
32	42	91.3	647	3 O59855	O59855 schizosacch
33	42	91.3	647	10 Q41027	Q41027 pisum sativ
34	42	91.3	650	5 Q9U777	Q9U777 stylophora
35	42	91.3	650	10 Q9ZS55	Q9ZS55 arabidopsis
36	42	91.3	650	10 Q9LHA8	Q9LHA8 arabidopsis
37	42	91.3	652	10 P93937	P93937 ascophyllum
38	42	91.3	653	5 Q94805	Q94805 trichoplusi
39	42	91.3	659	5 Q9XZJ2	Q9XZJ2 crassostrea
40	41	89.1	190	5 Q9U9B4	Q9U9B4 mytilus edu
41	41	89.1	221	5 P81157	P81157 aplysia cal
42	41	89.1	467	5 O44346	O44346 asbestoplum
43	41	89.1	467	5 O44347	O44347 petrosia fi
44	41	89.1	467	5 Q9GPM5	Q9GPM5 monosiga ov
45	41	89.1	639	13 O73922	O73922 oreochromis

## ALIGNMENTS

RESULT 1  
Q9U667 ID Q9U667 PRELIMINARY; PRT; 146 AA.  
AC Q9U667;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191828; AAF12787.1;  
DR HSSP; FL9120; LBA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 146  
SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

Query Match 91.3%; Score 42; DB 5; Length 146;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDY 9  
Db 79 SLFEGIDY 87

RESULT 2  
Q9U670 ID Q9U670 PRELIMINARY; PRT; 153 AA.  
AC Q9U670;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)



DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 GN HEAT-SHOCK PROTEIN (FRAGMENT).  
 DE HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191825; AAF12784.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 153  
 SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 91.3%; Score 42; DB 5; Length 153;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
 QY 1 SLFEGIDY 9  
 DB 80 SLFEGIDFY 88  
 RESULT 3  
 Q9U669 ID Q9U669 PRELIMINARY; PRT; 155 AA.  
 AC Q9U669  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191826; AAF12785.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 155  
 SQ SEQUENCE 155 AA; 17676 MW; C191F65B1F346C2 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 155;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
 QY 1 SLFEGIDY 9  
 DB 82 SLFEGIDFY 90  
 RESULT 4  
 Q9U665 ID Q9U665 PRELIMINARY; PRT; 157 AA.  
 AC Q9U665  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191830; AAF12789.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 157;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
 QY 1 SLFEGIDY 9  
 DB 84 SLFEGIDFY 92  
 RESULT 5  
 Q9U671 ID Q9U671 PRELIMINARY; PRT; 158 AA.  
 AC Q9U671  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191824; AAF12783.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 91.3%; Score 42; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
 QY 1 SLFEGIDY 9  
 DB 85 SLFEGIDFY 93  
 RESULT 6  
 Q9U668 ID Q9U668 PRELIMINARY; PRT; 158 AA.  
 AC Q9U668  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

Query Match 91.3%; Score 42; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;  
 QY 1 SLFEGIDY 9  
 DB 85 SLFEGIDFY 93  
 RESULT 6  
 Q9U668 ID Q9U668 PRELIMINARY; PRT; 158 AA.  
 AC Q9U668  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)



DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191827; AAF12786.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 91.3%; Score 42; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYI 9  
 |||||  
 Db 85 SLFEGIDFY 93

RESULT 7  
 Q90666 PRELIMINARY; PRT; 158 AA.  
 AC Q90666;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191829; AAF12788.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 91.3%; Score 42; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYI 9  
 |||||  
 Db 85 SLFEGIDFY 93

RESULT 8  
 P81159 PRELIMINARY; PRT; 220 AA.  
 ID P81159  
 AC P81159;  
 DT 01-JUN-1998 (TReMBLrel. 06, Created)

DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93077669; PubMed=1360013;  
 RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 the expression of BiP, the major protein chaperon of the ER.";  
 RL J. Cell Biol. 119:1069-1076(1992).  
 CC -I- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15039; CAA78757.1; -.  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 220 220  
 SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 91.3%; Score 42; DB 5; Length 220;  
 Best Local Similarity 88.9%; Pred. No. 2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYI 9  
 |||||  
 Db 138 SLFEGIDFY 146

RESULT 9  
 Q90520 PRELIMINARY; PRT; 278 AA.  
 ID Q90520;  
 AC Q90520;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=85036330; PubMed=6092938;  
 RA Kothary R.K., Jones D., Candido E.P.M.;  
 RT "70-Kilodalton heat shock polypeptides from rainbow trout:  
 characterization of cDNA sequences.";  
 RL Mol. Cell. Biol. 4:1785-1791(1984).  
 DR EMBL; K02549; AAA49562.1; -.  
 DR HSSP; P08109; 1CKR.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 278 278  
 SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 91.3%; Score 42; DB 13; Length 278;



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Best Local Similarity 88.9%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
Db 156 SLFEGIDFY 164

RESULT 10
Q98899 ID Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
GN HSP70-3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RN SEQUENCE FROM N.A.
RP Lim E.H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08578; CAA69892.1; -.
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.
FT NON_TER 367 367
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;

Query Match 91.3%; Score 42; DB 13; Length 367;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
Db 268 SLFEGIDFY 276

RESULT 11
Q63718 ID Q63718 PRELIMINARY; PRT; 455 AA.
AC Q63718;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT SHOCK ROTEN 70 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA D'Ambrosio E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z27118; CAA81642.1; -.
DR HSP; P08107; 1HJO.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.

Best Local Similarity 88.9%; Score 42; DB 5; Length 467;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
Db 252 SLFEGIDFY 260

RESULT 13
Q44352 ID Q44352 PRELIMINARY; PRT; 467 AA.
AC Q44352;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massilliana.
OC Eukaryota; Metazoa; Porifera; Calcareia; Calcaronea; Petroblionidae;
OC Petroblion.
OX NCBI_TaxID=68578;
RN [1]
RN SEQUENCE FROM N.A.
RP Borchhiellini C., Le Parco Y.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
FT NON_TER 467 467
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2B6EA96 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 467;
Best Local Similarity 88.9%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIY 9
Db 252 SLFEGIDFY 260

RESULT 13
Q44352 ID Q44352 PRELIMINARY; PRT; 467 AA.
AC Q44352;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massilliana.
OC Eukaryota; Metazoa; Porifera; Calcareia; Calcaronea; Petroblionidae;
OC Petroblion.
OX NCBI_TaxID=68578;
RN [1]
RN SEQUENCE FROM N.A.
RP Borchhiellini C., Le Parco Y.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.

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DR PRINTS; PRO0301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 467;  
Best Local Similarity 88.9%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIY 9  
|||||||  
Db 252 SLFEGIDFY 260

## RESULT 14

Q9NJ92 PRELIMINARY; PRT; 467 AA.

AC Q9NJ92;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
OS Guancha lacunosa.  
OC Eukaryota; Metazoa; Porifera; Calcarea; Clathrinida;  
OC Clathrinidae; Guancha.  
OX NCBI\_TaxID=115120;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Borchelli C., Le Parco Y.;  
RT "Sponges paraphyly and the origin of Metazoa."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF182195; AAF61297.1; -  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PRO0301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51318 MW; F36FC06CBIDEI131 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 467;  
Best Local Similarity 88.9%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIY 9  
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Db 252 SLFEGIDFY 260

## RESULT 15

O44349 PRELIMINARY; PRT; 468 AA.

AC O44349;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
GN HSP70.  
OS Funiculina quadrangularis.  
OC Eukaryota; Metazoa; Chldaria; Anthozoa; Alcyonaria; Funiculinidae;  
OC Funiculina.  
OX NCBI\_TaxID=68568;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borchelli C., Le Parco Y.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF026516; AAC05361.1; -  
DR HSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PRO0301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; UNKNOWN\_1.  
FT NON\_TER 1  
FT NON\_TER 468  
SQ SEQUENCE 468 AA; 51533 MW; EDED2B4699283FBC CRC64;

Query Match 91.3%; Score 42; DB 5; Length 468;  
Best Local Similarity 88.9%; Pred. No. 4.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIY 9  
|||||||  
Db 253 SLFEGIDFY 261

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Job time: 180 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:53:52 ; Search time 81.43 seconds  
(without alignments)  
2.487 Million cell updates/sec

Title: US-09-673-795-1  
Perfect score: 46  
Sequence: 1 SLFEGIDYIY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	89.1	643	4	US-08-797-358B-3
2	39	84.8	646	1	US-08-441-139-14
3	32	69.6	452	1	US-08-290-978A-5
4	32	69.6	452	2	US-08-780-869-5
5	32	69.6	458	4	US-09-457-046B-61
6	31	67.4	99	1	US-08-438-753B-22
7	31	67.4	99	1	US-08-443-883A-22
8	31	67.4	99	2	US-08-631-328-22
9	31	67.4	99	2	US-08-455-524B-22
10	31	67.4	99	2	US-08-455-021B-22
11	31	67.4	99	4	US-09-045-467-22
12	31	67.4	415	4	US-09-198-956-6
13	31	67.4	789	3	US-08-727-308-1
14	30	65.2	95	1	US-08-438-753B-24
15	30	65.2	95	1	US-08-443-883A-24
16	30	65.2	95	2	US-08-631-328-24
17	30	65.2	95	2	US-08-455-524B-24
18	30	65.2	95	2	US-08-455-021B-24
19	30	65.2	95	4	US-09-045-467-24
20	30	65.2	161	3	US-09-205-264-2
21	30	65.2	309	4	US-09-347-803-14
22	30	65.2	465	2	US-08-878-989-18
23	30	65.2	465	2	US-08-860-150-7
24	30	65.2	465	3	US-09-338-132-7
25	30	65.2	465	4	US-09-272-796-18
26	30	65.2	532	2	US-08-560-916-8
27	30	65.2	532	2	US-08-676-841-8

28	30	65.2	634	4	US-09-041-236-2	Sequence 2, Appli
29	30	65.2	666	4	US-09-240-410-2	Sequence 2, Appli
30	30	65.2	691	3	US-08-946-475-2	Sequence 2, Appli
31	30	65.2	691	4	US-09-340-479-2	Sequence 2, Appli
32	30	65.2	711	3	US-08-946-475-9	Sequence 9, Appli
33	30	65.2	711	4	US-09-340-479-9	Sequence 9, Appli
34	30	65.2	15281	2	US-08-471-119A-2	Sequence 2, Appli
35	29	63.0	36	1	US-08-487-890A-19	Sequence 19, Appli
36	29	63.0	36	2	US-08-478-435-19	Sequence 19, Appli
37	29	63.0	36	2	US-08-337-483-19	Sequence 19, Appli
38	29	63.0	36	2	US-08-478-373-19	Sequence 19, Appli
39	29	63.0	36	3	US-08-474-671-19	Sequence 19, Appli
40	29	63.0	36	3	US-08-483-577A-19	Sequence 19, Appli
41	29	63.0	36	4	US-08-897-438-19	Sequence 19, Appli
42	29	63.0	53	2	US-08-469-537A-7	Sequence 7, Appli
43	29	63.0	53	2	US-08-469-537A-20	Sequence 20, Appli
44	29	63.0	81	4	US-08-817-811-55	Sequence 55, Appli
45	29	63.0	120	4	US-08-679-006-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-FEB-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 89.1%; Score 41; DB 4; Length 643;  
Best Local Similarity 77.8%; Pred. No. 2;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDYIY 9



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Db 288 SLFEGVDYF 296
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RESULT 2
US-08-441-139-14
; Sequence 14, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS OR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 646 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-14

Query Match 84.8%; Score 39; DB 1; Length 646;
Best Local Similarity 77.8%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9
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Db 286 SLFEGIDYF 294

RESULT 3
US-08-290-978A-5
; Sequence 5, Application US/08290978A
; Patent No. 5624834
; GENERAL INFORMATION:
; APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
; APPLICANT: MULLER, YVONNE
; APPLICANT: KESTER, HERMANUS C.M.
; APPLICANT: VISSER, JACOB
; APPLICANT: VAN OOVEN, ALBERT J.J.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
; TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
; NUMBER OF SEQUENCES: 15

Query Match 69.6%; Score 32; DB 1; Length 452;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFEGIDI 8
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Db 203 LFDGIDI 209

RESULT 4
US-08-780-869-5
; Sequence 5, Application US/08780869
; Patent No. 5830737
; GENERAL INFORMATION:
; APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
; APPLICANT: MULLER, YVONNE
; APPLICANT: KESTER, HERMANUS C.M.
; APPLICANT: VISSER, JACOB
; APPLICANT: VAN OOVEN, ALBERT J.J.
; APPLICANT: ROLIN, CLAU
; TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
; TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,869
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/290,978  
; FILING DATE: 17-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 4615-0044.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-780-869-5

Query Match 69.6%; Score 32; DB 2; Length 452;  
Best Local Similarity 85.7%; Pred. No. 84;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFGGIDI 8  
||:||||  
Db 203 LFDGIDI 209

RESULT 5  
US-09-457-046B-61  
; Sequence 61, Application US/09457046B  
; Patent No. 6287835  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney et al.  
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
; FILE REFERENCE: 53679  
; CURRENT APPLICATION NUMBER: US/09/457,046B  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; US-09-457-046B-61

Query Match 69.6%; Score 32; DB 4; Length 458;  
Best Local Similarity 66.7%; Pred. No. 85;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9  
||:||||  
Db 165 SLFDGISAY 173

RESULT 6  
US-08-438-753B-22  
; Sequence 22, Application US/08438753B  
; Patent No. 5705363  
; GENERAL INFORMATION:  
; APPLICANT: Imakawa, Kazuhito  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,753B  
; FILING DATE: 10-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 5600-0001.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNtau6).  
; US-08-438-753B-22

Query Match 67.4%; Score 31; DB 1; Length 99;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9  
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Db 83 SYFGIHIY 91

RESULT 7  
US-08-443-883A-22  
; Sequence 22, Application US/08443883A  
; Patent No. 5738845  
; GENERAL INFORMATION:  
; APPLICANT: Bazer, Fuller W.  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; APPLICANT: Ott, Troy L.  
; APPLICANT: Van Heeke, Gino  
; APPLICANT: Imakawa, Kazuhito  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,883A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5600-0001.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNtau6).
US-08-443-883A-22

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Query Match 67.4%; Score 31; DB 1; Length 99;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 SLFEGIDIY 9
| | | | |
Db 83 SYFQGIHIY 91

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RESULT 8
US-08-631-328-22
; Sequence 22, Application US/08631328
; Patent No. 5939286
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Subramaniam, Prem S.
; TITLE OF INVENTION: Hybrid Interferon Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,328
; FILING DATE: 12-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 5600-0001.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNtau6).
US-08-631-328-22

```

```

Query Match 67.4%; Score 31; DB 2; Length 99;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

Qy 1 SLFEGIDIY 9
| | | | |
Db 83 SYFQGIHIY 91

```

```

RESULT 9
US-08-455-524B-22
; Sequence 22, Application US/08455524B
; Patent No. 5942223
; GENERAL INFORMATION:
; APPLICANT: Bazer, Fuller W.
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Ott, Troy L.
; APPLICANT: Van Heeke, Gino
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,524B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890

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; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 5600-0001.32  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNTau6).  
US-08-455-524B-22

Query Match 67.4%; Score 31; DB 2; Length 99;  
Best Local Similarity 66.7%; Pred. NO: 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 9  
| : : : : :  
Db 83 SYFQGIHIY 91

RESULT 10  
US-08-455-021B-22  
; Sequence 22, Application US/08455021B  
; GENERAL INFORMATION:  
; APPLICANT: Bazer, Fuller W.  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; APPLICANT: Ott, Troy L.  
; APPLICANT: Van Heeke, Gino  
; APPLICANT: Imakawa, Kazuhito  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455.021B  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615

; REFERENCE/DOCKET NUMBER: 5600-0001.31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNTau6).  
US-08-455-021B-22

Query Match 67.4%; Score 31; DB 2; Length 99;  
Best Local Similarity 66.7%; Pred. NO: 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDIY 9  
| : : : : :  
Db 83 SYFQGIHIY 91

RESULT 11  
US-09-045-467-22  
; Sequence 22, Application US/09045467  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/045,467  
; FILING DATE: 20-Mar-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/455,021  
; FILING DATE: 31-MAY-1995  
; APPLICATION NUMBER: US 08/438,753  
; FILING DATE: 10-MAY-1995  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dehlinger, Peter J.  
; REGISTRATION NUMBER: 28,006  
; REFERENCE/DOCKET NUMBER: 5600-0001.36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids



```

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; SEQUENCE DESCRIPTION: of SEQ ID NO:21 (HuIFNtau6).
; US-09-045-467-22

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```

Query Match          67.4%; Score 31; DB 4; Length 99;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 SLFEGIDIY 9
   | | | | |
DB 83 SYFQGIHY 91

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RESULT 12
US-09-198-956-6

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; Sequence 6, Application US/09198956
; Patent No. 6165769
; GENERAL INFORMATION:

```

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; APPLICANT: Andersen, Lene N.
; APPLICANT: Schulein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schnorr, Kirk

```

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; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; FILE REFERENCE: 5377-200-US

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; CURRENT APPLICATION NUMBER: US/09/198,956
; CURRENT FILING DATE: 1998-11-24

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; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 1344/97

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; EARLIER FILING DATE: 1997-12-02
; EARLIER APPLICATION NUMBER: 60/067,240

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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 6
; LENGTH: 415

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; TYPE: PRT
; ORGANISM: Bacillus licheniformis

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US-09-198-956-6

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Query Match          67.4%; Score 31; DB 4; Length 415;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 FEGIDIY 9
   | | | | |
DB 118 FEGVELY 124

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RESULT 13

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US-08-727-308-1

```

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; Sequence 1, Application US/08727308
; Patent No. 6020176

```

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; GENERAL INFORMATION:

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; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9

```

```

; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700

```

```

; CITY: Washington
; STATE: D.C.

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; COUNTRY: U.S.A.
; ZIP: 20005

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; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367

```

```

; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 202-371-8850
; TELEFAX:

```

```

; TELEX:

```

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; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:

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; LENGTH: 789 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; US-08-727-308-1

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Query Match          67.4%; Score 31; DB 3; Length 789;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SLFEGIDI 8
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DB 23 SLFPGVDV 30

```

```

RESULT 14

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```

US-08-438-753B-24

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; Sequence 24, Application US/08438753B
; Patent No. 5705363

```

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; GENERAL INFORMATION:

```

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; APPLICANT: Imakawa, Kazuhito
; TITLE OF INVENTION: Interferon Tau Compositions and

```

```

; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250

```

```

; CITY: Palo Alto
; STATE: CA

```

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; COUNTRY: USA
; ZIP: 94306

```

```

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,753B

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; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435

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```

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741

```

```

; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:

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```

; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890

```



; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 5600-0001.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 95 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).  
US-08-438-753B-24

Query Match 65.2%; Score 30; DB 1; Length 95;  
Best Local Similarity 55.6%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9  
| : : : : |  
Db 83 SYFQGIHVY 91

RESULT 15  
US-08-443-883A-24  
; Sequence 24, Application US/08443883A  
; Patent No. 5738845  
; GENERAL INFORMATION:  
; APPLICANT: Bazer, Fuller W.  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; APPLICANT: Ott, Troy L.  
; APPLICANT: Van Heeke, Gino  
; APPLICANT: Imakawa, Kazuhito  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,883A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fabian, Gary R.

; REGISTRATION NUMBER: 33,875  
; REFERENCE/DOCKET NUMBER: 5600-0001.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 95 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).  
US-08-443-883A-24

Query Match 65.2%; Score 30; DB 1; Length 95;  
Best Local Similarity 55.6%; Pred. No. 38;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 9  
| : : : : |  
Db 83 SYFQGIHVY 91

Search completed: December 6, 2001, 07:59:54  
Job time: 362 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:53 ; Search time 170.25 seconds  
(without alignments)  
7.732 Million cell updates/sec

Title: PEPL-MOD8G

Perfect score: 48

Sequence: 1 SLFEGIDGY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	83.3	289	12 Q98505	Q98505 paramecium
2	39	81.2	146	5 Q9U667	Q9U667 littorina p
3	39	81.2	153	5 Q9U670	Q9U670 littorina s
4	39	81.2	155	5 Q9U669	Q9U669 littorina s
5	39	81.2	157	5 Q9U665	Q9U665 littorina p
6	39	81.2	158	5 Q9U671	Q9U671 littorina s
7	39	81.2	158	5 Q9U668	Q9U668 littorina p
8	39	81.2	158	5 Q9U666	Q9U666 littorina p
9	39	81.2	220	5 P81159	P81159 aplysia cal
10	39	81.2	221	5 P81157	P81157 aplysia cal
11	39	81.2	278	13 Q90520	Q90520 oncorhynch
12	39	81.2	367	13 Q98899	Q98899 fugu rubrip
13	39	81.2	455	11 Q63718	Q63718 rattus norv
14	39	81.2	467	5 O44350	O44350 chondrosia
15	39	81.2	467	5 O44352	O44352 petrobiona
16	39	81.2	467	5 Q9NJ92	Q9NJ92 guancha lac
17	39	81.2	468	5 O44349	O44349 funiculina
18	39	81.2	469	5 O44351	O44351 eunicella c
19	39	81.2	526	13 Q98897	Q98897 fugu rubrip

20	39	81.2	617	10 Q9C7X7	Q9C7X7 arabidopsis
21	39	81.2	628	5 Q93147	Q93147 botryllus s
22	39	81.2	629	5 Q93146	Q93146 botryllus s
23	39	81.2	632	5 O15766	O15766 dictyostell
24	39	81.2	639	13 Q98900	Q98900 fugu rubrip
25	39	81.2	639	13 Q918F9	Q918F9 oryzias lat
26	39	81.2	640	5 Q93601	Q93601 caenorhabdi
27	39	81.2	640	13 Q93240	Q93240 paralichthy
28	39	81.2	641	11 Q63256	Q63256 rattus norv
29	39	81.2	641	11 Q9QWJ5	Q9QWJ5 mus musculu
30	39	81.2	645	5 O96541	O96541 setaria dig
31	39	81.2	645	5 Q9NJ7	Q9NJ7 wuchereria
32	39	81.2	645	5 Q9NGK9	Q9NGK9 wuchereria
33	39	81.2	645	10 O48563	O48563 brassica na
34	39	81.2	647	3 O59855	O59855 schizosacch
35	39	81.2	647	10 Q41027	Q41027 pisum sativ
36	39	81.2	650	5 Q9U777	Q9U777 stylophora
37	39	81.2	650	10 Q9ZS55	Q9ZS55 arabidopsis
38	39	81.2	650	10 Q9LHA8	Q9LHA8 arabidopsis
39	39	81.2	652	10 P93937	P93937 ascophyllum
40	39	81.2	653	5 Q94805	Q94805 trichoplusi
41	39	81.2	659	5 Q9XZJ2	Q9XZJ2 crassostrea
42	39	81.2	663	5 Q24952	Q24952 geodia cydo
43	38	79.2	190	5 Q9U9B4	Q9U9B4 mytilus edu
44	38	79.2	467	5 O44346	O44346 asbestoplum
45	38	79.2	467	5 O44347	O44347 petrosia fl

#### ALIGNMENTS

RESULT 1  
Q98505  
ID Q98505 PRELIMINARY; PRT; 289 AA.  
AC Q98505;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE GENOME, PARTIAL SEQUENCE.  
GN A454L.  
OS Paramecium bursaria chlorella virus 1 (PBCV-1).  
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.  
OX NCBI\_TaxID=10506;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96400190; PubMed=8806566;  
RA Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;  
RT "Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map  
RT positions 182 to 258";  
RL Virology 223:303-317(1996).  
DR EMBL; U42580; AAC96822.1; -.  
SQ SEQUENCE 289 AA; 31193 MW; BC8F7AF4A9E857F1 CRC64;

Query Match 83.3%; Score 40; DB 12; Length 289;  
Best Local Similarity 77.8%; Pred. No. 10;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||:  
Db 250 SLFEGLDGY 258

RESULT 2  
Q9U667  
ID Q9U667 PRELIMINARY; PRT; 146 AA.  
AC Q9U667;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.



OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OX Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 RN NCBI\_TaxID=31219;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191828; AAF12787.1; -  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

Query Match 81.2%; Score 39; DB 5; Length 146;  
 Best Local Similarity 88.9%; Pred. No. 7.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db ||||| 79 SLFEGIDFY 87

RESULT 3  
 Q9U670 PRELIMINARY; PRT; 153 AA.  
 ID Q9U670;  
 AC Q9U670;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OX Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 RN NCBI\_TaxID=31221;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191825; AAF12784.1; -  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 153 153  
 SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 81.2%; Score 39; DB 5; Length 153;  
 Best Local Similarity 88.9%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db ||||| 80 SLFEGIDFY 88

RESULT 4  
 Q9U669 PRELIMINARY; PRT; 155 AA.  
 ID Q9U669;  
 AC Q9U669;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191826; AAF12785.1; -  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 155 155  
 SQ SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 81.2%; Score 39; DB 5; Length 155;  
 Best Local Similarity 88.9%; Pred. No. 7.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db ||||| 82 SLFEGIDFY 90

RESULT 5  
 Q9U665 PRELIMINARY; PRT; 157 AA.  
 ID Q9U665;  
 AC Q9U665;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OX Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 RN NCBI\_TaxID=31219;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191830; AAF12789.1; -  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 157 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 81.2%; Score 39; DB 5; Length 157;  
 Best Local Similarity 88.9%; Pred. No. 7.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db ||||| 84 SLFEGIDFY 92

RESULT 6  
 Q9U671 PRELIMINARY; PRT; 158 AA.  
 ID Q9U671;  
 AC Q9U671;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;



OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191824; AAF12783.1; -;  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 81.2%; Score 39; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 7.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db 85 SLFEGIDFY 93

## RESULT 7

Q9U668 PRELIMINARY; PRT; 158 AA.  
 AC Q9U668;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191827; AAF12786.1; -;  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 81.2%; Score 39; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 7.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db 85 SLFEGIDFY 93

## RESULT 8

Q9U666 PRELIMINARY; PRT; 158 AA.  
 AC Q9U666;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191829; AAF12788.1; -;  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 81.2%; Score 39; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 7.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db 85 SLFEGIDFY 93

## RESULT 9

P81159 PRELIMINARY; PRT; 220 AA.  
 AC P81159;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-93077669; PubMed-1360013;  
 RX Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in the expression of BIP, the major protein chaperon of the ER.";  
 RL J. Cell Biol. 119:1069-1076(1992).  
 CC -|- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -|- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15039; CAA78757.1; -;  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 220  
 SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 81.2%; Score 39; DB 5; Length 220;  
 Best Local Similarity 88.9%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDGY 9  
 Db 138 SLFEGIDFY 146

## RESULT 10

P81157



ID P81157 PRELIMINARY; PRT; 221 AA.  
 AC 081157;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).  
 GN HSP70A.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93077669; PubMed=1360013;  
 RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 the expression of 81p, the major protein chaperon of the ER.";  
 RL J. Cell Biol. 119:1069-1076(1992).  
 CC -I- INDUCTION: BY HEAT SHOCK  
 CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15037; CAA78755.1; -.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 221 221  
 SQ SEQUENCE 221 AA; 24404 MW; 853F794106B83CC9 CRC64;

Query Match 81.2%; Score 39; DB 5; Length 221;  
 Best Local Similarity 88.9%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 SLFEGIDY 9  
 Db 139 SLFEGIDY 147  
 |||||

RESULT 11  
 Q90520  
 ID Q90520 PRELIMINARY; PRT; 278 AA.  
 AC Q90520;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=65036330; PubMed=6092938;  
 RA Kothary R.K., Jones D., Candido E.P.M.;  
 RT "70-Kilodalton heat shock polypeptides from rainbow trout:  
 characterization of cDNA sequences.";  
 RL Mol. Cell. Biol. 4:1785-1791(1984).  
 DR EMBL; K02549; AAA49562.1; -.  
 DR HSP; P08109; ICKR.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 278 278  
 SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 81.2%; Score 39; DB 13; Length 278;  
 Best Local Similarity 88.9%; Pred. No. 15;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 SLFEGIDY 9  
 Db 156 SLFEGIDY 164  
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 RESULT 12  
 Q98899  
 ID Q98899 PRELIMINARY; PRT; 367 AA.  
 AC Q98899;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 GN HSP70-3.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lim E.H.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y08578; CAA69892.1; -.  
 DR HSP; P19120; 3HSC.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock.  
 FT NON\_TER 367 367  
 FT NON\_TER 367 367  
 SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;

Query Match 81.2%; Score 39; DB 13; Length 367;  
 Best Local Similarity 88.9%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 SLFEGIDY 9  
 Db 268 SLFEGIDY 276  
 |||||  
 RESULT 13  
 Q63718  
 ID Q63718 PRELIMINARY; PRT; 455 AA.  
 AC Q63718;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT SHOCK ROPEIN 70 (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,  
 RA D'Ambrosio E.;  
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z27118; CAA81642.1; -.  
 DR HSP; P08107; 1HJO.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.



DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock.  
 FT NON\_TER 1  
 FT NON\_TER 455 455  
 SQ SEQUENCE 455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;

Query Match 81.2%; Score 39; DB 11; Length 455;  
 Best Local Similarity 88.9%; Pred. No. 27;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDGY 9  
 |||||  
 Db 254 SLFEGIDFY 262

## RESULT 14

O44350  
 ID O44350 PRELIMINARY; PRT; 467 AA.  
 AC O44350;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
 GN HSP70.  
 OS Chondrosia reniformis.  
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;  
 OC Chondrosida; Chondrillidae; Chondrosia.  
 OX NCBI\_TaxID=68574;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borchelliini C.; Le Parco Y.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026517; AAC05362.1; -.  
 DR HSSP; P08109; 1CKR.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467 467  
 SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 81.2%; Score 39; DB 5; Length 467;  
 Best Local Similarity 88.9%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDGY 9  
 |||||  
 Db 252 SLFEGIDFY 260

## RESULT 15

O44352  
 ID O44352 PRELIMINARY; PRT; 467 AA.  
 AC O44352;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
 GN HSP70.  
 OS Petrobiona massiliana.  
 OC Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;  
 OC Petrobiona.  
 OX NCBI\_TaxID=68578;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borchelliini C.; Le Parco Y.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026520; AAC05364.1; -.  
 DR HSSP; P08109; 1CKR.

DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467 467  
 SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;  
 Query Match 81.2%; Score 39; DB 5; Length 467;  
 Best Local Similarity 88.9%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 SLFEGIDGY 9  
 |||||  
 Db 252 SLFEGIDFY 260

Search completed: December 6, 2001, 07:56:53  
 Job time: 181 sec



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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:54 ; Search time 81.43 Seconds  
(without alignments)  
2.487 Million cell updates/sec

Title: PEPI-MOD8L  
Perfect score: 46  
Sequence: 1 SLFEGIDLY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	89.1	643	4	US-08-797-358B-3
2	39	84.8	646	1	US-08-441-139-14
3	33	71.7	415	4	US-09-198-956-6
4	32	69.6	161	3	US-09-205-264-2
5	32	69.6	309	4	US-09-347-803-14
6	32	69.6	458	4	US-09-457-046B-61
7	32	69.6	691	3	US-08-946-475-2
8	32	69.6	691	4	US-09-340-479-2
9	32	69.6	711	3	US-08-946-475-9
10	32	69.6	711	4	US-09-340-479-9
11	31	67.4	81	4	US-08-817-811-55
12	31	67.4	120	4	US-08-679-006-34
13	31	67.4	369	1	US-08-253-823-1
14	31	67.4	369	1	US-08-290-508-3
15	31	67.4	369	2	US-08-606-144-1
16	31	67.4	369	5	PCT-US94-02174-3
17	30	65.2	183	4	US-08-961-083-178
18	30	65.2	308	4	US-09-347-803-10
19	30	65.2	452	1	US-08-290-978A-5
20	30	65.2	452	2	US-08-780-869-5
21	30	65.2	465	2	US-08-878-989-18
22	30	65.2	465	2	US-08-860-150-7
23	30	65.2	465	3	US-09-338-132-7
24	30	65.2	465	4	US-09-272-796-18
25	30	65.2	532	2	US-08-560-916-8
26	30	65.2	532	2	US-08-676-841-8
27	29	63.0	11	2	US-08-486-839-10

28 29 63.0 11 3 US-09-151-011-10 Sequence 10, Appl  
29 29 63.0 11 4 US-09-343-623-10 Sequence 10, Appl  
30 29 63.0 53 2 US-08-469-537A-7 Sequence 7, Appl  
31 29 63.0 53 2 US-08-469-537A-20 Sequence 20, Appl  
32 29 63.0 99 1 US-08-438-753B-22 Sequence 22, Appl  
33 29 63.0 99 1 US-08-443-883A-22 Sequence 22, Appl  
34 29 63.0 99 2 US-08-631-328-22 Sequence 22, Appl  
35 29 63.0 99 2 US-08-455-524B-22 Sequence 22, Appl  
36 29 63.0 99 2 US-08-455-021B-22 Sequence 22, Appl  
37 29 63.0 99 4 US-09-045-467-22 Sequence 22, Appl  
38 29 63.0 229 4 US-09-045-973-7 Sequence 7, Appl  
39 29 63.0 376 3 US-09-025-691-3 Sequence 3, Appl  
40 29 63.0 481 4 US-07-912-122-4 Sequence 4, Appl  
41 29 63.0 481 5 PCT-US93-06404-4 Sequence 4, Appl  
42 29 63.0 581 2 US-08-989-386-7 Sequence 7, Appl  
43 29 63.0 603 2 US-08-687-865A-2 Sequence 2, Appl  
44 29 63.0 603 4 US-09-043-711-2 Sequence 2, Appl  
45 29 63.0 789 3 US-08-727-308-1 Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-Feb-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 89.1%; Score 41; DB 4; Length 643;  
Best Local Similarity 77.8%; Pred. No. 1.7;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9



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DB      288 SLFEGVDY 296
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; CURRENT FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1344/97
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/067,240
; EARLIER FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-198-956-6

Query Match      71.7%; Score 33; DB 4; Length 415;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 1 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 FEGIDLY 9
      |||:|
Db      118 FEGVELY 124

RESULT 4
US-09-205-264-2
; Sequence 2, Application US/09205264
; Patent No. 6114145
; GENERAL INFORMATION:
; APPLICANT: Olsen, et al.
; TITLE OF INVENTION: Synferon
; FILE REFERENCE: PF404
; CURRENT APPLICATION NUMBER: US/09/205,264
; CURRENT FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 60/067,746
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-264-2

Query Match      69.6%; Score 32; DB 3; Length 161;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 SLFEGIDLY 9
      |||:|
Db      120 SYFQGISLY 128

RESULT 5
US-09-347-803-14
; Sequence 14, Application US/09347803
; Patent No. 6274379
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hitz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Orozco, Buddy
; TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
; FILE REFERENCE: BB-1176
; CURRENT APPLICATION NUMBER: US/09/347,803
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,952
; EARLIER FILING DATE: July 15, 1998
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 309
; TYPE: PRT

DB      286 SLFEGIDY 294
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; CURRENT FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1344/97
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/067,240
; EARLIER FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-198-956-6

Query Match      84.8%; Score 39; DB 1; Length 646;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLFEGIDLY 9
      |||:|
Db      286 SLFEGIDY 294

RESULT 3
US-09-198-956-6
; Sequence 6, Application US/09198956
; Patent No. 6165769
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schuelein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schnorr, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; TITLE OF INVENTION: Licheniformis
; FILE REFERENCE: 5377.200-US
; CURRENT APPLICATION NUMBER: US/09/198,956

```



```
; ORGANISM: Glycine max
US-09-347-803-14

Query Match      69.6%; Score 32; DB 4; Length 309;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 300 AVFWGIDLY 308

RESULT 6
US-09-457-046B-61
; Sequence 61, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match      69.6%; Score 32; DB 4; Length 458;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 165 SLFDGISAY 173

RESULT 7
US-08-946-475-2
; Sequence 2, Application US/08946475
; Patent No. 6013505
; GENERAL INFORMATION:
; APPLICANT: Gwynn, Michael
; APPLICANT: Kallender, Howard
; APPLICANT: Palmer, Leslie
; TITLE OF INVENTION: TOPOISOMERASE I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,475
; FILING DATE: 08-OCT-1997
; APPLICATION NUMBER: 60/027,973
; FILING DATE: 08-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-340-479-2

; REFERENCE/DOCKET NUMBER: P50560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-946-475-2

Query Match      69.6%; Score 32; DB 3; Length 691;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFEIGIDL 8
Db 283 LYEGIDL 289

RESULT 8
US-09-340-479-2
; Sequence 2, Application US/09340479
; Patent No. 6274139
; GENERAL INFORMATION:
; APPLICANT: Gwynn, Michael
; APPLICANT: Kallender, Howard
; APPLICANT: Palmer, Leslie
; TITLE OF INVENTION: TOPOISOMERASE I
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,475
; FILING DATE: 08-OCT-1997
; APPLICATION NUMBER: 60/027,973
; FILING DATE: 08-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-340-479-2
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Query Match 69.6%; Score 32; DB 4; Length 691;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFEIGIDL 8  
DB 283 LYEGIDL 289

RESULT 9  
US-08-946-475-9  
; Sequence 9, Application US/08946475  
; Patent No. 6013505  
; GENERAL INFORMATION:  
; APPLICANT: Gwynn, Michael  
; APPLICANT: Kallender, Howard  
; APPLICANT: Palmer, Leslie  
; TITLE OF INVENTION: TOPOISOMERASE I  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,475  
; FILING DATE: 08-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/027,973  
; FILING DATE: 08-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimmil, Edward R  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: P50560  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 711 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-946-475-9

Query Match 69.6%; Score 32; DB 3; Length 711;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFEIGIDL 8  
DB 303 LYEGIDL 309

RESULT 10  
US-09-340-479-9  
; Sequence 9, Application US/09340479  
; Patent No. 6274139  
; GENERAL INFORMATION:  
; APPLICANT: Gwynn, Michael  
; APPLICANT: Kallender, Howard  
; APPLICANT: Palmer, Leslie

; TITLE OF INVENTION: TOPOISOMERASE I  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/340,479  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,475  
; FILING DATE: 08-OCT-1997  
; APPLICATION NUMBER: 60/027,973  
; FILING DATE: 08-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimmil, Edward R  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: P50560  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 711 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-340-479-9  
  
Query Match 69.6%; Score 32; DB 4; Length 711;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LFEIGIDL 8  
DB 303 LYEGIDL 309  
  
RESULT 11  
US-08-817-811-55  
; Sequence 55, Application US/08817811  
; Patent No. 6174528  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Juan A.  
; APPLICANT: Relf, Wendy A.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Saul, Allan J.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,811
; FILING DATE: 14-APR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 96/11944
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-817-811-55.

Query Match 67.4%; Score 31; DB 4; Length 81;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDL 9
I: ||: ||
DB 20 SILEGLNLY 28

RESULT 12
US-08-679-006-34
; Sequence 34, Application US/08679006
; Patent No. 6150500
; GENERAL INFORMATION:
; APPLICANT: Salerno, John C.
; TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF
; TITLE OF INVENTION: NOS ISOFORMS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,006
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: JCS96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-679-006-34
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Query Match 67.4%; Score 31; DB 4; Length 120;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGIDL 8
I: ||| ||
DB 46 LFEIGFDL 52

RESULT 13
US-08-253-823-1
; Sequence 1, Application US/08253823
; Patent No. 5541094
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: GLYCOLATE OXIDASE PRODUCTION
; NUMBER OF SEQUENCES: 1
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM
; OPERATING SYSTEM: MICROSOFT WINDOWS V3.0
; SOFTWARE: MICROSOFT WORD V2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,823
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/085,488
; FILING DATE: JULY 1, 1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-253-823-1

Query Match 67.4%; Score 31; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FEGIDL 8
I: |||||
DB 183 FEGIDL 188

RESULT 14
US-08-290-508-3
; Sequence 3, Application US/08290508
; Patent No. 5693490
; GENERAL INFORMATION:
; APPLICANT: PAYNE, MARK S.
; APPLICANT: ANTON, DAVID L.
; APPLICANT: DICOSIMO, ROBERT
; APPLICANT: GAVAGAN, JOHN E.
; TITLE OF INVENTION: Production of glycolate oxidase
; TITLE OF INVENTION: in methylotrophic yeast
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/290,508  
; FILING DATE: 15-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/025,495  
; FILING DATE: 03-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GALLEGOS, R. THOMAS  
; REGISTRATION NUMBER: 32,692  
; REFERENCE/DOCKET NUMBER: CR-9271  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-892-7342  
; TELEFAX: 302-892-7949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 369 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-290-508-3

Query Match 67.4%; Score 31; DB 1; Length 369;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FEGIDL 8  
Db 183 FEGIDL 188

RESULT 15  
US-08-606-144-1  
; Sequence 1, Application US/08606144  
; Patent No. 5834262  
; GENERAL INFORMATION:  
; APPLICANT: DAVID LEROY ANTON  
; TITLE OF INVENTION: OXIDATION OF GLYCOLIC ACID TO  
; TITLE OF INVENTION: GLYOXYLIC ACID USING A  
; TITLE OF INVENTION: MICROBIAL CELL TRANSFORMANT  
; TITLE OF INVENTION: AS CATALYST  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.JI.JDULPONTJDEJNEMOURS  
; ADDRESSEE: AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH 2.0 MB  
; COMPUTER: IBM COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WINDOWS, 3.1  
; SOFTWARE: MICROSOFT WORD VERSION 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/606,144  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/817,165  
; FILING DATE: JANUARY 6, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GREGORY, THEODORE C.  
; REGISTRATION NUMBER: 25,243  
; REFERENCE/DOCKET NUMBER: CH-2087-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-992-4925  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 369 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-606-144-1

Query Match 67.4%; Score 31; DB 2; Length 369;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FEGIDL 8  
Db 183 FEGIDL 188

Search completed: December 6, 2001, 07:59:54  
Job time: 362 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:26 ; Search time 88.19 Seconds  
(without alignments)  
7.774 Million cell updates/sec

Title: PEPL-MOD8L  
Perfect score: 46  
Sequence: 1 SLFEGIDLY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68: \*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	91.3	208	2 B44261	dnaK-type molecula
2	42	91.3	278	2 I51344	dnaK-type molecula
3	42	91.3	420	2 A26283	dnaK-type molecula
4	42	91.3	467	2 T45477	heat-shock protein
5	42	91.3	467	2 T45477	heat-shock protein
6	42	91.3	468	2 T45476	heat-shock protein
7	42	91.3	469	2 T45478	heat-shock protein
8	42	91.3	617	2 H96605	probable heat shoc
9	42	91.3	632	2 T45471	dnaK-type molecula
10	42	91.3	634	2 A25646	dnaK-type molecula
11	42	91.3	636	2 A48872	dnaK-type molecula
12	42	91.3	638	2 S31766	dnaK-type molecula
13	42	91.3	639	2 JCI391	dnaK-type molecula
14	42	91.3	639	2 S20139	dnaK-type molecula
15	42	91.3	640	1 HKHWA	dnaK-type molecula
16	42	91.3	640	2 A29160	dnaK-type molecula
17	42	91.3	640	2 S37394	dnaK-type molecula
18	42	91.3	640	2 T21394	hypothetical prote
19	42	91.3	640	2 T43724	dnaK-type molecula
20	42	91.3	641	2 S53357	dnaK-type molecula
21	42	91.3	641	2 S35718	dnaK-type molecula
22	42	91.3	641	2 I54542	dnaK-type molecula
23	42	91.3	641	2 A45871	dnaK-type molecula
24	42	91.3	642	1 HHBYA1	dnaK-type molecula
25	42	91.3	642	2 JH0095	dnaK-type molecula
26	42	91.3	642	2 B36590	dnaK-type molecula
27	42	91.3	644	2 A45635	dnaK-type molecula
28	42	91.3	645	2 I51129	dnaK-type molecula
29	42	91.3	646	2 T46650	heat shock protein

30	42	91.3	647	1 HHXL70	dnaK-type molecula
31	42	91.3	647	2 S44168	dnaK-type molecula
32	42	91.3	647	2 T41121	heat shock protein
33	42	91.3	650	2 JC7088	heat shock protein
34	41	89.1	209	2 A44261	dnaK-type molecula
35	41	89.1	214	2 A03309	dnaK-type molecula
36	41	89.1	372	2 PQ0138	dnaK-type molecula
37	41	89.1	379	2 T46588	dnaK-type molecula
38	41	89.1	467	2 T45473	heat-shock protein
39	41	89.1	467	2 T45474	heat-shock protein
40	41	89.1	641	2 JN0668	dnaK-type molecula
41	41	89.1	641	2 FC7036	heat shock protein
42	41	89.1	643	2 S25585	dnaK-type molecula
43	41	89.1	643	2 S09036	dnaK-type molecula
44	41	89.1	651	2 T45517	heat shock protein
45	41	89.1	651	2 JC7132	heat shock protein

## ALIGNMENTS

RESULT 1

B44261  
dnaK-type molecular chaperone HSC70 - California sea hare (fragment)  
N:Alternate names: heat shock protein 70 homolog HSC70  
C:Species: Aplysia californica (California sea hare)  
C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999  
C:Accession: B44261  
R:Kuhl, D.; Kennedy, T.E.; Barzilal, A.; Kandel, E.R.  
J. Cell Biol. 119, 1069-1076, 1992  
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr  
A:Reference number: A44261; MUID:93077669  
A:Accession: B44261  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-208 <KUH>  
A:Note: sequence extracted from NCBI backbone (NCBIP:118950)  
C:Genetics:  
A:Gene: HSC70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 208;  
Best Local Similarity 88.9%; Pred. No. 0.39;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
DB 132 SLFEGIDFY 140

RESULT 2

I51344  
dnaK-type molecular chaperone (clone pHS70.7) - rainbow trout (fragment)  
N:Alternate names: 70K heat shock protein  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999  
C:Accession: I51344  
R:Kothary, R.K.; Jones, D.; Candido, E.P.M.  
Mol. Cell. Biol. 4, 1785-1791, 1984  
A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o  
A:Reference number: I51344; MUID:85036330  
A:Accession: I51344  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-278 <KOT>  
A:Cross-references: GB:X02549; NID:g213803; PIDN:AAA49562.1; PID:g213804  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70



C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 278;  
Best Local Similarity 88.9%; Pred. No. 0.54;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
|||||||

Db 156 SLFEGIDFY 164

#### RESULT 3

A26283

QnaK-type molecular chaperone - mouse (fragment)

N:Alternate names: heat shock protein 68

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999

C:Accession: A26283

R:Low, D.G.; Moran, L.A.

J. Biol. Chem. 261, 2102-2112, 1986

A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he

A:Reference number: A26283; MUID:86111900

A:Accession: A26283

A:Molecule type: mRNA

A:Residues: 1-420 <LOW>

A:Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208

A:Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein compl

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 420;  
Best Local Similarity 88.9%; Pred. No. 0.85;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
|||||||

Db 65 SLFEGIDFY 73

#### RESULT 4

T45477

heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

C:Species: Chondrosia reniformis

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45477

R:Borchellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45477

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 0.96;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
|||||||

Db 252 SLFEGIDFY 260

#### RESULT 5

T45479

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)  
C:Species: Eunicella cavolini

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45479

R:Borchellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45479

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 0.96;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
|||||||

Db 252 SLFEGIDFY 260

#### RESULT 6

T45476

heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)

C:Species: Funiculina quadrangularis

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45476

R:Borchellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45476

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-468 <BOR>

A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match 91.3%; Score 42; DB 2; Length 468;  
Best Local Similarity 88.9%; Pred. No. 0.96;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
|||||||

Db 253 SLFEGIDFY 261

#### RESULT 7

T45478

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C:Species: Eunicella cavolini

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45478

R:Borchellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45478

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-469 <BOR>

A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70



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Query Match          91.3%; Score 42; DB 2; Length 469;
Best Local Similarity 88.9%; Pred. No. 0.96;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 254 SLFEGIDFY 262
|||||||

RESULT 8
H96605
probable heat shock protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: H96605
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96605
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-617 <STO>
A:Cross-references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GN00141
C:Genetics:
A:Gene: F13N6.9
A:Map position: 1
C:Superfamily: heat shock protein 70

Query Match          91.3%; Score 42; DB 2; Length 617;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 292 SLFEGIDFY 300
|||||||

RESULT 9
T45471
dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N:Alternate names: heat shock cognate protein 70
C:Species: Dictyostelium discoideum
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C:Accession: T45471
R:Boves, H.; Mintert, U.; Dittich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22980
A:Accession: T45471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-632 <BOV>
A:Cross-references: EMBL:AF025951; PIDN:AA81865.1
A:Experimental source: strain AX3
C:Genetics:
A:Gene: hsc70
A:Note: localized to filopodias and cortex
C:Superfamily: heat shock protein 70

Query Match          91.3%; Score 42; DB 2; Length 632;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 292 SLFEGIDFY 300
|||||||

RESULT 9
T45471
dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N:Alternate names: heat shock cognate protein 70
C:Species: Dictyostelium discoideum
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C:Accession: T45471
R:Boves, H.; Mintert, U.; Dittich, W.; Faix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z22980
A:Accession: T45471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-632 <BOV>
A:Cross-references: EMBL:AF025951; PIDN:AA81865.1
A:Experimental source: strain AX3
C:Genetics:
A:Gene: hsc70
A:Note: localized to filopodias and cortex
C:Superfamily: heat shock protein 70

Query Match          91.3%; Score 42; DB 2; Length 636;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 280 SLFEGIDFY 288
|||||||

RESULT 12
S31766
dnak-type molecular chaperone hsp70 - green monkey
N:Alternate names: heat shock protein 70
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

Query Match          91.3%; Score 42; DB 2; Length 634;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 289 SLFEGIDFY 297
|||||||

RESULT 11
A48872
dnak-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein
C:Species: Dictyostelium discoideum
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C:Accession: A48872
R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with
A:Reference number: A48872; MUID:94043116
A:Accession: A48872
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-636 <EDD>
A:Cross-references: GB:L22736; NID:9433179; PIDN:AAA33219.1; PID:9433180
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match          91.3%; Score 42; DB 2; Length 634;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 289 SLFEGIDFY 297
|||||||

RESULT 11
A48872
dnak-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein
C:Species: Dictyostelium discoideum
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C:Accession: A48872
R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with
A:Reference number: A48872; MUID:94043116
A:Accession: A48872
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-636 <EDD>
A:Cross-references: GB:L22736; NID:9433179; PIDN:AAA33219.1; PID:9433180
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match          91.3%; Score 42; DB 2; Length 636;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 280 SLFEGIDFY 288
|||||||

RESULT 12
S31766
dnak-type molecular chaperone hsp70 - green monkey
N:Alternate names: heat shock protein 70
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
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C;Accession: S31766; I36927  
 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 submitted to the EMBL Data Library, January 1993  
 A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
 A;Reference number: S31766  
 A;Accession: S31766  
 A;Molecule type: mRNA  
 A;Residues: 1-638 <SAI>  
 R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FEBS Lett. 355, 282-286, 1994  
 A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me  
 A;Reference number: I36927; MUID:95080396  
 A;Accession: I36927  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-638 <RES>  
 A;Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
 A;Experimental source: kidney; cell line COS-1  
 C;Genetics:  
 A;Gene: hsp70  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein comp  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 638;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 284 SLFEGIDFY 292

RESULT 13  
 JCI391

dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
 N;Alternate names: heat shock protein 70IV; hsp70IV protein  
 C;Species: Paracentrotus lividus (common urchin)  
 C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C;Accession: JCI391  
 R;Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
 A;Reference number: JCI391; MUID:93077053  
 A;Accession: JCI391  
 A;Molecule type: DNA  
 A;Residues: 1-639 <SCO>  
 A;Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
 C;Genetics:  
 A;Gene: hsp70IV  
 A;Introns: 61/2  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein comp  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 91.3%; Score 42; DB 2; Length 639;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 286 SLFEGIDFY 294

RESULT 14  
 S20139

dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: heat shock protein YG102; protein L0971; protein YLL024c  
 C;Species: Saccharomyces cerevisiae

C;Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C;Accession: S20139; S64772; S64775; S69383  
 R;Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A;Reference number: S20139; MUID:89128457  
 A;Accession: S20139  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-639 <SLA>  
 A;Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
 R;Goffeau, A.; Purnelle, B.  
 submitted to the Protein Sequence Database, May 1996  
 A;Reference number: S64761  
 A;Accession: S64772  
 A;Molecule type: DNA  
 A;Residues: 1-639 <GOF>  
 A;Cross-references: EMBL:X73129; NID:gl360201; PIDN:CAA97472.1; PID:gl360202; MIPS:YL  
 A;Experimental source: strain S288C  
 R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, May 1996  
 A;Reference number: S64775  
 A;Accession: S64775  
 A;Molecule type: DNA  
 A;Residues: 72-639 <DUE>  
 A;Cross-references: EMBL:X73129; MIPS:YLL024c  
 A;Experimental source: strain S288C  
 R;Purnelle, B.; Goffeau, A.  
 submitted to the EMBL Data Library, April 1996

A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals  
 mly and a new ABC transporter homologous to the human multidrug resistance protein.  
 A;Reference number: S69380  
 A;Accession: S69383  
 A;Molecule type: DNA  
 A;Residues: 1-639 <PUR>  
 A;Cross-references: EMBL:X97560; NID:gl297003; PIDN:CAA66167.1; PID:gl297007  
 C;Genetics:  
 A;Gene: SGP:SSA2  
 A;Cross-references: MIPS:YLL024c; SGD:S0003947  
 A;Map position: 12L  
 C;Function:  
 A;Description: involved in protein folding and assembling/disassembling of protein co  
 C;Superfamily: heat shock protein 70  
 C;Keywords: ATP; molecular chaperone

Query Match 91.3%; Score 42; DB 2; Length 639;  
 Best Local Similarity 88.9%; Pred. No. 1.4;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 283 SLFEGIDFY 291

RESULT 15  
 HHKW7A

dnak-type molecular chaperone hsp70A - Caenorhabditis elegans  
 N;Alternate names: heat shock protein 70 A  
 C;Species: Caenorhabditis elegans  
 C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
 C;Accession: JT0285  
 R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
 Gene 64, 241-255, 1988

A;Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri  
 A;Reference number: JT0285; MUID:88297155  
 A;Accession: JT0285  
 A;Molecule type: DNA; mRNA  
 A;Residues: 1-640 <SNU>

A;Cross-references: GB:M18540; NID:gl56351; PIDN:AAA28078.1; PID:gl56352  
 N;Alternate names: genomic clones representing six distinct members of the hsp70 gene family wer  
 A;Note: transcripts of hsp70A are abundant in control worms and also increase two- to  
 A;Note: one of the three introns in hsp70A is in a position similar to an intron in D



C:Genetics:  
A:Gene: hsp70A  
A:Map position: IV  
A:Introns: 69/1; 331/3; 558/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 91.3%; Score 42; DB 1; Length 640;  
Best Local Similarity 88.9%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SLFEGIDLY 9  
| | | | | | | |  
Db 287 SLFEGIDFY 295

Search completed: December 6, 2001, 07:58:26  
Job time: 274 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:50 ; Search time 50.21 Seconds  
(without alignments)  
6.572 Million cell updates/sec

Title: PEPL-MOD8L  
Perfect score: 46  
Sequence: 1 SLFEGIDLY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	93.5	638	1 HS70_CERCA	P1902 ceratitis c
2	42	91.3	322	1 HS70_ONCVO	P11503 onchocerca
3	42	91.3	420	1 HS73_MOUSE	Q61696 mus musculus
4	42	91.3	503	1 HS70_PENCI	Q92260 penicillium
5	42	91.3	634	1 HS70_CHICK	P08106 gallus galli
6	42	91.3	638	1 HS71_CERAE	Q28222 cercopithec
7	42	91.3	638	1 HS72_YEAST	P10592 saccharomyc
8	42	91.3	639	1 HS74_PARLI	Q06248 paracentrot
9	42	91.3	640	1 HS7A_CAEEL	P09446 caenorhabdi
10	42	91.3	640	1 HS7C_DICDI	P36415 dictyosteli
11	42	91.3	641	1 HS7L_BOVIN	Q27975 bos taurus
12	42	91.3	641	1 HS7L_HUMAN	P08107 homo sapien
13	42	91.3	641	1 HS71_MOUSE	P17879 mus musculus
14	42	91.3	641	1 HS71_PIG	P34930 sus scrofa
15	42	91.3	641	1 HS71_RAT	Q07439 rattus norv
16	42	91.3	641	1 HS71_YEAST	P10591 saccharomyc
17	42	91.3	641	1 HS72_BOVIN	Q27965 bos taurus
18	42	91.3	641	1 HS74_YEAST	P22202 saccharomyc
19	42	91.3	644	1 HS70_BRUMA	P27541 brugia mala
20	42	91.3	644	1 HS70_ONCTS	Q91233 oncorhynch
21	42	91.3	645	1 HS70_PLEWA	Q91291 pleurodeles
22	42	91.3	646	1 HS70_NEUCR	Q01233 neurospora
23	42	91.3	647	1 HS70_XENLA	P02827 xenopus lae
24	42	91.3	649	1 HS70_BLAEM	P48720 blastoclad
25	42	91.3	652	1 HS7D_MANSE	Q9u639 manduca sex
26	41	89.1	214	1 HS7A_DROSI	P02826 drosophila
27	41	89.1	372	1 HS72_PARLI	P22623 paracentrot
28	41	89.1	379	1 HS7X_PIG	P34934 sus scrofa
29	41	89.1	641	1 HS7A_DROME	P29843 drosophila
30	41	89.1	643	1 HS76_HUMAN	P17066 homo sapien
31	41	89.1	643	1 HS76_PIG	Q04967 sus scrofa
32	41	89.1	648	1 HS71_PUGGR	Q01877 puccinia gr
33	39	84.8	641	1 HS73_RAT	P55063 rattus norv

34 39 84.8 641 1 HS7H\_HUMAN P34931 homo sapien  
35 39 84.8 641 1 HS7T\_MOUSE P16627 mus musculus  
36 39 84.8 642 1 HS72\_PICAN P53623 pichia angu  
37 39 84.8 643 1 HS71\_SCHPO Q10265 schizosacch  
38 39 84.8 644 1 HS71\_PICAN P53421 pichia angu  
39 39 84.8 644 1 HS72\_LYCES P27322 lycopersico  
40 39 84.8 645 1 HS70\_SOYBN P26413 glycine max  
41 39 84.8 646 1 HS7C\_CRIGR P19378 cricetus  
42 39 84.8 646 1 HS7C\_HUMAN P11142 homo sapien  
43 39 84.8 646 1 HS7C\_MOUSE P08109 mus musculus  
44 39 84.8 649 1 HS70\_PARRR P87047 paracoccidi  
45 39 84.8 649 1 HS73\_ARATH O65719 arabidopsis

## ALIGNMENTS

RESULT 1  
HS70\_CERCA STANDARD; PRT; 638 AA.  
AC P91902;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (HSP70).  
OS Ceratitis capitata (Mediterranean fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Tephritoidea; Tephritidae; Ceratitis.  
OX NCBI\_TaxID=7213;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mintzas A.C.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
DR EMBL; Y08955; CAA70153.1; -  
DR HSSP; P19120; IATR  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock.  
SQ SEQUENCE 638 AA; 70068 MW; EE86A60E861C36D7 CRC64;

Query Match 93.5%; Score 43; DB 1; Length 638;  
Best Local Similarity 88.9%; Pred. No. 0.5;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLFEGIDLY 9  
:|||||||  
Db 283 ALFEGIDLY 291

RESULT 2  
HS70\_ONCVO STANDARD; PRT; 322 AA.  
AC P11503;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).



```
OS Onchocerca volvulus.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
CC Onchocercidae; Onchocerca.
CC NCBI_TaxID=6282;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=89201313; PubMed=2704388;
CC Rothstein N.M., Higashi G., Yates J., Rajan T.V.;
CC "Onchocerca volvulus heat shock protein 70 is a major immunogen in
CC microfilaricidal individuals from a filariasis-endemic area.";
CC Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A
CC MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL; J04006; AAA29417.1; -.
CC HSP; P19120; IATR.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; PARTIAL.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Heat shock.
CC NON_TER 1
CC FT NON_TER 1
CC SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;
CC -----
Query Match 91.3%; Score 42; DB 1; Length 322;
Best Local Similarity 88.9%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDLY 9
DB 43 SLFEGIDFY 51
|||||||
RESULT 3
HS73_MOUSE STANDARD; PRT; 420 AA.
AC Q61696; Q61697;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).
GN HSP70-3 OR HSP70A1.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=86111900; PubMed=2868009;
CC Lowe D.G., Moran L.A.;
CC "Molecular cloning and analysis of DNA complementary to three mouse
CC Mr = 68,000 heat shock protein mRNAs.";
CC J. Biol. Chem. 261:2102-2112(1986).
CC [2]
CC SEQUENCE OF 155-420 FROM N.A.
CC MEDLINE=94357449; PubMed=8076831;
CC Perry M.D., Aujame L., Shtang S., Moran L.A.;
CC "Structure and expression of an inducible HSP70-encoding gene from
CC Mus musculus.";
CC Gene 146:273-278(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC -----
CC Onchocerca volvulus.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
CC Onchocercidae; Onchocerca.
CC NCBI_TaxID=6282;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=89201313; PubMed=2704388;
CC Rothstein N.M., Higashi G., Yates J., Rajan T.V.;
CC "Onchocerca volvulus heat shock protein 70 is a major immunogen in
CC microfilaricidal individuals from a filariasis-endemic area.";
CC Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A
CC MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL; M12571; AAA57234.1; -.
CC EMBL; M12572; AAA57235.1; -.
CC HSP; P19120; IATR.
CC MGD; MGI:96244; Hsp70-3.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; PARTIAL.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC NON_TER 1
CC FT NON_TER 1
CC SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;
CC -----
Query Match 91.3%; Score 42; DB 1; Length 420;
Best Local Similarity 88.9%; Pred. No. 0.51;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDLY 9
DB 65 SLFEGIDFY 73
|||||||
RESULT 4
HS70_PENCI STANDARD; PRT; 503 AA.
AC Q92260;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
GN HSP70.
OS Penicillium citrinum.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
CC NCBI_TaxID=5077;
CC [1]
CC SEQUENCE FROM N.A.
CC Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
CC "Molecular cloning and expression of a Penicillium citrinum
CC allergen with sequence homology and antigenic cross-reactivity to
CC a hsp70 human heat shock protein.";
CC Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; U64207; AAB06397.1; -.
CC -----
```



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DR HSP: P19120; 3HSC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Allergen.
FT NON_TER 1
SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAE1320 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 503;
Best Local Similarity 88.9%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
DB 154 SLFEGIDFY 162

RESULT 5
HS71_CHICK
ID HS71_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL: J02579; AAA48825.1; -
CC PIR: A25646; A25646.
CC HSP: P19120; LATR.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70; 1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00329; HSP70_1; 1.
CC PROSITE: PS00297; HSP70_2; 1.
CC PROSITE: PS00329; HSP70_3; 1.
CC PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 91.3%; Score 42; DB 1; Length 634;
Best Local Similarity 88.9%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
DB 289 SLFEGIDFY 297

RESULT 6
HS71_CERAE
ID HS71_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL: X70684; CA450019.1; -
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70; 1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
SQ SEQUENCE 638 AA; 69920 MW; D53076A0FFABGAB3 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 638;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
DB 284 SLFEGIDFY 292

RESULT 7
HS72_YEAST
ID HS72_YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YLL024C OR L0931.
```



OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC MEDLINE=69128457; PubMed=2644626;  
 RX STRAIN=S288C;  
 RA Slater M.R., Craig E.A.;  
 RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
 RL Nucleic Acids Res. 17:805-806(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC MEDLINE=69128457; PubMed=2644626;  
 RX STRAIN=S288C;  
 RA Purnelle B., Goffeau A.;  
 RT Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 71-638 FROM N.A.

RC Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 91-97 AND 325-341.

RC MEDLINE=95203288; PubMed=7895733;  
 RX STRAIN=S288C;  
 RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RT Volpe T., Warner J.R., McLaughlin C.S.;  
 RL "Protein identifications for a Saccharomyces cerevisiae protein  
 database.";  
 RL Electrophoresis 15:1466-1486(1994).  
 RN [5]  
 RP SEQUENCE OF 186-195.

RC STRAIN=ATCC 38531 / Y41;  
 RX MEDLINE=97089742; PubMed=8935650;  
 RA Norbeck J., Blomberg A.;  
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
 Saccharomyces cerevisiae.";  
 RL FEMS Microbiol. Lett. 137:1-8(1996).  
 RN [6]  
 RP ACETYLATION, AND PHOSPHORYLATION.

RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
 CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
 CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
 CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE  
 CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -!- PTM: PHOSPHORYLATED.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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 CC -----

DR EMBL: X12927; CAA31394.1; -;  
 DR EMBL: X73129; CAA97472.1; -;  
 DR EMBL: X97560; CAA66167.1; -;  
 DR PIR: S20139; S20139.  
 DR HSSP: P19120; INGI.  
 DR SWISS-2DPAGE: P10592; YEAST.  
 DR YEPD: 9800; -;

DR SGB: S0003947; SSA2.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.

KW Heat shock; ATP-binding; Multigene family; Acetylation;  
 KW Phosphorylation.  
 FT INIT\_MET 0  
 FT MOD\_RES 1 1 ACETYLATION.  
 SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 638;  
 Best Local Similarity 88.9%; Pred. No. 0.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 282 SLFEGIDFY 290

RESULT 8  
 HS74\_PARLI  
 ID HS74\_PARLI STANDARD; PRT; 639 AA.  
 AC Q06248;

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).  
 GN HSP70IV.

OS Paracentrotus lividus (Common sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;  
 OC Paracentrotus.  
 OX NCBI\_TaxID=7656;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=93077053; PubMed=1339375;

RA Sconzo G., Scardina G., Ferraro M.G.;  
 RT "Characterization of a new member of the sea urchin Paracentrotus  
 RT lividus hsp70 gene family and its expression.";  
 RL Gene 121:353-358(1992).  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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 CC -----

DR EMBL: X61379; CAA43653.1; -;  
 DR PIR: JC1391; JC1391.  
 DR HSSP: P19120; INGI.

DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW ATP-binding; Heat shock; Multigene family.  
 SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 91.3%; Score 42; DB 1; Length 639;  
 Best Local Similarity 88.9%; Pred. No. 0.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 286 SLFEGIDFY 294

RESULT 9  
 HS7A\_CAEEL  
 ID HS7A\_CAEEL STANDARD; PRT; 640 AA.  
 AC P09446;



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DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
RX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
RL Gene 64:241-255(1988).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC -----
CC EMBL; M18540; AAA28078.1; -.
DR PIR; J70285; HKW7A.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
DB 287 SLFEGIDFY 295

RESULT 10
HS7C_DICDI
ID HS7C_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RL cap32/34.";
RN EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN=AX3;

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RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; X75263; CAA53039.1; -.
DR EMBL; I22736; AAA33219.1; -.
DR PIR; S37394; S37394.
DR HSP; P19120; INGI.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone.
FT CONFLICT 1 29
FT CONFLICT 32 32
FT CONFLICT 64 64
FT CONFLICT 180 180
FT CONFLICT 237 237
FT CONFLICT 240 240
FT CONFLICT 341 341
FT CONFLICT 352 352
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;

Query Match 91.3%; Score 42; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
DB 284 SLFEGIDFY 292

RESULT 11
HS7I_BOVIN
ID HS7I_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;

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RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerriero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An Alu polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; U09861; AAA73914.1; -
CC EMBL; U02891; AAA03450.1; -
CC HSP; P19120; INGC.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70; 1
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
SQ

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Query Match 91.3%; Score 42; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SLFEGIDLY 9
Db 286 SLFEGIDFY 294
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RESULT 12
ID HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQM0; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=91055806; PubMed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RN Immunogenetics 32:242-251(1990).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Hunt C., Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison
RT with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
RN [3]
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RX MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major
RT heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
RN [5]
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RX MEDLINE=87066768; PubMed=3786141;
RA Drabant B., Genthe A., Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts
RT prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RX MEDLINE=99234376; PubMed=10216320;
RA Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; M59828; AAA63226.1; -
CC EMBL; M59830; AAA63227.1; -
CC EMBL; AF134726; AAD21816.1; -
CC EMBL; AF134726; AAD21815.1; -
CC EMBL; M11717; AAA52697.1; -
CC EMBL; M24743; AAA59844.1; -
CC EMBL; M24744; AAA59845.1; -
CC EMBL; X04677; CAA28381.1; -
CC EMBL; X04677; CAA28382.1; -
CC PIR; A29160; A29160.
CC PIR; A45871; A45871.
CC PIR; A25773; A25773.

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DR PDB; LHJO; 21-OCT-98.
DR SWISS-2DPAGE; P08107; HUMAN.
DR MIM; 140550; -.
DR MIM; 603012; -.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
KW 3D-structure. 7
KW CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 370 370 A -> D (IN REF. 3); AAD21816.
FT CONFLICT 370 370 A -> G (IN REF. 2).
FT CONFLICT 469 469 MISSING (IN REF. 2).
FT CONFLICT 499 499 N -> S (IN REF. 3); AAD21815.
FT CONFLICT 499 499 N -> S (IN REF. 3); AAD21815.
SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 286 SLFEGIDFY 294

RESULT 13
HS71_MOUSE
ID HS71_MOUSE STANDARD; PRT; 641 AA.
AC P17879; O61689;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169;
RA Hunt C.; Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
RL expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible Hsp70-encoding gene from
RL Mus musculus.";
RL Gene 146:273-278(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; M69100; -; NOT_ANNOTATED_CDS.
CC PIR; S35718; S35718.
CC HSSP; P19120; INGC.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.

```



DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family.  
SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;  
  
Query Match 91.3%; Score 42; DB 1; Length 641;  
Best Local Similarity 88.9%; Pred. No. 0.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDLY 9  
| | | | | | | | | |  
DB 286 SLFEGIDFY 294

## RESULT 15

HSP71\_RAT STANDARD; PRT; 641 AA.  
ID HSP71\_RAT  
AC Q07439; P42853;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).  
GN HSP70-1 AND HSP70-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94096443; PubMed=8271311;  
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,  
RA Massa S.M., Sharp F.R.;  
RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal  
RT and injured rat brain.";  
RL J. Neurosci. Res. 36:325-335(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LEW.IW/GUN;  
RX MEDLINE=95012453; PubMed=7927536;  
RA Walter L., Rauh F., Guenther E.;  
RT "Comparative analysis of the three major histocompatibility complex-  
RT linked heat shock protein 70 (Hsp70) genes of the rat.";  
RL Immunogenetics 40:325-330(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
RX MEDLINE=94368874; PubMed=8086479;  
RA Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;  
RT "Cloning, nucleotide sequence and expression of rat heat inducible  
RT hsp70 gene.";  
RL Biochim. Biophys. Acta 1219:64-72(1994).

CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
CC -!- INDUCTION: BY HEAT SHOCK.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L15764; AAA17441.1; -.

DR EMBL; X77208; CAA544423.1; -.  
DR EMBL; X77207; CAA544422.1; -.  
DR EMBL; X74271; CAA52328.1; -.  
DR HSSP; P19120; INGC.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
FT CONFLICT 71 72 KR -> NG (IN REF. 3).  
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).  
FT CONFLICT 408 408 G -> A (IN REF. 3).  
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 91.3%; Score 42; DB 1; Length 641;  
Best Local Similarity 88.9%; Pred. No. 0.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
| | | | | | | | | |  
DB 286 SLFEGIDFY 294

Search completed: December 6, 2001, 08:00:50  
Job time: 418 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:52 ; Search time 170.25 Seconds  
(without alignments)  
7.732 Million cell updates/sec

Title: PEPL-MOD8L

Perfect score: 46

Sequence: 1 SLFEGIDLY 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL17:\*

1: sp-archaea:\*

2: sp-bacteria:\*

3: sp-fungi:\*

4: sp-human:\*

5: sp-invertebrate:\*

6: sp-mammal:\*

7: sp-mhc:\*

8: sp-organelle:\*

9: sp-phase:\*

10: sp-plant:\*

11: sp-rodent:\*

12: sp-virus:\*

13: sp-vertebrate:\*

14: sp-unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	93.5	645	3 094106	094106 pneumocysti
2	43	93.5	647	3 094104	094104 pneumocysti
3	42	91.3	146	5 090667	090667 littorina p
4	42	91.3	153	5 090670	090670 littorina s
5	42	91.3	155	5 090669	090669 littorina s
6	42	91.3	157	5 090665	090665 littorina p
7	42	91.3	158	5 090671	090671 littorina s
8	42	91.3	158	5 090668	090668 littorina p
9	42	91.3	158	5 090666	090666 littorina p
10	42	91.3	220	5 091159	091159 aplysia cal
11	42	91.3	278	13 090520	090520 oncorhynch
12	42	91.3	367	13 098899	098899 fugu rubrip
13	42	91.3	455	11 063718	063718 rattus norv
14	42	91.3	467	5 044350	044350 chondrosia
15	42	91.3	467	5 044352	044352 petrobiona
16	42	91.3	467	5 09NJ92	09NJ92 guancha lac
17	42	91.3	468	5 044349	044349 funiculina
18	42	91.3	469	5 044351	044351 eunicella c
19	42	91.3	526	13 098897	098897 fugu rubrip

20	42	91.3	617	10 09C7X7	09c7x7 arabidopsis
21	42	91.3	628	5 093147	093147 botryllus s
22	42	91.3	629	5 093146	093146 botryllus s
23	42	91.3	632	5 015766	015766 dictyosteli
24	42	91.3	639	13 098900	098900 fugu rubrip
25	42	91.3	639	13 0918F9	0918f9 oryzias lat
26	42	91.3	640	5 093601	093601 caenorhabdi
27	42	91.3	640	13 093240	093240 paralichthy
28	42	91.3	641	11 063256	063256 rattus norv
29	42	91.3	641	11 090WJ5	090WJ5 mus musculu
30	42	91.3	645	5 096541	096541 setaria dig
31	42	91.3	645	5 09NJB7	09njb7 wuchereria
32	42	91.3	645	5 09NGK9	09ngk9 wuchereria
33	42	91.3	645	10 048563	048563 brassica na
34	42	91.3	647	3 059855	059855 schizosacch
35	42	91.3	647	10 041027	041027 pisum sativ
36	42	91.3	650	5 090777	090777 stylophora
37	42	91.3	650	10 092S55	092s55 arabidopsis
38	42	91.3	650	10 09LHA8	09lha8 arabidopsis
39	42	91.3	652	10 093937	093937 ascomphyllum
40	42	91.3	653	5 094805	094805 trichoplusi
41	42	91.3	659	5 09XZJ2	09xzj2 crassostrea
42	41	89.1	190	5 0909B4	0909b4 mytilus edu
43	41	89.1	221	5 091157	091157 aplysia cal
44	41	89.1	467	5 044346	044346 asbestoplum
45	41	89.1	467	5 044347	044347 petrosia fi

## ALIGNMENTS

RESULT	1
094106	
ID	094106 PRELIMINARY; PRT; 645 AA.
AC	094106;
DT	01-MAY-1999 (TREMREL. 10, Created)
DT	01-MAY-1999 (TREMREL. 10, Last sequence update)
DT	01-JUN-2001 (TREMREL. 17, Last annotation update)
DE	HEAT SHOCK PROTEIN 70 (FRAGMENT).
GN	PCSA1.
OS	Pneumocystis carinii f. sp. carinii.
OC	Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC	Pneumocystis.
OX	NCBI_TaxID=38081;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97045128; PubMed=8890193;
RA	Stedman T.T., Buck G.A.;
RT	"Identification, characterization, and expression of the Bip
RT	endoplasmic reticulum resident chaperonins in Pneumocystis carinii.";
RL	Infect. Immun. 64:4463-4471(1996).
DR	EMBL; U0967; AAB00455.1; -.
DR	HSSP; P19120; 3HSC.
DR	InterPro; IPR001023; HSP70.
DR	InterPro; IPR000169; Thiolprot_act_site.
DR	Pfam; PF00012; HSP70; 1.
DR	PRINTS; PR00301; HEATSHOCK70.
DR	PROSITE; PS00297; HSP70_1; UNKNOWN_1.
DR	PROSITE; PS00329; HSP70_2; 1.
DR	PROSITE; PS01036; HSP70_3; 1.
DR	PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW	Heat shock.
FT	NON_TER. 645 645
SQ	SEQUENCE 645 AA; 70884 MW; 6D8CF90433BB163F CRC64;

Query Match 93.5%; Score 43; DB 3; Length 645;

Best Local Similarity 88.9%; Pred. No. 3.7;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDLY 9

||:|||||

Db 286 SLYEGIDLY 294



Tue Dec 11 08:45:50 2001

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 Db 79 SLFEGIDFY 87

RESULT 4  
 Q9U670 PRELIMINARY; PRT; 153 AA.  
 AC Q9U670;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70;  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191825; AAF12784.1; -.  
 DR HSP; P19120; IBAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR NON\_TER 1  
 FT NON\_TER 153  
 SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 91.3%; Score 42; DB 5; Length 153;  
 Best Local Similarity 88.9%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 Db 80 SLFEGIDFY 88

RESULT 5  
 Q9U669 PRELIMINARY; PRT; 155 AA.  
 AC Q9U669;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70;  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191826; AAF12785.1; -.  
 DR HSP; P19120; IBAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR NON\_TER 1  
 FT NON\_TER 155  
 SQ SEQUENCE 155 AA; 17676 MW; C191F65B1F346C2 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 155;  
 Best Local Similarity 88.9%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2  
 Q94104 PRELIMINARY; PRT; 647 AA.  
 AC Q94104;  
 DT 01-MAY-1999 (TREMELrel. 10, Created)  
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
 GN HSP70.  
 OS Pneumocystis carinii.  
 OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;  
 OC Pneumocystis.  
 OX NCBI\_TaxID=4754;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Paul S.P., Graves D.C.;  
 RT "Phylogeny and sequence analysis of Pneumocystis carinii HSP70.";  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U71151; AAD09565.1; -.  
 DR HSP; P19120; 3HSC.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF000169; Thiolprot\_act\_site.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; UNKNOWN\_1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; UNKNOWN\_1.  
 KW Heat shock.  
 FT NON\_TER 1  
 SQ SEQUENCE 647 AA; 71176 MW; 92F94963999380F9 CRC64;

Query Match 93.5%; Score 43; DB 3; Length 647;  
 Best Local Similarity 88.9%; Pred. No. 3.8;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 Db 288 SLFEGIDLY 296

RESULT 3  
 Q9U667 PRELIMINARY; PRT; 146 AA.  
 AC Q9U667;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191828; AAF12787.1; -.  
 DR HSP; P19120; IBAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR NON\_TER 1  
 FT NON\_TER 146  
 SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

Query Match 91.3%; Score 42; DB 5; Length 146;  
 Best Local Similarity 88.9%; Pred. No. 1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 SLFEGIDLY 9  
 |||||  
 Db 82 SLFEGIDFY 90

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6  
 Q90665  
 ID Q90665 PRELIMINARY; PRT; 157 AA.  
 AC Q90665;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191830; AAF12789.1; -.  
 DR HSSP; PI9120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 157;  
 Best Local Similarity 88.9%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 84 SLFEGIDFY 92

RESULT 7  
 Q90671  
 ID Q90671 PRELIMINARY; PRT; 158 AA.  
 AC Q90671;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191824; AAF12783.1; -.  
 DR HSSP; PI9120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 91.3%; Score 42; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 1.1;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 85 SLFEGIDFY 93

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8  
 Q90668  
 ID Q90668 PRELIMINARY; PRT; 158 AA.  
 AC Q90668;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191827; AAF12786.1; -.  
 DR HSSP; PI9120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 91.3%; Score 42; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
 |||||  
 Db 85 SLFEGIDFY 93

RESULT 9  
 Q90666  
 ID Q90666 PRELIMINARY; PRT; 158 AA.  
 AC Q90666;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191829; AAF12788.1; -.  
 DR HSSP; PI9120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 91.3%; Score 42; DB 5; Length 158;



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DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; Multigene family.
FT NON_TER 1
FT NON_TER 278
SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match          91.3%; Score 42; DB 13; Length 278;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches      8; Conservative    0; Mismatches   1; Indels     0; Gaps     0;

QY      1 SLFEGIDLY 9
DB      |||||I
       156 SLFEGIDFY 164

RESULT 12
ID Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
GN HSP70-3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Lim E.H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y08578; CAA69892.1; -.
DR HSSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.
FT NON_TER 367
FT NON_TER 367
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;

Query Match          91.3%; Score 42; DB 13; Length 367;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches      8; Conservative    0; Mismatches   1; Indels     0; Gaps     0;

Qy      1 SLFEGIDLY 9
Db      |||||I
       268 SLFEGIDFY 276

RESULT 13
ID Q63718 PRELIMINARY; PRT; 455 AA.
AC Q63718;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEAT SHOCK ROETEIN 70 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

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RN  SEQUENCE FROM N.A.
RP  Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA  D'Ambrosio E.; 1993) to the EMBL/GenBank/DBJ databases.
RL  Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; 227118; CA981642.1; -.
DR  HSSP; P08107; 1HJO.
DR  InterPro; IPR001023; HSP70.
DR  Pfam; PF00012; HSP70; 1.
DR  PRINTS; PR00301; HEATSHOCK70.
DR  PROSITE; PS00329; HSP70_2; 1.
DR  PROSITE; PS01036; HSP70_3; 1.
KW  Heat shock.
FT  NON_TER 1
FT  NON_TER 455
SQ  SEQUENCE 455 AA; 5040 MW; 0F45F12CBALE2971 CRC64;

Query Match 91.3%; Score 42; DB 11; Length 455;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 254 SLFEGIDFY 260

RESULT 14
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ID O44350 PRELIMINARY; PRT; 467 AA.
AC O44350;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Chondrosia reniformis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Chondrosida; Chondrillidae; Chondrosia.
OX NCBI_TaxID=68574;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelli C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026517; AAC05362.1; -.
DR HSSP; P08109; ICKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 467
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 467;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 252 SLFEGIDFY 260

RESULT 15
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ID O44352 PRELIMINARY; PRT; 467 AA.
AC O44352;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massilliana.
OC Eukaryota; Metazoa; Porifera; Calcareae; Petrobionidae;
OC Petrobiona.
OX NCBI_TaxID=68578;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelli C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSSP; P08109; ICKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 467
SQ SEQUENCE 467 AA; 51458 MW; 23BE28FFD1873DA6 CRC64;

Query Match 91.3%; Score 42; DB 5; Length 467;
Best Local Similarity 88.9%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9
Db 252 SLFEGIDFY 260

Search completed: December 6, 2001, 07:56:52
Job time: 180 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:54 ; Search time 81.43 seconds  
(without alignments)  
2.487 Million cell updates/sec

Title: PEPL-MOD8V  
Perfect score: 46  
Sequence: 1 SLFEGIDVY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	40	87.0	643	4	US-08-797-358B-3
2	38	82.6	646	1	US-08-441-139-14
3	33	71.7	458	4	US-09-457-046B-61
4	32	69.6	789	3	US-08-727-308-1
5	31	67.4	95	1	US-08-438-753B-24
6	31	67.4	95	1	US-08-443-883A-24
7	31	67.4	95	2	US-08-631-328-24
8	31	67.4	95	2	US-08-455-524B-24
9	31	67.4	95	2	US-08-455-021B-24
10	31	67.4	95	4	US-09-045-467-24
11	31	67.4	452	1	US-08-290-978A-5
12	31	67.4	452	2	US-08-780-869-5
13	31	67.4	634	4	US-09-041-236-2
14	31	67.4	666	4	US-09-240-410-2
15	30	65.2	99	1	US-08-438-753B-22
16	30	65.2	99	1	US-08-443-883A-22
17	30	65.2	99	2	US-08-631-328-22
18	30	65.2	99	2	US-08-455-524B-22
19	30	65.2	99	4	US-08-455-021B-22
20	30	65.2	99	4	US-09-045-467-22
21	30	65.2	415	4	US-09-198-956-6
22	30	65.2	465	2	US-08-878-989-18
23	30	65.2	465	2	US-08-860-150-7
24	30	65.2	465	3	US-09-338-132-7
25	30	65.2	465	4	US-09-272-796-18
26	30	65.2	532	2	US-08-560-916-8
27	30	65.2	532	2	US-08-676-841-8

28	30	65.2	603	2	US-08-687-865A-2	Sequence 2, Appli
29	30	65.2	603	4	US-09-043-711-2	Sequence 2, Appli
30	29	63.0	43	1	US-07-998-003A-22	Sequence 22, Appl
31	29	63.0	43	1	US-08-453-274B-22	Sequence 22, Appl
32	29	63.0	43	1	US-08-453-695A-22	Sequence 22, Appl
33	29	63.0	43	1	US-08-268-161A-22	Sequence 22, Appl
34	29	63.0	43	2	US-08-453-702A-22	Sequence 22, Appl
35	29	63.0	43	4	US-09-099-639-22	Sequence 22, Appl
36	29	63.0	43	5	PCT-US93-12588-22	Sequence 22, Appl
37	29	63.0	43	5	PCT-US95-08071-22	Sequence 22, Appl
38	29	63.0	53	2	US-08-469-537A-7	Sequence 7, Appli
39	29	63.0	53	2	US-08-469-537A-20	Sequence 2, Appli
40	29	63.0	161	3	US-09-205-264-2	Sequence 32, Appl
41	29	63.0	303	2	US-08-599-171A-32	Sequence 32, Appl
42	29	63.0	303	2	US-08-646-590B-32	Sequence 32, Appl
43	29	63.0	303	3	US-09-069-226-32	Sequence 32, Appl
44	29	63.0	303	4	US-09-412-184-32	Sequence 32, Appl
45	29	63.0	309	4	US-09-347-803-14	Sequence 14, Appl

## ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-Feb-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 87.0%; Score 40; DB 4; Length 643;  
Best Local Similarity 77.8%; Pred. No. 3.1;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9



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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match
Best Local Similarity 71.7%; Score 33; DB 4; Length 458;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   |||:| |
Db 165 SLFDGISAY 173

RESULT 4
US-08-727-308-1
; Sequence 1, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-727-308-1

Query Match
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDV 8
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Db 23 SLFFGVDV 30

RESULT 5
US-08-438-753B-24
; Sequence 24, Application US/08438753B
; Patent No. 5705363
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match
Best Local Similarity 71.7%; Score 33; DB 4; Length 458;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
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Db 165 SLFDGISAY 173

RESULT 4
US-08-727-308-1
; Sequence 1, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-727-308-1

Query Match
Best Local Similarity 69.6%; Score 32; DB 3; Length 789;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDV 8
   ||| | | |
Db 23 SLFFGVDV 30

RESULT 5
US-08-438-753B-24
; Sequence 24, Application US/08438753B
; Patent No. 5705363
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match
Best Local Similarity 71.7%; Score 33; DB 4; Length 458;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   |||:| |
Db 165 SLFDGISAY 173

RESULT 4
US-08-727-308-1
; Sequence 1, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-727-308-1

Query Match
Best Local Similarity 69.6%; Score 32; DB 3; Length 789;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDV 8
   ||| | | |
Db 23 SLFFGVDV 30

RESULT 5
US-08-438-753B-24
; Sequence 24, Application US/08438753B
; Patent No. 5705363
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match
Best Local Similarity 71.7%; Score 33; DB 4; Length 458;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   |||:| |
Db 165 SLFDGISAY 173

RESULT 4
US-08-727-308-1
; Sequence 1, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,308
; FILING DATE: October 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-727-308-1

Query Match
Best Local Similarity 69.6%; Score 32; DB 3; Length 789;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDV 8
   ||| | | |
Db 23 SLFFGVDV 30

RESULT 5
US-08-438-753B-24
; Sequence 24, Application US/08438753B
; Patent No. 5705363
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match
Best Local Similarity 71.7%; Score 33; DB 4; Length 458;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   |||:| |
Db 165 SLFDGISAY 173

RESULT 4
US-08-727-308-1
; Sequence 1, Application US/08727308
; Patent No. 6020176
; GENERAL INFORMATION:
; APPLICANT: YUJI KAMIYA et al.
; TITLE OF INVENTION: KAURENE SYNTHASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 646 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-139-14

Query Match
Best Local Similarity 82.6%; Score 38; DB 1; Length 646;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   ||:| | | |
Db 286 SLXEGIDFY 294

RESULT 3
US-09-457-046B-61
; Sequence 61, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457.046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 458
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APPLICANT: Imakawa, Kazuhito  
TITLE OF INVENTION: Interferon Tau Compositions and  
METHODS OF USE  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/438,753B  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,891  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,741  
FILING DATE: 09-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/318,050  
FILING DATE: 02-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/969,890  
FILING DATE: 30-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 5600-0001.30  
TELEPHONE: 415-324-0880  
TELEFAX: 415-324-0960  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 95 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).  
US-08-438-753B-24

Query Match 67.4%; Score 31; DB 1; Length 95;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
| : : : : |  
Db 83 SYFQGIHVY 91

RESULT 6  
US-08-443-883A-24  
Sequence 24, Application US/08443883A  
Patent No. 5738845  
GENERAL INFORMATION:  
APPLICANT: Bazer, Fuller W.  
APPLICANT: Johnson, Howard M.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Ott, Troy L.  
APPLICANT: Van Heeke, Gino  
APPLICANT: Imakawa, Kazuhito  
TITLE OF INVENTION: Interferon Tau Compositions and  
METHODS OF USE

NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,883A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,891  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,741  
FILING DATE: 09-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/318,050  
FILING DATE: 02-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/969,890  
FILING DATE: 30-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 5600-0001.30  
TELEPHONE: 415-324-0880  
TELEFAX: 415-324-0960  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 95 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).  
US-08-443-883A-24

Query Match 67.4%; Score 31; DB 1; Length 95;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
| : : : : |  
Db 83 SYFQGIHVY 91

RESULT 7  
US-08-631-328-24  
Sequence 24, Application US/08631328  
Patent No. 5939286  
GENERAL INFORMATION:  
APPLICANT: Johnson, Howard M.  
APPLICANT: Pontzer, Carol H.  
APPLICANT: Subramaniam, Prem S.  
TITLE OF INVENTION: Hybrid Interferon Compositions and  
METHODS OF USE  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA



Tue Dec 11 08:45:51 2001

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; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,328
; FILING DATE: 12-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 5600-0001.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).
; US-08-631-328-24

```

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Query Match 67.4%; Score 31; DB 2; Length 95;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

Qy 1 SLFEGIDVY 9
| | : | | |
Db 83 SYFOGIHVY 91

```

```

RESULT 8
US-08-455-524B-24
; Sequence 24, Application US/08455524B
; Patent No. 5942223
; GENERAL INFORMATION:
; APPLICANT: Bazer, Fuller W.
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Ott, Troy L.
; APPLICANT: Van Heeke, Gino
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,524B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753

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; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 5600-0001.32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; INDIVIDUAL ISOLATE: of SEQ ID NO:23 (HuIFNtau7).
; US-08-455-524B-24

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```

Query Match 67.4%; Score 31; DB 2; Length 95;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

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Qy 1 SLFEGIDVY 9
| | : | | |
Db 83 SYFOGIHVY 91

```

```

RESULT 9
US-08-455-021B-24
; Sequence 24, Application US/08455021B
; GENERAL INFORMATION:
; APPLICANT: Bazer, Fuller W.
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Ott, Troy L.
; APPLICANT: Van Heeke, Gino
; APPLICANT: Imakawa, Kazuhito
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,021B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993

```



```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 5600-0001.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; of SEQ ID NO:23 (HuIFNtau7).
;
; US-08-455-021B-24

Query Match 67.4%; Score 31; DB 2; Length 95;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
DB 83 SYFQGIHVY 91

RESULT 10
US-09-045-467-24
; Sequence 24, Application US/09045467
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; METHODS OF USE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,467
; FILING DATE: 20-Mar-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/455,021
; FILING DATE: 31-MAY-1995
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
```

```
;
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 5600-0001.36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence
; of SEQ ID NO:23 (HuIFNtau7).
;
; US-09-045-467-24

Query Match 67.4%; Score 31; DB 4; Length 95;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
DB 83 SYFQGIHVY 91

RESULT 11
US-08-290-978A-5
; Sequence 5, Application US/08290978A
; Patent No. 5624834
; GENERAL INFORMATION:
; APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
; APPLICANT: MULLER, YVONNE
; APPLICANT: KESTER, HERMANUS C.M.
; APPLICANT: VISSER, JACOB
; APPLICANT: VAN Ooyen, ALBERT J.J.
; APPLICANT: ROLIN, CLAUDE
; TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
; TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,978A
; FILING DATE: 17-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4615-0044.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
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```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-290-978A-5

Query Match          67.4%; Score 31; DB 1; Length 452;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFGIDV 8
DB 203 LFDGIDI 209

RESULT 12
US-08-780-869-5
; Sequence 5, Application US/08780869
; Patent No. 5830737
; GENERAL INFORMATION:
; APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.
; APPLICANT: MULLER, YVONNE
; APPLICANT: KESTER, HERMANUS C.M.
; APPLICANT: VISSER, JACOB
; APPLICANT: VAN OUYEN, ALBERT J.J.
; APPLICANT: ROLIN, CLAUD
; TITLE OF INVENTION: CLONING AND EXPRESSION OF THE
; EXO-POLYGLACTURONASE GENE FROM ASPERGILLUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,869
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,978
; FILING DATE: 17-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4615-0044.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-780-869-5

Query Match          67.4%; Score 31; DB 2; Length 452;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LFGIDV 8
DB 203 LFDGIDI 209
```

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RESULT 13
US-09-041-236-2
; Sequence 2, Application US/09041236
; Patent No. 6225285
; GENERAL INFORMATION:
; APPLICANT: Luo, Yuling
; APPLICANT: Xiomei, Xu
; TITLE OF INVENTION: Semaphorin K1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,236
; FILING DATE: March 11, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: EXEL98-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-041-236-2

Query Match          67.4%; Score 31; DB 4; Length 634;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFGIDVY 9
DB 149 LFGDEVY 156

RESULT 14
US-09-240-410-2
; Sequence 2, Application US/09240410
; Patent No. 6197544
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: HAYES, PHILIP DAVID
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,410
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; FILING DATE: 27-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK APPLICATION NO. TO BE ASSIGNED  
; FILING DATE: 20-JAN-1999  
; APPLICATION NUMBER: EP APPLICATION NO. 98300694.1  
; FILING DATE: 30-JAN-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GP-30039  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0700  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 666 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-240-410-2

Query Match 67.4%; Score 31; DB 4; Length 666;  
Best Local Similarity 75.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDVY 9  
Db 181 LFEGDEVY 188

## RESULT 15

US-08-438-753B-22  
; Sequence 22, Application US/08438753B  
; Patent No. 5705363  
; GENERAL INFORMATION:  
; APPLICANT: Inakawa, Kazuhito  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,753B  
; FILING DATE: 10-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 5600-0001.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-324-0880  
; TELEFAX: 415-324-0960  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: Of SEQ ID NO:21 (Hu1ENTau6).  
; US-08-438-753B-22

Query Match 65.2%; Score 30; DB 1; Length 99;  
Best Local Similarity 55.6%; Pred. No. 39;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
Db 83 SYFOGIHY 91

Search completed: December 6, 2001, 07:59:55  
Job time: 363 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:26 ; Search time 88.19 Seconds  
(without alignments)  
7.774 Million cell updates/sec

Title: PEP1-MOD8V

Perfect score: 46

Sequence: 1 SLFEGIDVY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	89.1	208	2 B44261	dnak-type molecule
2	41	89.1	209	2 A44261	dnak-type molecule
3	41	89.1	278	2 I51344	dnak-type molecule
4	41	89.1	372	2 P00138	dnak-type molecule
5	41	89.1	420	2 A26283	dnak-type molecule
6	41	89.1	467	2 T45477	heat-shock protein
7	41	89.1	467	2 T45479	heat-shock protein
8	41	89.1	468	2 T45476	heat-shock protein
9	41	89.1	469	2 T45478	heat-shock protein
10	41	89.1	617	2 H96605	probable heat shock
11	41	89.1	632	2 T45471	dnak-type molecule
12	41	89.1	634	2 A25646	dnak-type molecule
13	41	89.1	636	2 A48872	dnak-type molecule
14	41	89.1	638	2 S31766	dnak-type molecule
15	41	89.1	639	2 JC1391	dnak-type molecule
16	41	89.1	639	2 S20139	dnak-type molecule
17	41	89.1	640	1 HHKW7A	dnak-type molecule
18	41	89.1	640	2 A29160	dnak-type molecule
19	41	89.1	640	2 S37394	dnak-type molecule
20	41	89.1	640	2 T21394	hypothetical prote
21	41	89.1	640	2 T43724	dnak-type molecule
22	41	89.1	641	2 S53357	dnak-type molecule
23	41	89.1	641	2 S35718	dnak-type molecule
24	41	89.1	641	2 I54542	dnak-type molecule
25	41	89.1	641	2 A45871	dnak-type molecule
26	41	89.1	642	1 HHBYA1	dnak-type molecule
27	41	89.1	642	2 JH0095	dnak-type molecule
28	41	89.1	642	2 B36590	dnak-type molecule
29	41	89.1	644	2 A45635	dnak-type molecule

```

30      41      89.1      645      2      I51129      dnak-type molecule
31      41      89.1      646      2      T46650      heat shock protein
32      41      89.1      647      1      HXL70       dnak-type molecule
33      41      89.1      647      2      S44168      dnak-type molecule
34      41      89.1      647      2      T41121      heat shock protein
35      41      89.1      650      2      JC7088      heat shock protein
36      40      87.0      214      2      A03309      dnak-type molecule
37      40      87.0      379      2      I46588      dnak-type molecule
38      40      87.0      467      2      T45473      heat-shock protein
39      40      87.0      467      2      T45474      heat-shock protein
40      40      87.0      641      2      JN0668      dnak-type molecule
41      40      87.0      641      2      PC7036      heat shock protein
42      40      87.0      643      2      S25585      dnak-type molecule
43      40      87.0      643      2      S09036      dnak-type molecule
44      40      87.0      651      2      T45517      heat shock protein
45      40      87.0      651      2      JC7132      heat shock protein

```

#### ALIGNMENTS

RESULT 1

B44261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KUH>

A>Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

A:Gene: HSC70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

```

Query Match      89.1%; Score 41; DB 2; Length 208;
Best Local Similarity 88.9%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 SLFEGIDVY 9

Db 132 SLFEGIDVY 140

RESULT 2

A44261

dnak-type molecular chaperone HSP70a - California sea hare (fragment)

N:Alternate names: heat shock protein 70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: A44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: A44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-209 <KUH>

A>Note: sequence extracted from NCBI backbone (NCBIP:118951)

C:Genetics:

A:Gene: HSP70a

C:Function:



A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 209;  
Best Local Similarity 88.9%; Pred. No. 0.61;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 133 SLFEGIDY 141

RESULT 3  
I51344  
dnaK-type molecular chaperone (clone pHS70.7) - rainbow trout (fragment)  
N:Alternate names: 70K heat shock protein  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999  
C:Accession: I51344  
R:Kothary, R.K.; Jones, D.; Candido, E.P.M.  
Mol. Cell. Biol. 4, 1785-1791, 1984  
A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of  
A:Reference number: I51344; MUID:85036330  
A:Accession: I51344  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-278 <KOT>  
A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 278;  
Best Local Similarity 88.9%; Pred. No. 0.84;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 156 SLFEGIDFY 164

RESULT 4  
PQ0138  
dnaK-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)  
N:Alternate names: heat shock protein 70  
C:Species: Paracentrotus lividus (common urchin)  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 20-Aug-1999  
C:Accession: PQ0138  
R:Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.  
Gene 96, 295-300, 1990  
A:Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.  
A:Reference number: PQ0138; MUID:91099690  
A:Accession: PQ0138  
A:Molecule type: DNA  
A:Residues: 1-372 <ROS>  
A:Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001  
C:Genetics:  
A:Gene: hsp70 II  
A:Introns: 68/1; 137/1; 188/3; 281/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 372;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 286 SLFEGIDY 294

RESULT 5  
A26283  
dnaK-type molecular chaperone - mouse (fragment)  
N:Alternate names: heat shock protein 58  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A26283  
R:Lowe, D.G.; Moran, L.A.  
J. Biol. Chem. 261, 2102-2112, 1986  
A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr-68,000  
A:Reference number: A26283; MUID:86111900  
A:Accession: A26283  
A:Molecule type: mRNA  
A:Residues: 1-420 <LOW>  
A:Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208  
A:Note: the authors translated the codon CTG for residue 173 as Val and CGC for resid  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 420;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 65 SLFEGIDFY 73

RESULT 6  
T45477  
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)  
C:Species: Chondrosia reniformis  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45477  
R:Borchelli, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45477  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 89.1%; Score 41; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 252 SLFEGIDFY 260

RESULT 7  
T45479  
heat-shock protein 70 [imported] - Eunicella cavollini (fragment)  
C:Species: Eunicella cavollini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45479  
R:Borchelli, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983



A:Accession: T45479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 89.1%; Score 41; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
|||||||  
Db 252 SLFEGIDFY 260

RESULT 8  
T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
C:Species: Funiculina quadrangularis  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45476  
R:Borchliellini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: 222983  
A:Accession: T45476  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-468 <BOR>  
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 89.1%; Score 41; DB 2; Length 468;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
|||||||  
Db 253 SLFEGIDFY 261

RESULT 9  
T45478  
heat-shock protein 70 [imported] - Eunicella cavollini (fragment)  
C:Species: Eunicella cavollini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45478  
R:Borchliellini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: 222983  
A:Accession: T45478  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-469 <BOR>  
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 89.1%; Score 41; DB 2; Length 469;  
Best Local Similarity 88.9%; Pred. No. 1.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
|||||||  
Db 254 SLFEGIDFY 262

RESULT 10  
H96605

Probable heat shock protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001

C:Accession: H96605

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: H96605

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-617 <STO>

A:Cross-references: GB:AF005173; NID:gl1024845; PIDN:AAG26930.1; GSPDB:GN00141

C:Genetics:

A:Gene: F13N6.9

A:Map position: 1

C:Superfamily: heat shock protein 70

Query Match 89.1%; Score 41; DB 2; Length 617;  
Best Local Similarity 88.9%; Pred. No. 2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
|||||||  
Db 292 SLFEGIDFY 300

RESULT 11  
T45471

dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum

N:Alternate names: heat shock cognate protein 70

C:Species: Dictyostelium discoideum

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T45471

R:Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.

submitted to the EMBL Data Library, September 1997

A:Reference number: 222980

A:Accession: T45471

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-632 <BOV>

A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1

A:Experimental source: strain AX3

C:Genetics:

A:Gene: hsc70

A:Note: localized to filopodias and cortex

C:Superfamily: heat shock protein 70

Query Match 89.1%; Score 41; DB 2; Length 632;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
|||||||  
Db 285 SLFEGIDFY 293

RESULT 12  
A25646

dnak-type molecular chaperone - chicken



N:Alternate names: heat shock protein 70  
C:Species: Gallus gallus (chicken)  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25646  
R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
J. Biol. Chem. 261, 12692-12699, 1986  
A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.  
A:Reference number: A25646; MUID:86304452  
A:Accession: A25646  
A:Molecule type: DNA  
A:Residues: 1-634 <MOR>  
A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941  
A:Note: The authors translated the codon TCG for residue 583 as Trp  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 634;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 289 SLFEGIDFY 297

RESULT 13  
A48872  
dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)  
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein aginactin  
C:Species: Dictyostelium discoideum  
C>Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
C:Accession: A48872  
R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
J. Biol. Chem. 268, 23267-23274, 1993  
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an  
A:Reference number: A48872; MUID:94043116  
A:Accession: A48872  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-636 <EDD>  
A:Cross-references: GB:L12736; NID:g433179; PIDN:AAA33219.1; PID:g433180  
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Val  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 636;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 280 SLFEGIDFY 288

RESULT 14  
S31766  
dnaK-type molecular chaperone hsp70 - green monkey  
N:Alternate names: heat shock protein 70  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S31766; I36927  
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
submitted to the EMBL Data Library, January 1993  
A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
A:Reference number: S31766  
A:Accession: S31766  
A:Molecule type: mRNA

A:Residues: 1-638 <SAI>  
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
FEBS Lett. 355, 282-286, 1994  
A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible  
A:Reference number: I36927; MUID:95080396  
A:Accession: I36927  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-638 <RES>  
A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
A:Experimental source: kidney; cell line COS-1  
C:Genetics:  
A:Gene: hsp70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 89.1%; Score 41; DB 2; Length 638;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 284 SLFEGIDFY 292

RESULT 15  
JC1391  
dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
N:Alternate names: heat shock protein 70IV; hsp70IV protein  
C:Species: Paracentrotus lividus (common urchin)  
C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
C:Accession: JC1391  
R:Sconzo, G.; Scardina, G.; Ferraro, M.G.  
Gene 121, 353-358, 1992  
A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp  
A:Reference number: JC1391; MUID:93077053  
A:Accession: JC1391  
A:Molecule type: DNA  
A:Residues: 1-639 <SCO>  
A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
C:Genetics:  
A:Gene: hsp70IV  
A:Introns: 61/2  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 89.1%; Score 41; DB 2; Length 639;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 286 SLFEGIDFY 294

Search completed: December 6, 2001, 07:58:26  
Job time: 274 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:50 ; Search time 50.21 Seconds  
(without alignments)  
6.572 Million cell updates/sec

Title: PEPL-MOD8V  
Perfect score: 46  
Sequence: 1 SLFEGIDVY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	41	89.1	322	1 HS70_ONCVO	P11503 onchocerca
2	41	89.1	372	1 HS72_PARLI	P22623 paracentrot
3	41	89.1	420	1 HS73_MOUSE	Q61696 mus musculus
4	41	89.1	503	1 HS70_PENCI	Q92260 penicillium
5	41	89.1	634	1 HS70_CHICK	P08106 gallus gall
6	41	89.1	638	1 HS71_CERAE	Q28222 cercopithec
7	41	89.1	638	1 HS72_YEAST	P10592 saccharomyc
8	41	89.1	639	1 HS74_PARLI	Q06248 paracentrot
9	41	89.1	640	1 HS7A_CAEEL	P09446 caenorhabdi
10	41	89.1	640	1 HS7C_DICDI	P36415 dictyosteli
11	41	89.1	641	1 HS71_BOVIN	Q27975 bos taurus
12	41	89.1	641	1 HS71_HUMAN	P08107 homo sapien
13	41	89.1	641	1 HS71_MOUSE	P17879 mus musculus
14	41	89.1	641	1 HS71_PIG	P34930 sus scrofa
15	41	89.1	641	1 HS71_RAT	Q07439 rattus norv
16	41	89.1	641	1 HS71_YEAST	P10591 saccharomyc
17	41	89.1	641	1 HS72_BOVIN	Q27965 bos taurus
18	41	89.1	641	1 HS74_YEAST	P22202 saccharomyc
19	41	89.1	644	1 HS70_BRUNA	P27541 bruglia mala
20	41	89.1	644	1 HS70_ONCTYS	Q91233 oncorhynch
21	41	89.1	645	1 HS70_PLEWA	Q91291 pleurodeles
22	41	89.1	646	1 HS70_NEUCR	Q01223 neurospora
23	41	89.1	647	1 HS70_XENLA	P02827 xenopus lae
24	41	89.1	649	1 HS70_BLAEM	P48720 blastoclad
25	41	89.1	652	1 HS7D_MANSE	Q90639 manduca sex
26	40	87.0	214	1 HS7A_DROSI	P02826 drosophila
27	40	87.0	379	1 HS7X_PIG	P34934 sus scrofa
28	40	87.0	638	1 HS70_CERCA	P1902 ceratitidis c
29	40	87.0	641	1 HS7A_DROME	P29843 drosophila
30	40	87.0	643	1 HS76_HUMAN	P17066 homo sapien
31	40	87.0	643	1 HS76_PIG	Q04967 sus scrofa
32	40	87.0	648	1 HS71_PUCGR	Q01877 puccinia gr
33	38	82.6	641	1 HS73_RAT	P55063 rattus norv

34 HS7H\_HUMAN 641 1 HS7H\_HUMAN P34931 homo sapien  
35 HS7T\_MOUSE 641 1 HS7T\_MOUSE P16627 mus musculus  
36 HS72\_PICAN 642 1 HS72\_PICAN P53623 pichia angu  
37 HS71\_SCHPO 643 1 HS71\_SCHPO Q10265 schizosacch  
38 HS71\_PICAN 644 1 HS71\_PICAN P11142 pichia angu  
39 HS72\_LYCES 644 1 HS72\_LYCES P27322 lycopersico  
40 HS70\_SOYBN 645 1 HS70\_SOYBN P26413 glycine max  
41 HS7C\_CRIGR 646 1 HS7C\_CRIGR P19378 cricetus  
42 HS7C\_HUMAN 646 1 HS7C\_HUMAN P11142 homo sapien  
43 HS7C\_MOUSE 646 1 HS7C\_MOUSE P08109 mus musculus  
44 HS70\_PARRR 649 1 HS70\_PARRR P87047 paracoccidi  
45 HS73\_ARATH 649 1 HS73\_ARATH O65719 arabidopsis

## ALIGNMENTS

RESULT 1  
HS70\_ONCVO STANDARD: PRT; 322 AA.  
AC P11503;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DE 01-FEB-1996 (Rel. 33, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89201313; PubMed=2704388;  
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;  
RT Onchocerca volvulus heat shock protein 70 is a major immunogen in  
amicrofilaremic individuals from a filariasis-endemic area.;  
RL Mol. Biochem. Parasitol. 33:229-236(1989).  
CC -! DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A  
MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  
CC -! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC -----  
CC EMBL; J04006; AAA29417.1; -  
DR HSSP; P19120; IATR.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock.  
FT NON\_TER 1  
FT NON\_TER 322 322  
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 89.1%; Score 41; DB 1; Length 322;  
Best Local Similarity 88.9%; Pred No. 0.57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVY 9  
Db 43 SLFEGIDFY 51  
Query Match 89.1%; Score 41; DB 1; Length 322;  
Best Local Similarity 88.9%; Pred No. 0.57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVY 9  
Db 43 SLFEGIDFY 51

RESULT 2  
HS72\_PARLI STANDARD: PRT; 372 AA.  
ID HS72\_PARLI



AC P22623;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).  
GN HSP70II.  
OS Paracentrotus lividus (Common sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinozoa; Echinacea; Echinoida; Echinidae;  
OC Paracentrotus.  
OX NCBI\_TaxID=7656;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Gonad;  
RX MEDLINE=9109690; PubMed=2269441;  
RA la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.;  
RT "Sequence of a sea urchin hsp70 gene and its 5' flanking region.";  
RL Gene 96:295-300(1990).  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC -----  
DR EMBL; X16544; CAA34544.1; --  
DR PIR; P00138; P00138.  
DR HSSP; P19120; INGI.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70.1.  
DR PROSITE; PS00297; HSP70.1; 1.  
DR PROSITE; PS00329; HSP70.2; PARTIAL.  
DR PROSITE; PS01036; HSP70.3; 1.  
DR ATP-binding; Heat shock; Multigene family.  
KW NON\_TER 372  
FT SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;  
SQ  
  
Query Match 89.1%; Score 41; DB 1; Length 372;  
Best Local Similarity 88.9%; Pred. No. 0.67;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDVY 9  
Db 286 SLFEGIDY 294  
|||||||  
  
RESULT 3  
HS73\_MOUSE  
ID HS73\_MOUSE STANDARD; PRT; 420 AA.  
AC Q61696; Q61697;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).  
GN HSP70-3 OR HSP70A1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8611900; PubMed=2868009;  
RA Lowe D.G., Moran L.A.;  
RT "Molecular cloning and analysis of DNA complementary to three mouse  
RT Mr = 68,000 heat shock protein mRNAs.";  
RL J. Biol. Chem. 261:2102-2112(1986).  
RN [2]  
RP SEQUENCE OF 155-420 FROM N.A.  
RX MEDLINE=94357449; PubMed=8076831;

RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
RT "Structure and expression of an inducible HSP70-encoding gene from  
RT Mus musculus.";  
RL Gene 146:273-278(1994).  
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC OF NEWLY TRANSLATED PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
CC -1- INDUCTION: BY HEAT SHOCK.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC -----  
DR EMBL; M12571; AAA57234.1; --  
DR EMBL; M12572; AAA57235.1; --  
DR HSSP; P19120; IATR.  
DR MGD; MGI:96244; Hsp70-3.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70.1.  
DR PROSITE; PS00297; HSP70.1; PARTIAL.  
DR PROSITE; PS00329; HSP70.2; PARTIAL.  
DR PROSITE; PS01036; HSP70.3; 1.  
DR ATP-binding; Chaperone; Heat shock; Multigene family.  
KW NON\_TER 188  
FT VARIANT 188 188 V -> G.  
SQ SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;  
SQ  
  
Query Match 89.1%; Score 41; DB 1; Length 420;  
Best Local Similarity 88.9%; Pred. No. 0.76;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDVY 9  
Db 65 SLFEGIDFY 73  
|||||||  
  
RESULT 4  
HS70\_PENCI  
ID HS70\_PENCI STANDARD; PRT; 503 AA.  
AC Q92260;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
GN HSP70.  
OS Penicillium citrinum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
OX NCBI\_TaxID=5077;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;  
RT "Molecular cloning and expression of a penicillium citrinum  
RT allergen with sequence homology and antigenic cross-reactivity to  
RT a hsp70 human heat shock protein.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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DR EMBL; U64207; AAB06397.1; -  
DR HSP; P19120; 3HSC.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Allergen.  
FT NON\_TER 1  
SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEAL320 CRC64;

Query Match 89.1%; Score 41; DB 1; Length 503;  
Best Local Similarity 88.9%; Pred. No. 0.92;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
Db 154 SLFEGIDFY 162  
|||||

RESULT 5  
HS70\_CHICK  
ID HS70\_CHICK STANDARD; PRT; 634 AA.  
AC P08106;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86304452; PubMed=3017985;  
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
RT "Organization, nucleotide sequence, and transcription of the chicken  
HSP70 gene."  
RL J. Biol. Chem. 261:12692-12699(1986).  
CC - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----

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CC -----

DR EMBL; J02579; AAA48825.1; -  
DR PIR; A25646; A25646.  
DR HSP; P19120; 1A7R.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock; Multigene family.  
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 89.1%; Score 41; DB 1; Length 634;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9

Db 289 SLFEGIDFY 297  
|||||

RESULT 6  
HS71\_CERAE  
ID HS71\_CERAE STANDARD; PRT; 638 AA.  
AC Q28222;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN 1.  
GN HSPAL.  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
RX MEDLINE=95080396; PubMed=7988690;  
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;  
RT "The hsc70 gene which is slightly induced by heat is the main virus  
inducible member of the hsp70 gene family."  
RL FEBS Lett. 355:282-286(1994).  
CC - FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING  
CC STRESS-INDUCED DAMAGE.

CC - INDUCTION: BY HEAT SHOCK.  
CC - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----

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DR EMBL; X70684; CAA50019.1; -  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 89.1%; Score 41; DB 1; Length 638;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
Db 284 SLFEGIDFY 292  
|||||

RESULT 7  
HS72\_YEAST  
ID HS72\_YEAST STANDARD; PRT; 638 AA.  
AC P10592;



01-JUL-1989 (Rel. 11, Created)  
01-OCT-1994 (Rel. 30, Last sequence update)  
01-OCT-1996 (Rel. 34, Last annotation update)  
HEAT SHOCK PROTEIN SSA2  
SSA2 OR YLL024C OR L0931.  
Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=S288C;  
RX MEDLINE=89128457; PubMed=2644626;  
RA Slater M.R., Craig E.A.;  
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
RL Nucleic Acids Res. 17:805-806(1989).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=S288C;  
RX MEDLINE=89128457; PubMed=2644626;  
RA Slater M.R., Craig E.A.;  
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
RL Nucleic Acids Res. 17:805-806(1989).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=S288C;  
RX MEDLINE=89128457; PubMed=2644626;  
RA Slater M.R., Craig E.A.;  
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
RL Nucleic Acids Res. 17:805-806(1989).  
RN [4]  
RN SEQUENCE OF 91-97 AND 325-341.  
RP STRAIN=S288C;  
RX MEDLINE=95203288; PubMed=7895733;  
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
RA Volpe T., Warner J.R., McLaughlin C.S.;  
RT "Protein identifications for a Saccharomyces cerevisiae protein  
database.";  
RL Electrophoresis 15:1466-1486(1994).  
RN [5]  
RN SEQUENCE OF 186-195.  
RP STRAIN=ATCC 38531 / Y41;  
RX MEDLINE=97089742; PubMed=8935650;  
RA Norbeck J., Blomberg A.;  
RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
Saccharomyces cerevisiae.";  
RL FEMS Microbiol. Lett. 137:1-8(1996).  
RN [6]  
RN ACETYLATION, AND PHOSPHORYLATION.  
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
RA Volpe T., Warner J.R., McLaughlin C.S.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
CC -1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE  
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- PTM: PHOSPHORYLATED.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC  
CC EMBL; X12927; CAA31394.1; -;  
CC EMBL; X73129; CAA97472.1; -;  
CC EMBL; X97560; CAA66167.1; -;  
CC PIR; S20139; S20139.  
CC HSP; P19120; INGJ.  
CC SWISS-2DPAGE; P10592; YEAST.  
CC YEPD; 9800; -;  
CC SGD; S0003947; SSA2.  
CC InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; ATP-binding; Multigene family; Acetylation;  
KW Phosphorylation.  
FT INIT\_MET 0  
FT MOD\_RES 1  
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;  
  
Query Match 89.1%; Score 41; DB 1; Length 638;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDVY 9  
DB 282 SLFEGIDFY 290  
  
RESULT 8.  
HS74\_PARLI  
ID HS74\_PARLI STANDARD; PRT; 639 AA.  
AC Q06248;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).  
GN HSP70IV.  
OS Paracentrotus lividus (Common sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;  
OC Paracentrotus.  
OX NCBI\_TaxID=7656;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=93077053; PubMed=1339375;  
RA Sconzo G., Scardina G., Ferraro M.G.;  
RT "Characterization of a new member of the sea urchin Paracentrotus  
RT lividus hsp70 gene family and its expression.";  
RL Gene 121:353-358(1992).  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC  
CC EMBL; X61379; CAA43653.1; -;  
CC PIR; JC1391; JC1391.  
CC HSP; P19120; INGJ.  
CC InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock; Multigene family.  
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;  
  
Query Match 89.1%; Score 41; DB 1; Length 639;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDVY 9  
DB 286 SLFEGIDFY 294



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RT cap32/34.";
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RX STRAIN-AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -|- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -|- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; X75263; CAA53039.1; -
DR EMBL; L22736; AAA33219.1; -
DR PIR; S37394; S37394.
DR HSSP; P19120; INGI.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone.
FT CONFLICT 1 29
FT CONFLICT 32 32
FT CONFLICT 64 64
FT CONFLICT 180 180
FT CONFLICT 237 237
FT CONFLICT 240 240
FT CONFLICT 341 341
FT CONFLICT 352 352
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;
MSSIGIDLTGYTSCVGVWMDRVEIAND ->
IHNNHGNATVWVSGPVPSEVLSFN (IN REF. 2).
N -> T (IN REF. 2).
V -> A (IN REF. 2).
R -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
I -> L (IN REF. 2).
F -> P (IN REF. 2).

Query Match 89.1%; Score 41; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
Db 284 SLFEGIDFY 292
|||||||

RESULT 11
HST1_BOVIN
ID HST1_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

RT cap32/34.";
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RX STRAIN-AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -|- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -|- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X75263; CAA53039.1; -
DR EMBL; L22736; AAA33219.1; -
DR PIR; S37394; S37394.
DR HSSP; P19120; INGI.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone.
FT CONFLICT 1 29
FT CONFLICT 32 32
FT CONFLICT 64 64
FT CONFLICT 180 180
FT CONFLICT 237 237
FT CONFLICT 240 240
FT CONFLICT 341 341
FT CONFLICT 352 352
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;
MSSIGIDLTGYTSCVGVWMDRVEIAND ->
IHNNHGNATVWVSGPVPSEVLSFN (IN REF. 2).
N -> T (IN REF. 2).
V -> A (IN REF. 2).
R -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
I -> L (IN REF. 2).
F -> P (IN REF. 2).

Query Match 89.1%; Score 41; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
Db 287 SLFEGIDFY 295
|||||||

RESULT 10
HST7_DICDI
ID HST7_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-AX3;
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerliero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An AluI polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; U09861; AAA73914.1; -
CC EMBL; U02891; AAA03450.1; -
CC HSP; P19120; INGC.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
KW SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
SQ

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Query Match      89.18; Score 41; DB 1; Length 641;
Best Local Similarity 88.98; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 SLFEGIDVY 9
   |||||
Db 286 SLFEGIDFY 294

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RESULT 12
HS71_HUMAN
ID HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q90040; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91055806; PubMed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Hunt C., Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison
RT with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
RN [3]
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RX MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major
RT heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
RN [5]
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RX MEDLINE=87066768; PubMed=3786141;
RA Drabant B., Genthe A., Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts
RT prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RX MEDLINE=99234376; PubMed=10216320;
RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; M59828; AAA63226.1; -
CC EMBL; M59830; AAA63227.1; -
CC EMBL; AF134726; AAD21816.1; -
CC EMBL; AF134726; AAD21815.1; -
CC EMBL; M11717; AAA52697.1; -
CC EMBL; M24743; AAA59844.1; -
CC EMBL; M24744; AAA59845.1; -

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DR EMBL; X04676; CAA28381.1; -.
DR EMBL; X04677; CAA28382.1; -.
DR PIR; A29160; A29160.
DR PIR; A45871; A45871.
DR PIR; A25773; A25773.
DR PDB; 1HJO; 21-OCT-98..
DR SWISS-2DPAGE; P08107; HUMAN.
DR MIM; 140550; -.
DR MIM; 603012; -.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
KW 3D-structure.
FT CONFLICT 7 7 I -> V (IN REF. 2).
FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).
FT CONFLICT 370 370 A -> G (IN REF. 2).
FT CONFLICT 469 469 MISSING (IN REF. 2).
FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).
FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).
SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;

Query Match 89.1%; Score 41; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   |||||
Db 286 SLFEGIDFY 294

RESULT 13
HS71_MOUSE
ID HS71_MOUSE STANDARD; PRT; 641 AA.
AC P17879; O61689;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169;
RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
RL expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from
RL Mus musculus.";
RL Gene 146:273-278(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; M69100; -; NOT_ANNOTATED_CDS.
CC PIR; S35718; S35718.

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CC
CC EMBL; M35021; AAA37864.1; -.
CC EMBL; M76613; AAA57233.1; -.
CC PIR; JH0095; JH0095.
CC HSP; P19120; INGC.
CC MGD; MGI:99517; Hsp70-1.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 342 342 A -> R (IN REF. 1).
FT CONFLICT 627 627 P -> PP (IN REF. 1).
SQ SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 89.1%; Score 41; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
   |||||
Db 286 SLFEGIDFY 294

RESULT 14
HS71_PIG
ID HS71_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPA1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
RT Bouquet Y.H.;
RL "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; M69100; -; NOT_ANNOTATED_CDS.
CC PIR; S35718; S35718.
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CC -----  
 DR HSP; P19120; INGC.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family.  
 SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match 89.1%; Score 41; DB 1; Length 641;  
 Best Local Similarity 88.9%; Pred. No. 1.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
 |||||  
 Db 286 SLFEGIDFY 294

## RESULT 15

HS7L\_RAT STANDARD; PRT; 641 AA.  
 AC Q07439; P42853;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).  
 GN HSP70-1 AND HSP70-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94096443; PubMed=8271311;  
 RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,  
 RA Massa S.M., Sharp F.R.;  
 RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal  
 RT and injured rat brain.";  
 RL J. Neurosci. Res. 36:325-335(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LEW.1W/GUN;  
 RX MEDLINE=95012453; PubMed=7927536;  
 RA Walter L., Rauh F., Guenther E.;  
 RT "Comparative analysis of the three major histocompatibility complex-  
 RT linked heat shock protein 70 (Hsp70) genes of the rat.";  
 RL Immunogenetics 40:325-330(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
 RX MEDLINE=94368874; PubMed=8086479;  
 RA Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;  
 RA "Cloning, nucleotide sequence and expression of rat heat inducible  
 RT hsp70 gene.";  
 RL Biochim. Biophys. Acta 1219:64-72(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way

Query Match 89.1%; Score 41; DB 1; Length 641;  
 Best Local Similarity 88.9%; Pred. No. 1.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
 |||||  
 Db 286 SLFEGIDFY 294

Search completed: December 6, 2001, 08:00:51  
 Job time: 419 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: December 6, 2001, 07:56:52 ; Search time 170.25 seconds  
(without alignments)  
7.732 Million cell updates/sec

Title: PEP1-MOD8V

Perfect score: 46

Sequence: 1 SLFEGIDVY 9

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp.vertibrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	89.1	146	5 Q9U667	Q9U667 littorina p
2	41	89.1	153	5 Q9U670	Q9U670 littorina s
3	41	89.1	155	5 Q9U669	Q9U669 littorina s
4	41	89.1	157	5 Q9U665	Q9U665 littorina p
5	41	89.1	158	5 Q9U671	Q9U671 littorina s
6	41	89.1	158	5 Q9U668	Q9U668 littorina p
7	41	89.1	158	5 Q9U666	Q9U666 littorina p
8	41	89.1	220	5 P81159	P81159 aplysia cal
9	41	89.1	221	5 P81157	P81157 aplysia cal
10	41	89.1	278	13 Q9U520	Q9U520 oncorhynch
11	41	89.1	367	13 Q98899	Q98899 fugu rubrip
12	41	89.1	455	11 Q63718	Q63718 rattus norv
13	41	89.1	467	5 Q44350	Q44350 chondrosia
14	41	89.1	467	5 Q44352	Q44352 petrobion
15	41	89.1	467	5 Q9NJ92	Q9NJ92 guancha lac
16	41	89.1	468	5 Q44349	Q44349 funiculina
17	41	89.1	469	5 Q44351	Q44351 eunicella c
18	41	89.1	526	13 Q98897	Q98897 fugu rubrip
19	41	89.1	617	10 Q9C7X7	Q9C7X7 aradidopsis

20	41	89.1	628	5 Q93147	Q93147 botryllus s
21	41	89.1	629	5 Q93146	Q93146 botryllus s
22	41	89.1	632	5 Q15766	Q15766 dictyosteli
23	41	89.1	639	13 Q98900	Q98900 fugu rubrip
24	41	89.1	639	13 Q918F9	Q918F9 oryzias lat
25	41	89.1	640	5 Q93601	Q93601 caenorhabdi
26	41	89.1	640	13 Q93240	Q93240 paralichthy
27	41	89.1	641	11 Q63256	Q63256 rattus norv
28	41	89.1	641	11 Q9QWJ5	Q9QWJ5 mus musculu
29	41	89.1	645	5 Q96541	Q96541 setaria dfg
30	41	89.1	645	5 Q9NJB7	Q9NJB7 wuchereria
31	41	89.1	645	5 Q9NGK9	Q9NGK9 wuchereria
32	41	89.1	645	10 Q48563	Q48563 brassica na
33	41	89.1	647	3 Q59855	Q59855 schizosacch
34	41	89.1	647	10 Q41027	Q41027 pisum sativ
35	41	89.1	650	5 Q9U777	Q9U777 stylophora
36	41	89.1	650	10 Q9ZS55	Q9ZS55 arabidopsis
37	41	89.1	650	10 Q9LHA8	Q9LHA8 arabidopsis
38	41	89.1	652	10 P93937	P93937 ascophyllum
39	41	89.1	653	5 Q94805	Q94805 trichoplusi
40	41	89.1	659	5 Q9XZJ2	Q9XZJ2 crassostrea
41	41	89.1	663	5 Q24952	Q24952 geodia cydo
42	40	87.0	190	5 Q9U9B4	Q9U9B4 mytilus edu
43	40	87.0	467	5 Q44346	Q44346 asbestoplum
44	40	87.0	467	5 Q44347	Q44347 petrosia fi
45	40	87.0	467	5 Q9GPM5	Q9GPM5 monosiga ov

#### ALIGNMENTS

```

RESULT 1
Q9U667 ID Q9U667 PRELIMINARY; PRT; 146 AA.
AC Q9U667;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Littorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF191828; AAF12787.1; -.
DR HSSP: P19120; 1BAL.
DR InterPro: IPR001023; HSP70.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

Query Match 89.1%; Score 41; DB 5; Length 146;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
Db |||||
79 SLFEGIDFY 87

RESULT 2
Q9U670 ID Q9U670 PRELIMINARY; PRT; 153 AA.
AC Q9U670;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

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DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191825; AAF12784.1; -  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 153 153  
FT NON\_TER 153 153  
SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 89.1%; Score 41; DB 5; Length 153;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 80 SLFEGIDFY 88

RESULT 3  
Q9U669 PRELIMINARY; PRT; 155 AA.  
AC Q9U669;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191826; AAF12785.1; -  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 155 155  
FT NON\_TER 155 155  
SQ SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 89.1%; Score 41; DB 5; Length 155;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 82 SLFEGIDFY 90

RESULT 4  
Q9U665 PRELIMINARY; PRT; 157 AA.  
AC Q9U665;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191830; AAF12789.1; -  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 157 157  
FT NON\_TER 157 157  
SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 89.1%; Score 41; DB 5; Length 157;  
Best Local Similarity 88.9%; Pred. No. 2.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 84 SLFEGIDFY 92

RESULT 5  
Q9U671 PRELIMINARY; PRT; 158 AA.  
AC Q9U671;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191824; AAF12783.1; -  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 158 158  
FT NON\_TER 158 158  
SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 89.1%; Score 41; DB 5; Length 158;  
Best Local Similarity 88.9%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDVY 9  
|||||||  
Db 85 SLFEGIDFY 93

RESULT 6  
Q9U668 PRELIMINARY; PRT; 158 AA.  
AC Q9U668;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)



DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191827; AAF12786.1; -.  
DR HSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 89.1%; Score 41; DB 5; Length 158;  
Best Local Similarity 88.9%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
DB 85 SLFEGIDFY 93

RESULT 7  
Q90666 PRELIMINARY; PRT; 158 AA.  
ID Q90666  
AC Q90666;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191829; AAF12788.1; -.  
DR HSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 89.1%; Score 41; DB 5; Length 158;  
Best Local Similarity 88.9%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
DB 85 SLFEGIDFY 93

RESULT 8  
P81159 PRELIMINARY; PRT; 220 AA.  
ID P81159  
AC P81159;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
GN HSC70.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93077669; Pubmed=1360013;  
RA Kuhl D.; Kennedy T.; Barzilai A.; Kandel E.;  
RT "Long-term sensitization training in Aplysia leads to an increase in  
the expression of Bip, the major protein chaperon of the ER.";  
RL J. Cell Biol. 119:1069-1076(1992).  
CC -!- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL; Z15039; CAA78757.1; -.  
DR HSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 220  
SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 89.1%; Score 41; DB 5; Length 220;  
Best Local Similarity 88.9%; Pred. No. 3.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9  
DB 138 SLFEGIDFY 146

RESULT 9  
P81157 PRELIMINARY; PRT; 221 AA.  
ID P81157  
AC P81157;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).  
GN HSP70A.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93077669; Pubmed=1360013;  
RA Kuhl D.; Kennedy T.; Barzilai A.; Kandel E.;  
RT "Long-term sensitization training in Aplysia leads to an increase in  
the expression of Bip, the major protein chaperon of the ER.";  
RL J. Cell Biol. 119:1069-1076(1992).  
CC -!- INDUCTION: BY HEAT SHOCK.  
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL; Z15037; CAA78755.1; -.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 221  
SQ SEQUENCE 221 AA; 24404 MW; 853F794106E83CC9 CRC64;



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Query Match      89.1%; Score 41; DB 5; Length 221;
Best Local Similarity 88.9%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
DB 139 SLFEGIDVY 147

RESULT 10
Q90520 ID Q90520 PRELIMINARY; PRT; 278 AA.
AC Q90520;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036330; PubMed=6092938;
RA Kothary R.K., Jones D., Candido E.P.M.;
RT "70-Kilodalton heat shock polypeptides from rainbow trout:
RT characterization of cDNA sequences.";
RL Mol. Cell. Biol. 4:1785-1791(1984).
DR EMBL; K02549; AAA49562.1; -.
DR HSSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR Heat shock; Multigene family.
KW NON_TER 1
FT NON_TER 278 278
SQ SEQUENCE 278 AA; 30327 MW; B4C745DE584C17A CRC64;

Query Match      89.1%; Score 41; DB 13; Length 278;
Best Local Similarity 88.9%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
DB 156 SLFEGIDVY 164

RESULT 11
Q98899 ID Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
GN HSP70-3.
OS Fuqu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Lim E.H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08578; CAA69892.1; -.
DR HSSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.

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DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.
FT NON_TER 367 367
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;.

Query Match      89.1%; Score 41; DB 13; Length 367;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
DB 268 SLFEGIDVY 276

RESULT 12
Q63718 ID Q63718 PRELIMINARY; PRT; 455 AA.
AC Q63718;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT SHOCK ROEIN 70 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA D'Ambrosio E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z27118; CAA81642.1; -.
DR HSSP; P08107; 1HJO.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.
FT NON_TER 1 1
FT NON_TER 455 455
SQ SEQUENCE 455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;

Query Match      89.1%; Score 41; DB 11; Length 455;
Best Local Similarity 88.9%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDVY 9
DB 254 SLFEGIDVY 262

RESULT 13
O44350 ID O44350 PRELIMINARY; PRT; 467 AA.
AC O44350;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Chondrosia reniformis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Chondrosida; Chondrillidae; Chondrosia.
OX NCBI_TaxID=68574;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelli C., Le Parco Y.;

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RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026517; AAC05362.1; -;  
 DR HSSP; P08109; 1CKR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467 467  
 SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 89.1%; Score 41; DB 5; Length 467;  
 Best Local Similarity 88.9%; Pred. No. 7.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
 |||||  
 Db 252 SLFEGIDFY 260

## RESULT 14

O44352  
 ID 044352 PRELIMINARY; PRT; 467 AA.  
 AC O44352;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
 GN HSP70.  
 OS Petrobionta massilliana.  
 OC Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Petrobionidae;  
 OC Petrobionta.  
 OX NCBI\_TaxID=68578;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borchelliini C., Le Parco Y.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026520; AAC05364.1; -;  
 DR HSSP; P08109; 1CKR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467 467  
 SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 89.1%; Score 41; DB 5; Length 467;  
 Best Local Similarity 88.9%; Pred. No. 7.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
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 Db 252 SLFEGIDFY 260

## RESULT 15

O9NJ92  
 ID O9NJ92 PRELIMINARY; PRT; 467 AA.  
 AC O9NJ92;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
 OS Guancha lacunosa.  
 OC Eukaryota; Metazoa; Porifera; Calcarea; Clathrinida;  
 OC Clathrinidae; Guancha.  
 OX NCBI\_TaxID=115120;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Borchelliini C., Le Parco Y.;  
 RT "Sponges paraphyly and the origin of Metazoa.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF182195; AAF61297.1; -;  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467 467  
 SQ SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match 89.1%; Score 41; DB 5; Length 467;  
 Best Local Similarity 88.9%; Pred. No. 7.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDVY 9  
 |||||  
 Db 252 SLFEGIDFY 260

Search completed: December 6, 2001, 07:56:52  
 Job time: 180 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:58 ; Search time 81.43 Seconds  
(without alignments)  
2.764 Million cell updates/sec

Title: PEP2-MOD8A

Perfect score: 51

Sequence: 1 SLFEGIDAYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA:\*
- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	86.3	643	4	US-08-797-358B-3
2	42	82.4	646	1	US-08-441-139-14
3	37	72.5	458	4	US-09-457-046B-61
4	36	70.6	495	3	US-09-079-415-4
5	36	70.6	533	2	US-08-225-488-2
6	33	64.7	800	6	5183745-3
7	32	62.7	303	2	US-08-599-171A-32
8	32	62.7	303	2	US-08-646-590B-32
9	32	62.7	303	3	US-09-069-226-32
10	32	62.7	303	4	US-09-412-184-32
11	32	62.7	617	4	US-08-867-611-30
12	32	62.7	617	5	PCT-US92-06965A-35
13	32	62.7	3011	1	US-08-453-552-2
14	32	62.7	3011	2	US-08-710-637-2
15	32	62.7	3011	5	PCT-US93-00907-2
16	31	60.8	20	4	US-08-612-973-71
17	31	60.8	20	4	US-08-927-597-71
18	31	60.8	43	4	US-09-312-183A-8
19	31	60.8	45	1	US-08-262-037-88
20	31	60.8	55	1	US-08-262-037-89
21	31	60.8	60	1	US-08-262-037-90
22	31	60.8	87	1	US-07-867-194-6
23	31	60.8	88	4	US-08-444-818-83
24	31	60.8	108	2	US-08-483-695-42
25	31	60.8	108	2	US-07-965-285-42
26	31	60.8	108	2	US-08-487-231-42
27	31	60.8	108	4	US-09-201-912-42

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6288478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/797,358B  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-FEB-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 86.3%; Score 44; DB 4; Length 643;  
Best Local Similarity 80.0%; Pred. No. 0.63;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10







;; TITLE OF INVENTION: NO. 5846802a1 Fungal Protease  
;; NUMBER OF SEQUENCES: 18  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Ciba-Geigy Corporation  
;; STREET: 7 Skyline Drive  
;; CITY: Hawthorne  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 10532  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,488  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/047,214  
;; FILING DATE: 13-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Spruill, W. Murray  
;; REGISTRATION NUMBER: 32,943  
;; REFERENCE/DOCKET NUMBER: 4-19055/A/CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 919-541-8615  
;; TELEFAX: 919-541-8689  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 533 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-225-488-2

Query Match 70.6%; Score 36; DB 2; Length 533;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EGDVAYT 10

Db 173 EGVDAVT 179

RESULT 6

5183745-3  
;; Patent No. 5183745  
;; APPLICANT: DANCHIN, ANTOINE; GLASER, PHILLIPPE; KRIN, EVELYN;  
;; BARZU, OCTAVIEN; LADANT, DANIEL; ULLMAN, AGNES  
;; TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR  
;; BIOLOGICAL USES  
;; NUMBER OF SEQUENCES: 13  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/426,541  
;; FILING DATE: 25-OCT-1989  
;; SEQ ID NO: 3:  
;; LENGTH: 800  
5183745-3

Query Match 64.7%; Score 33; DB 6; Length 800;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDAY 9

Db 721 SIFRGIQAY 729

RESULT 7

US-08-599-171A-32

;; Sequence 32, Application US/08599171A  
;; Patent No. 5814473  
;; GENERAL INFORMATION:  
;; APPLICANT: WARREN, Patrick V.  
;; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
;; NUMBER OF SEQUENCES: 32  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
;; STREET: 6 BECKER FARM ROAD  
;; CITY: ROSELAND  
;; STATE: NEW JERSEY  
;; COUNTRY: USA  
;; ZIP: 07068  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 INCH DISKETTE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: WORD PERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/599,171A  
;; FILING DATE: Concurrently  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: HERRON, CHARLES J.  
;; REGISTRATION NUMBER: 28,019  
;; REFERENCE/DOCKET NUMBER: 331400-38  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 303 AMINO ACIDS  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PROTEIN  
US-08-599-171A-32

Query Match 62.7%; Score 32; DB 2; Length 303;  
Best Local Similarity 66.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDAY 9

Db 34 SIFEGIRCY 42

RESULT 8

US-08-646-590B-32  
;; Sequence 32, Application US/08646590B  
;; Patent No. 5962283  
;; GENERAL INFORMATION:  
;; APPLICANT: Warren, Patrick V.  
;; APPLICANT: Swanson, Ronald V.  
;; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
;; NUMBER OF SEQUENCES: 42  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 4225 Executive Square, Suite 1400  
;; CITY: La Jolla  
;; STATE: CA  
;; COUNTRY: US  
;; ZIP: 92037  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSEQ for Windows Version 2.0



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/646,590B  
;; FILING DATE: 08-May-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/599,171  
;; FILING DATE: 09-FEB-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US97/01094  
;; FILING DATE: 21-January-1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Haile, Ph.D., Lisa A.  
;; REGISTRATION NUMBER: 38,347  
;; REFERENCE/DOCKET NUMBER: 09010/017001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619/678-5070  
;; TELEFAX: 619/678-5099  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 303 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: internal  
;; US-08-646-590B-32

Query Match 62.7%; Score 32; DB 2; Length 303;  
Best Local Similarity 66.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
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Db 34 SIFEGIRGY 42

RESULT 9  
;; US-09-069-226-32  
;; Sequence 32, Application US/09069226  
;; Patent No. 6013509  
;; GENERAL INFORMATION:  
;; APPLICANT: WARREN, Patrick V.  
;; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
;; NUMBER OF SEQUENCES: 32  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
;; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
;; STREET: 6 BECKER FARM ROAD  
;; CITY: ROSELAND  
;; STATE: NEW JERSEY  
;; COUNTRY: USA  
;; ZIP: 07068  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 INCH DISKETTE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: WORD PERFECT 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/069,226  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/599,171  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: HERRON, CHARLES J.  
;; REGISTRATION NUMBER: 28,019  
;; REFERENCE/DOCKET NUMBER: 331400-38  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 32:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 303 AMINO ACIDS  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PROTEIN  
;; US-09-069-226-32

Query Match 62.7%; Score 32; DB 3; Length 303;  
Best Local Similarity 66.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
|:|||||  
Db 34 SIFEGIRGY 42

RESULT 10  
;; US-09-412-184-32  
;; Sequence 32, Application US/09412184  
;; Patent No. 6268188  
;; GENERAL INFORMATION:  
;; APPLICANT: Warren, Patrick V.  
;; APPLICANT: Swanson, Ronald V.  
;; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
;; NUMBER OF SEQUENCES: 42  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 4225 Executive Square, Suite 1400  
;; CITY: La Jolla  
;; STATE: CA  
;; COUNTRY: US  
;; ZIP: 92037  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/412,184  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/646,590  
;; FILING DATE: 08-May-1996  
;; APPLICATION NUMBER: 08/599,171  
;; FILING DATE: 09-FEB-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US97/01094  
;; FILING DATE: 21-January-1997  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Haile, Ph.D., Lisa A.  
;; REGISTRATION NUMBER: 38,347  
;; REFERENCE/DOCKET NUMBER: 09010/017001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619/678-5070  
;; TELEFAX: 619/678-5099  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 303 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FRAGMENT TYPE: internal  
;; US-09-412-184-32

Query Match 62.7%; Score 32; DB 4; Length 303;  
Best Local Similarity 66.7%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9



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DB      34 SIFEGIRGY 42      1:||||| |
Query Match      62.7%; Score 32; DB 4; Length 617;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
US-08-867-611-30
; Sequence 30, Application US/08867611
; Patent No. 6172189
; GENERAL INFORMATION:
; APPLICANT: DEVARE, SUSHIL G
; APPLICANT: DESAI, SURESH M
; APPLICANT: CASEY, JAMES M
; APPLICANT: DAILEY, STEPHEN H
; APPLICANT: DAWSON, GEORGE J
; APPLICANT: GUTIERREZ, ROBIN A
; APPLICANT: LESNIEWSKI, RICHARD R
; APPLICANT: STEWART, JAMES L
; APPLICANT: RUPPRECHT, KEVIN R
; TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
; ANTIGENS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,611
; FILING DATE: 02-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,757
; FILING DATE:
; APPLICATION NUMBER: US/08/179,896
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/572,822
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/614,069
; FILING DATE: 07-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,561
; FILING DATE: 21-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,565
; FILING DATE: 21-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,566
; FILING DATE: 21-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 4834.US.P6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-9556
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 617 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-867-611-30

Query Match      62.7%; Score 32; DB 5; Length 617;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
PCT-US92-06965A-35
; Sequence 35, Application PC/TUS9206965A
; GENERAL INFORMATION:
; APPLICANT: DEVARE, S.
; APPLICANT: DESAI, S.
; APPLICANT: DAILEY, S.
; TITLE OF INVENTION: HCV SYNTHETIC PEPTIDE FROM NS1 REGION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: ILLINOIS
; COUNTRY: U.S.
; ZIP: 60065-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06965A
; FILING DATE: 19920821
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 4834PC.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 617 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-06965A-35

Query Match      62.7%; Score 32; DB 5; Length 617;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
US-08-453-552-2
; Sequence 2, Application US/08453552
; Patent No. 5667992
; GENERAL INFORMATION:
; APPLICANT: CASEY, JAMES M.
; APPLICANT: BODE, SUZANNE L.
; APPLICANT: ZECK, BILLY J.
; APPLICANT: YAMAGUCHI, JULIE
; APPLICANT: FRAIL, DONALD E.
; APPLICANT: DESAI, SURESH M.
; APPLICANT: DEVARE, SUSHIL G.
; TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
; PROTEINS
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NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: ONE ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,552  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5131.US.D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-937-9556  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3011 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-453-552-2

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Best Local Similarity 66.7%; Pred. No. 8.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 377 LFSGVDAAT 385

RESULT 14  
US-08-710-637-2  
Sequence 2, Application US/08710637  
Patent No. 5854001  
GENERAL INFORMATION:  
APPLICANT: CASEY, JAMES M.  
APPLICANT: BODE, SUZANNE L.  
APPLICANT: ZECK, BILLY J.  
APPLICANT: YAMAGUCHI, JULIE  
APPLICANT: FRAIL, DONALD E.  
APPLICANT: DESAI, SURESH M.  
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: ONE ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,637  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/144,099  
FILING DATE:  
APPLICATION NUMBER: US 07/830,024  
FILING DATE: 01-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5131.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-937-9556  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3011 amino acids  
TYPE: amino acid  
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US-08-710-637-2

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Db 377 LFSGVDAAT 385

RESULT 15  
PCT-US93-00907-2  
Sequence 2, Application PC/TUS9300907  
GENERAL INFORMATION:  
APPLICANT: CASEY, JAMES M.  
APPLICANT: BODE, SUZANNE L.  
APPLICANT: ZECK, BILLY J.  
APPLICANT: YAMAGUCHI, JULIE  
APPLICANT: FRAIL, DONALD E.  
APPLICANT: DESAI, SURESH M.  
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: ONE ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/00907  
FILING DATE: 19930129  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5131.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-937-9556  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3011 amino acids  
TYPE: AMINO ACID



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; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US93-00907-2

Query Match 62.7%; Score 32; DB 5; Length 3011;  
Best Local Similarity 66.7%; Pred. No. 8.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 377 LFSGVDAAT 385

Search completed: December 6, 2001, 07:59:59  
Job time: 367 sec

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GenCore version 4.5  
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(without alignments)  
370.404 Million cell updates/sec

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Perfect score: 37  
Sequence: 1 gggcaagcttggaactcagaatctccccagagccgag 37

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: gb.ba.\*
- 2: gb.btg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
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- 17: em.hum.\*
- 18: em.in.\*
- 19: em.om.\*
- 20: em.or.\*
- 21: em.ov.\*
- 22: em.pat.\*
- 23: em.ph.\*
- 24: em.pl.\*
- 25: em.ro.\*
- 26: em.sts.\*
- 27: em.sy.\*
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- 29: em.vi.\*
- 30: em.htgo\_hum.\*
- 31: em.htgo\_inv.\*
- 32: em.htgo\_rod.\*
- 33: em.htg\_hum.\*
- 34: em.htg\_inv.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3

Result No.	Score	Match	Length	DB	ID	Description
1	37	100.0	37	6	AX012955	Sequence
2	27.4	74.1	3190	9	HS295141	AX012955 Homo sapi
3	27.4	74.1	3190	9	HS295140	AX012955 Homo sapi
4	27.4	74.1	3196	9	HS295140	AX012955 Homo sapi
5	27.4	74.1	3199	9	HS295140	AX012955 Homo sapi
6	27	73.0	27	6	AX105685	AX105685 Sequence
7	26	70.3	190	9	GORMHIE	L38651 Gorilla gor
8	25.8	69.7	100000	9	AP000520	AP000520 Homo sapi
9	25.8	69.7	162227	9	AB023056	AB023056 Homo sapi
10	25.4	68.6	39	6	AX021171	AX021171 Sequence
11	25.4	68.6	165	9	HLACW301	U31372 Human class
12	25.4	68.6	184	9	ORAMHC1AC	L32844 Pongo pygma
13	25.4	68.6	186	9	CHPMHC1AA	L32845 Pan troglod
14	25.4	68.6	186	9	CHPMHC1AC	L32855 Pan troglod
15	25.4	68.6	186	9	GORMHC1AC	L32849 Gorilla gor
16	25.4	68.6	186	9	GORMH1A	L38647 Gorilla gor
17	25.4	68.6	186	9	HUMHC1AA	L32851 Homo sapien
18	25.4	68.6	186	9	ORAMHC1AB	L32843 Pongo pygma
19	25.4	68.6	187	9	CHPMHC1AE	L32857 Pan troglod
20	25.4	68.6	215	9	HUMHCW18	M58631 Human MHC c
21	25.4	68.6	216	9	HUMHCW5	M58630 Human MHC c
22	25.4	68.6	287	9	HSB13HLA	X82906 H.sapiens H
23	25.4	68.6	287	9	HSB27HLA	X82908 H.sapiens H
24	25.4	68.6	287	9	HSB44HLA	X82904 H.sapiens H
25	25.4	68.6	287	9	HSB51HLA	X82898 H.sapiens H
26	25.4	68.6	287	9	HSBLAB18	X82909 H.sapiens H
27	25.4	68.6	287	9	HSBLAB35	X82897 H.sapiens H
28	25.4	68.6	287	9	HSBLAB37	X82907 H.sapiens H
29	25.4	68.6	287	9	HSBLAB400	X82920 H.sapiens H
30	25.4	68.6	287	9	HSBLAB41	X82903 H.sapiens H
31	25.4	68.6	287	9	HSBLAB45	X82901 H.sapiens H
32	25.4	68.6	287	9	HSBLAB47	X82905 H.sapiens H
33	25.4	68.6	287	9	HSBLAB49	X82926 H.sapiens H
34	25.4	68.6	287	9	HSBLAB50	X82927 H.sapiens H
35	25.4	68.6	287	9	HSBLAB52	X82899 H.sapiens H
36	25.4	68.6	287	9	HSBLAB53	X82900 H.sapiens H
37	25.4	68.6	287	9	HSBLAB57	X82925 H.sapiens H
38	25.4	68.6	287	9	HSBLAB58	X82919 H.sapiens H
39	25.4	68.6	287	9	HSBLAB60	X82902 H.sapiens H
40	25.4	68.6	287	9	HSBLAB62	X82922 H.sapiens H
41	25.4	68.6	287	9	HSBLAB63	X82921 H.sapiens H
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ALIGNMENTS

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LOCUS	AX012955	Sequence	37 bp	DNA	PAT	07-SEP-2000
DEFINITION	Sequence	3 from Patent	WO9954464.			
ACCESSION	AX012955					
VERSION	AX012955.1	GI:10040205				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 37)  
Gaudin,C. and Triebel,F.  
Mutated peptide compounds, derived from hsp70, useful in cancer immunotherapy  
Patent: WO 9954464-A 3 28-OCT-1999;  
ROUSSY INST GUSTAVE (FR); GAUDIN CATHERINE (FR); TRIEBEL FREDERIC (FR)  
Location/Qualifiers  
1..37  
SOURCE



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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS      Homo sapiens HLA gene for MHC class I antigen, B*4701 allele, exons
DEFINITION      1-7.
ACCESSION      AJ295141
VERSION      AJ295141.1 GI:11493145
KEYWORDS      B*4701 allele; HLA-B gene; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      Cox,S.T.
AUTHORS      1 (bases 1 to 3190)
TITLE      Confirmation of HLA B*4701
JOURNAL      Unpublished
REFERENCE      Cox,S.T.
AUTHORS      2 (bases 1 to 3190)
TITLE      Direct Submission
JOURNAL      Submitted (27-OCT-2000) Cox S.T., Dept of HLA Sequencing, Anthony
Nolan Research, The Royal Free Hospital, Pond Street, Hampstead,
London, NW3 2QG, UNITED KINGDOM
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DTAAQITQRKEAARVAEOLRLAYLEGECVEMLRRLYENKGTQLQADPPKTHVTHPI
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Best Local Similarity 83.8%; Pred. No. 30;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 3
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LOCUS      Homo sapiens HLA-B gene for MHC class I antigen, B*4006 allele.
ACCESSION      AJ300180
VERSION      AJ300180.1 GI:11125668
KEYWORDS      B*4006 allele; HLA-B gene; human leucocyte antigen B; major
histocompatibility complex; MHC class I antigen.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      Cox,S.T.
AUTHORS      1 (bases 1 to 3190)
TITLE      Variant B*4006 with difference in exon 2
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 3190)
AUTHORS      Cox,S.T.
TITLE      Direct Submission
JOURNAL      Submitted (03-NOV-2000) Cox S.T., Dept of HLA Sequencing, Anthony
Nolan Research, The Royal Free Hospital, Pond Street, Hampstead,
London, NW3 2QG, UNITED KINGDOM
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 2734..2777

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 Best Local Similarity 83.8%; Pred. No. 30;  
 Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 gggcaagcttgactcagaatctctccacagaccgag 37  
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 Db 64 GGGCGTCGACGACTCAGAATCTCCCGACGCCGAG 100  
 RESULT 4  
 HSA295140 3196 bp DNA PRI 29-NOV-2000  
 LOCUS  
 DEFINITION Homo sapiens HLA gene for MHC class I antigen, B\*1501101 allele,  
 exons 1-7.  
 ACCESSION AJ295140  
 VERSION AJ295140.1 GI:11493143  
 KEYWORDS B\*1501101 allele; HLA-B gene; human leucocyte antigen B; major  
 histocompatibility complex; MHC class I antigen.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 3196)  
 AUTHORS Cox,S.T.  
 TITLE Confirmatory sequence of HLA B\*1501101  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3196)  
 AUTHORS Cox,S.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-OCT-2000) Cox S.T., Dept of HLA Sequencing, Anthony  
 Nolan Research, The Royal Free Hospital, Pond Street, Hampstead,  
 London, NW3 2QG, UNITED KINGDOM  
 FEATURES  
 source  
 1..3196  
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 /chromosome="6p21.31"  
 /cell\_line="pp"  
 /tissue\_type="blood"  
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 /gene="HLA-B"  
 98..170  
 /gene="HLA-B"  
 /number=1  
 join(98..170,300..569,815..1090,1666..1941,2046..2162,  
 2604..2636,2743..2786)  
 /gene="HLA-B"  
 /function="antigen presentation"  
 /note="B\*1501101 allele"  
 /codon\_start=1  
 /product="MHC class I antigen"  
 /protein\_id="CAC17462.1"  
 /db\_xref="GI:11493144"  
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 RFIAYGVDDTFVRFDSDAASPRMAPRWIEQEGPEYWDRETOISKNTQTYRESL  
 RNLRGYVNSAGSHTLQRMVGCDDVGPGRLLRGHNOYAYDGKDYIALNEDLSWTAA  
 DTAQITQRKWEAAKVAQLRAYLEGECEWMLRRYLENGKETLQADPPKTHVTHPI  
 SDHEATLRCWALGFYPAEITLTWQDGEDQDTDELVELTRPAGDRTFOKWAAYVPSG  
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 171..299  
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 /number=1  
 300..569  
 /gene="HLA-B"  
 /number=2  
 570..814  
 /gene="HLA-B"  
 intron  
 exon  
 intron



exon	/number=2 815. .1090 /gene="HLA-B" /number=3 1091. .1665 /gene="HLA-B" /number=3 1666. .1941 /gene="HLA-B" /number=4 1942. .2045 /gene="HLA-B" /number=4 2046. .2162 /gene="HLA-B" /number=5 2163. .2603 /gene="HLA-B" /number=5 2604. .2636 /gene="HLA-B" /number=6 2637. .2742 /gene="HLA-B" /number=6 2743. .2786 /gene="HLA-B" /number=7	590 a	922 c	1016 g	668 t	
BASE COUNT						
ORIGIN						
Query Match	74.1%;	Score 27.4;	DB 9;	Length 3196;		
Best Local Similarity	83.8%;	Pred. No. 30;				
Matches	31;	Conservative	0;	Mismatches	6;	Indels
					0;	Gaps
						0;
Qy	1	ggcgaagcttgactcagaatctcccgagcgag	37			
Db	61	GGGGTCTGACGACTCAGAACTCTCCCGAGCGCGAG	97			
RESULT	5					
HSA300181						
LOCUS	HSA300181	3199 bp	DNA	PRI	29-JAN-2001	
DEFINITION	Homo sapiens HLA-B gene for MHC class I antigen, B*1517 allele.					
ACCESSION	AJ300181					
VERSION	AJ300181.1	GI:11125670				
KEYWORDS	B*1517 allele; HLA-B gene; human leucocyte antigen B; major histocompatibility complex; MHC class I antigen.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 3199)					
AUTHORS	Cox, S.					
TITLE	HLA B*1517 variant with differences in exon 2					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 3199)					
AUTHORS	Cox, S.T.					
TITLE	Direct Submission					
JOURNAL	Submitted (03-NOV-2000) Cox S.T., Dept of HLA Sequencing, Anthony Nolan Research, The Royal Free Hospital, Pond Street, Hampstead, London, NW3 2QG, UNITED KINGDOM					
FEATURES	Location/Qualifiers					
source	1. .3199					
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	/db_xref="taxon:9606"					
	/chromosome="6"					
	/map="6p21.31"					
	/tissue_type="blood"					
mRNA	Join(101. .173,302. .571,817. .1092,1668. .1943,2048. .2164, 2606. .2638,2745. .2788)					
	/gene="HLA-B"					
gene	/note="B*1517 allele"					
	Join(101. .173,174. .301,302. .571,572. .816,817. .1092, 1093. .1667,1668. .1943,1944. .2047,2048. .2164,2165. .2605, 2606. .2638,2639. .2744,2745. .2788)					
	/gene="HLA-B"					
exon	101. .173					
	/gene="HLA-B"					
	/note="B*1517"					
	/number=1					
CDS	Join(101. .173,302. .571,817. .1092,1668. .1943,2048. .2164, 2606. .2638,2745. .2788)					
	/gene="HLA-B"					
	/function="antigen presentation"					
	/note="B*1517 allele"					
	/codon_start=1					
	/product="MHC class I antigen"					
	/protein_id="CAC15502.1"					
	/db_xref="GI:11125671"					
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intron	174. .301					
	/gene="HLA-B"					
	/note="B*1517"					
	/number=1					
exon	302. .571					
	/gene="HLA-B"					
	/note="B*1517"					
	/number=2					
intron	572. .816					
	/gene="HLA-B"					
	/note="B*1517"					
	/number=2					
exon	817. .1092					
	/gene="HLA-B"					
	/note="B*1517"					
	/number=3					
intron	1093. .1667					
	/gene="HLA-B"					
	/note="B*1517"					
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exon	1668. .1943					
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exon	2048. .2164					
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exon	2745. .2788					
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27



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BASE COUNT      589 a      922 c      1021 g      667 t
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/ gene="B*1517"
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Best Local Similarity 83.8%; Pred. No. 30;
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 99gcaggttgactcagaatctccccagacgcgcag 37
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Db 64 GGGCTCGACGACTCAGAATCTCCCGACGCGCGAG 100

RESULT 6
AX105685
LOCUS AX105685 27 bp DNA PAT 30-APR-2001
DEFINITION Sequence 25 from Patent WO0125271.
ACCESSION AX105685
VERSION AX105685.1 GI:13921707
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hanada,K.I. and Yang,J.C.
TITLE Fibroblast growth factor-5 (fgf-5) is a tumor associated t-cell
JOURNAL antigen
PATENT: WO 0125271-A 25 12-APR-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source
1. .27
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer that can be used to clone HLA-A3."
BASE COUNT      7 a      10 c      7 g      3 t
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Query Match      73.0%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaactcagaatctccccagacgcgcag 37
|||||
Db 1 GGACTCAGAAATCTCCCGACGCGCGAG 27

RESULT 7
GORMHIE
LOCUS GORMHIE 190 bp DNA PRI 03-AUG-1995
DEFINITION Gorilla gorilla (clone Sha7), MHC class I Gogo-A gene promoter.
ACCESSION L38651
VERSION L38651.1 GI:632919
KEYWORDS class I gene promoter; germline; major histocompatibility complex.
SOURCE Gorilla gorilla (individual isolate Shamba).
ORGANISM Gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
REFERENCE 1 (bases 1 to 190)
AUTHORS Vallejo,A.N. and Pease,L.R.
TITLE Structure of the MHC A and B locus promoters in hominoids. Insights
on the evolution of the class I MHC multigene family
JOURNAL J. Immunol. 154 (8), 3912-3921 (1995)
MEDLINE 95221896
FEATURES
Location/Qualifiers
source
1. .190
/organism="Gorilla gorilla"
/isolate="Shamba"
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/cell_type="EBV-transformed B-lymphoblast"
/germline
/clone="SHA7"

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promoter 1. .190
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misc_feature 8. .19
enhancer 86. .95
/note="interferon responsive element"
/note="Enhancer B"
CAAT_signal 111. .116
BASE COUNT 31 a 62 c 45 g 52 t
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Query Match 70.3%; Score 26; DB 9; Length 190;
Best Local Similarity 85.3%; Pred. No. 2.6e+02;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 caagcttgactcagaatctccccagacgcgcag 37
|||||
Db 156 CACATTGGGACTCAGATTCTCCCGACGCGCGAG 189

RESULT 8
AP000520/c
LOCUS AP000520 100000 bp DNA PRI 30-MAR-2000
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 19/20.
ACCESSION AP000520
VERSION AP000520.1 GI:5926709
KEYWORDS
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Shiina,S., Tamiya,G., Oka,A. and Inoko,H.
TITLE Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
JOURNAL Published Only in DataBase (1999) In press
REFERENCE 2 (bases 1 to 100000)
AUTHORS Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) to the DDBJ/EMBL/GenBank databases. Mika
Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
Japan (E-mail:mika@tokyo.jst.go.jp,
URL:http://www.alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470)
This sequence is conducted by Tokai University as a JST sequencing
Team.
Principal Investigator: Hidetoshi Inoko Ph.D
Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
For further information about this sequences, please visit our
sequence archive web site (http://www.alis.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www.alis.tokyo.jst.go.jp.
Location/Qualifiers
source
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sequences."
STS
gene
misc_feature

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RESULT	10
AX021171	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	



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BASE COUNT      29 a      63 c      45 g      28 t
ORIGIN

Query Match      68.6%; Score 25.4; DB 9; Length 165;
Best Local Similarity 96.3%; Pred. No. 4.2e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagccgcgag 37
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Db 61 GGACTCAGATTCTCCCGAGACGCCGAG 87

RESULT 12
ORAMHCIAAC      184 bp      DNA      PRI      03-AUG-1995
LOCUS
DEFINITION      Pongo pygmaeus (clone C632) MHC class I Popy-A gene, promoter
region.
ACCESSION      L32844
VERSION      L32844.1 GI:625047
KEYWORDS      class I gene promoter; major histocompatibility complex.
SOURCE      Pongo pygmaeus
ORGANISM      Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 184)
Vallejo,A.N. and Pease,L.R.
AUTHORS
TITLE      Structure of the MHC A and B locus promoters in hominoids. Insights
on the evolution of the class I MHC multigene family
JOURNAL      J. Immunol. 154 (8), 3912-3921 (1995)
MEDLINE
FEATURES
Location/Qualifiers
source      1..184
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/cell_line="CP81"
/cell_type="EBV-transformed B-lymphoblastoid cell"
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promoter      1..184
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factor site NFkB and first ATG"
protein_bind      8..19
enhancer      82..92
CAAT_signal      107..112
TATA_signal      133..139
BASE COUNT      32 a      65 c      43 g      44 t
ORIGIN

Query Match      68.6%; Score 25.4; DB 9; Length 184;
Best Local Similarity 96.3%; Pred. No. 4e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagccgcgag 37
||||| ||||| ||||| ||||| ||||| |||||
Db 157 GGACTCAGATTCTCCCGAGACGCCGAG 183

RESULT 13
CHPMHCIAA      186 bp      DNA      PRI      03-AUG-1995
LOCUS
DEFINITION      Pan troglodytes (clone K1811) MHC class I Patr-B gene, promoter
region.
ACCESSION      L32845
VERSION      L32845.1 GI:625016
KEYWORDS      class I gene promoter; major histocompatibility complex.
SOURCE      Pan troglodytes
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 186)
Vallejo,A.N. and Pease,L.R.
AUTHORS
TITLE      Structure of the MHC A and B locus promoters in hominoids. Insights
on the evolution of the class I MHC multigene family
JOURNAL      J. Immunol. 154 (8), 3912-3921 (1995)
MEDLINE
FEATURES
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source      1..186
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promoter      1..186
/note="5' proximal promoter region between transcription
factor site NFkB and first ATG"
protein_bind      9..20
enhancer      84..94
CAAT_signal      109..114
TATA_signal      135..141
BASE COUNT      33 a      69 c      41 g      43 t
ORIGIN

REFERENCE 1 (bases 1 to 186)
AUTHORS      Vallejo,A.N. and Pease,L.R.
TITLE      Structure of the MHC A and B locus promoters in hominoids. Insights
on the evolution of the class I MHC multigene family
JOURNAL      J. Immunol. 154 (8), 3912-3921 (1995)
MEDLINE
FEATURES
Location/Qualifiers
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promoter      1..186
/note="5' proximal promoter region between transcription
factor site NFkB and first ATG"
protein_bind      9..20
enhancer      84..94
CAAT_signal      109..114
TATA_signal      135..141
BASE COUNT      33 a      71 c      39 g      43 t
ORIGIN

Query Match      68.6%; Score 25.4; DB 9; Length 186;
Best Local Similarity 96.3%; Pred. No. 4e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagccgcgag 37
||||| ||||| ||||| ||||| ||||| |||||
Db 160 GGACTCAGATTCTCTCAGACGCCGAG 186

RESULT 14
CHPMHCIAAC      186 bp      DNA      PRI      03-AUG-1995
LOCUS
DEFINITION      Pan troglodytes (clone T1725) MHC class I Patr-B gene, promoter
region.
ACCESSION      L32855
VERSION      L32855.1 GI:625018
KEYWORDS      class I gene promoter; major histocompatibility complex.
SOURCE      Pan troglodytes
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 186)
Vallejo,A.N. and Pease,L.R.
AUTHORS
TITLE      Structure of the MHC A and B locus promoters in hominoids. Insights
on the evolution of the class I MHC multigene family
JOURNAL      J. Immunol. 154 (8), 3912-3921 (1995)
MEDLINE
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/germline
promoter      1..186
/note="5' proximal promoter region between transcription
factor site NFkB and first ATG"
protein_bind      9..20
enhancer      84..94
CAAT_signal      109..114
TATA_signal      135..141
BASE COUNT      33 a      69 c      41 g      43 t
ORIGIN

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Query Match 68.6%; Score 25.4; DB 9; Length 186;  
 Best Local Similarity 96.3%; Pred. No. 4e+02;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 11 ggactcagaatctcccgagccgag 37  
 Db 160 GGACTCAGAACTCTCTCAGACGCCGAG 186

RESULT 15  
 GORMHICAC 186 bp DNA PRI 03-AUG-1995  
 LOCUS  
 DEFINITION Gorilla gorilla (clone OS20) MHC class I Gogo-A gene, promoter region.  
 ACCESSION L32849  
 VERSION L32849.1 GI:625033  
 KEYWORDS class I gene promoter; major histocompatibility complex.  
 SOURCE Gorilla gorilla.  
 ORGANISM Gorilla gorilla  
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 1 (bases 1 to 186)  
 Vallejo, A.N. and Pease, L.R.  
 Structure of the MHC A and B locus promoters in hominoids. Insights on the evolution of the class I MHC multigene family  
 J. Immunol. 154 (8), 3912-3921 (1995)  
 JOURNAL MEDLINE 95221896  
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 /germline  
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 /note="5' proximal promoter region between transcription factor site NFkB and first ATG"  
 8..19  
 /bound\_moiety="interferon responsive element"  
 83..93  
 /note="B"  
 CAAT\_signal 108..113  
 TATA\_signal 134..140  
 BASE COUNT 35 a 63 c 43 g 45 t  
 ORIGIN

Query Match 68.6%; Score 25.4; DB 9; Length 186;  
 Best Local Similarity 96.3%; Pred. No. 4e+02;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 11 ggactcagaatctcccgagccgag 37  
 Db 159 GGACTCAGAACTCTCTCAGACGCCGAG 185

Search completed: December 6, 2001, 09:57:28  
 Job time: 4032 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2001, 08:50:16 ; Search time 230.64 Seconds  
(without alignments)  
137.535 Million cell updates/sec

Title: US-09-673-795-3

Perfect score: 37

Sequence: 1 ggccaagcttgactcagaatctcccgagcgag 37

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	37	AA222705	Human HLA allele a
2	27	73.0	27	AA222705	Reverse RT-PCR pri
3	26.2	70.8	1441	AA222705	Human secreted pro
4	25.4	68.6	39	AA222705	HLA-B*0702/mouse C
5	25.4	68.6	707	AA222705	Human HLA-A2 templ
6	25.4	68.6	3357	AA222705	Human polynucleoti
7	25.4	68.6	3874	AA222705	Sequence of genomi
8	25.4	68.6	6553	AA222705	HLA B27 consensus
9	25	67.6	447	AA222705	Human secreted pro
10	25	67.6	529	AA222705	Human secreted pro
11	24.6	66.5	432	AA222705	Human secreted pro

12	24	64.9	358	21	AA222705	Human secreted pro
13	24	64.9	527	21	AA222705	Human secreted pro
14	23.8	64.3	3357	22	AA222705	Human polynucleoti
15	23.8	64.3	3372	22	AA222705	Human polynucleoti
16	23.8	64.3	3372	22	AA222705	Human polynucleoti
17	23.4	63.2	480	21	AA222705	Human secreted pro
18	22.2	60.0	2069	22	AA222705	Human polynucleoti
19	20.6	55.7	512	22	AA222705	Rhesus monkey EST-
20	20.6	55.7	645	21	AA222705	Aspergillus oryzae
21	20.6	55.7	2046	22	AA222705	Human polynucleoti
22	20.6	55.7	3983	21	AA222705	Plant SDF polynuci
23	19.6	53.0	758	20	AA222705	Human validated ca
24	19.6	53.0	824	22	AA222705	Human cDNA clone (
25	19.6	53.0	1380	22	AA222705	Human cDNA sequenc
26	19.6	53.0	1971	22	AA222705	Human polynucleoti
27	19.6	53.0	1974	22	AA222705	Human cDNA sequenc
28	19.6	53.0	2008	22	AA222705	Human cDNA sequenc
29	19.6	53.0	2794	22	AA222705	Human polynucleoti
30	19.6	53.0	2795	21	AA222705	Human ORF3140
31	19.2	51.9	300	21	AA222705	Downstream region
32	19.2	51.9	1419	16	AA222705	PDI promoter. Hom
33	19.2	51.9	1419	18	AA222705	PDI promoter regio
34	19.2	51.9	2010	22	AA222705	Nucleotide sequenc
35	19	51.4	152	21	AA222705	Human secreted pro
36	19	51.4	318	20	AA222705	Human secreted pro
37	19	51.4	424	21	AA222705	Human secreted pro
38	19	51.4	474	22	AA222705	Probe #3463 for ge
39	19	51.4	474	22	AA222705	Probe #3577 used t
40	19	51.4	474	22	AA222705	Probe #3408 used t
41	19	51.4	907	20	AA222705	Human prostate tum
42	19	51.4	1580	21	AA222705	Human cancer assoc
43	19	51.4	2178	17	AA222705	Neural cell adhesi
44	18.8	50.8	270	17	AA222705	Human cdc25C gene
45	18.8	50.8	414	22	AA222705	C glutamicum codin

#### ALIGNMENTS

RESULT	1
AA222705	AA222705 standard; DNA; 37 BP.
ID	AA222705 standard; DNA; 37 BP.
XX	
AC	AA222705;
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Human HLA allele amplification primer 5p2-H.
XX	
KW	Human; heat shock protein 70; hsp70; identification; tumour; mutation;
KW	T cell response; amplification; vector; bacterium; cancer; allele;
KW	cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;
KW	immune defence; immunogenicity; specificity; human leucocyte antigen;
KW	PCR; primer; amplification; ss.
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9954464-A1.
XX	
PD	28-OCT-1999.
XX	
PF	22-APR-1999; 99WO-FR00957.
XX	
PR	22-APR-1998; 98FR-0005033.
XX	
PA	(INSR ) INST ROUSSY GUSTAVE.
XX	
PI	Triebel F, Gaudin C;
XX	
DR	WPI; 2000-013251/01.
XX	
PT	Identifying mutant peptides from heat-shock protein 70, for treatment



```

PT of cancer -
XX
PS Example 7; Page 24; 56pp; French.
XX
CC The invention relates to a method of identifying peptides, derived from
CC hsp70 that stimulate a tumour-specific T cell response (e.g. AA44199
CC and AA44200) . Identification of the hsp70 peptides that have at least
CC one mutation or identification compared with the native sequence, and induce
CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70
CC encoding DNA from one or more tumours; (ii) cloning the amplified
CC sequences into a vector that can be replicated in bacteria; (iii)
CC sequencing fragments in each cultured bacterial colony to identify any
CC hsp70 mutations, and (iv) determining the immunogenicity of the mutant
CC peptides identified. The peptides, optionally formulated with an agent
CC that induces cellular stress, are used for treatment of cancer,
CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,
CC cancers of head and neck, particularly kidney cancer). The peptides may
CC also be used to increase the proportion of tumour-specific cytotoxic T
CC lymphocytes in a cell culture and/or induce these cells to secrete
CC cytotoxic factors (specifically interleukin-2, interferon-gamma and
CC tumour necrosis factor). Particularly where the cells are used to
CC stimulate immune defences. The method identifies peptides with high
CC immunogenicity and high specificity for particular HLA (human leucocyte
CC antigen) alleles. The primers AAZ22705-22706 were used to PCR amplify
CC HLA alleles for the method of the invention.
XX
SQ Sequence 37 BP; 9 A; 12 C; 11 G; 5 T; 0 other;

Query Match 100.0%; Score 37; DB 21; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggcaagcttgagctcagaatctccccagacgcgag 37
| | | | | | | | | | | | | | | | | | | | |
Db 1 gggcaagcttgagctcagaatctccccagacgcgag 37

RESULT 2
AAD03948
ID AAD03948 standard; DNA; 27 BP.
XX
AC AAD03948;
XX
DT 02-JUL-2001 (first entry)
XX
DE Reverse RT-PCR primer for cloning human leucocyte antigen-A3 gene.
XX
KW Human; fibroblast growth factor-5; FGF-5; neoplasm; cytostatic; RCC;
KW renal cell carcinoma; immunomodulator; gene therapy; carcinoma; breast;
KW prostate; bladder; pancreas; TAA; tumour associated antigen;
KW horseshoe kidney; Hippel-Lindau disease; acquired renal cystic disease;
KW adult polycystic kidney disease; RT-PCR primer; human leucocyte antigen;
KW HLA-A3 gene; ss.
XX
OS Homo sapiens.
XX
PN W0200125271-A2.
XX
PD 12-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US26689.
XX
PR 02-OCT-1999; 99US-0157103.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Hanada K, Yang JC;
XX
WPI; 2001-290607/30.
XX
PT Treating a subject having a neoplasm expressing fibroblast growth
factor-5 (FGF-5), e.g. prostate, breast, bladder, or pancreas

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PT carcinoma, comprises modulating an immune response to FGF-5 or
XX modulating FGF-5 expression or activity -
XX
PS Example 3; Page 24; 101pp; English.
XX
CC The present invention relates to a method for treating a subject having
CC neoplasm expressing fibroblast growth factor-5 (FGF-5) comprises
CC modulating an immune response to FGF-5 or FGF-5 expression or activity.
CC FGF is a tumour associated antigen (TAA). The method is useful for
CC treating or preventing a neoplasm such as prostate carcinoma, breast
CC carcinoma, bladder carcinoma, pancreas carcinoma, and renal cell
CC carcinoma (RCC) and diseases, such as Hippel-Lindau disease, horseshoe
CC kidneys, adult polycystic kidney disease and acquired renal cystic
CC disease. FGF-5 polypeptides may be used as immunogen in the production
CC of antibodies, which are useful in quantitative immunoassays that
CC determine concentrations of antigen-bearing substances in biological
CC samples, and to (semi-)quantitatively identify the presence of antigen
CC expressing or overexpressing tumours by decreasing FGF-5 activity, as
CC diagnostic agents to monitor the progression or regression of an FGF-5
CC expressing or overexpressing tumour in a patient undergoing therapy for
CC the treatment of neoplasm. FGF-5 cDNA is also useful in gene therapy.
CC The present sequence is reverse RT-PCR primer used for cloning
CC human leucocyte antigen (HLA-A3) gene from autologous 1764 RCC to
CC introduce HLA-A3 into non-HLA-A3-expressing cells. The HLA-A3 gene
XX was then subcloned into retroviral vector pRX-INES-Bsr.
XX
SQ Sequence 27 BP; 7 A; 10 C; 7 G; 3 T; 0 other;

Query Match 73.0%; Score 27; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggactcagaatctccccagacgcgag 37
| | | | | | | | | | | | | | | | | | | | |
Db 1 ggactcagaatctccccagacgcgag 27

RESULT 3
AAD08377
ID AAD08377 standard; cDNA; 1441 BP.
XX
AC AAD08377;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human secreted protein-encoding gene 33 cDNA clone HTXDC77, SEQ ID NO:43.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angioenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery;
KW cell culture; chemotaxis; food additive; gene therapy;
KW binding partner identification; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..520
FT /tag= a
FT /product= "Human secreted protein precursor"
FT /transl_except= (pos:74..76, aa:Xaa)
FT /transl_except= (pos:89..91, aa:Xaa)
FT /transl_except= (pos:104..106, aa:Xaa)
FT /transl_except= (pos:113..115, aa:Xaa)
FT /transl_except= (pos:170..172, aa:Xaa)
FT /transl_except= (pos:269..271, aa:Xaa)

```



FT /transl\_except= (pos:275..277, aa:Xaa)  
 FT /transl\_except= (pos:323..325, aa:Xaa)  
 FT /transl\_except= (pos:338..340, aa:Xaa)  
 FT /transl\_except= (pos:347..349, aa:Xaa)  
 FT /transl\_except= (pos:386..388, aa:Xaa)  
 FT /transl\_except= (pos:419..421, aa:Xaa)  
 FT /transl\_except= (pos:512..514, aa:Xaa)  
 FT /note= "Xaa equals any of the naturally occurring  
 FT L-amino acids"  
 FT 65..118  
 FT /\*tag= b  
 FT mat\_peptide 119..517  
 FT /\*tag= c  
 FT /product= "Mature human secreted protein"  
 XX

PN WO200077022-A1.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 01-JUN-2000; 2000WO-US15136.  
 XX  
 XX 11-JUN-1999; 99US-0138629.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM, Komatsoulis GA;  
 PI  
 XX  
 DR WPI; 2001-367020/38.  
 DR P-PSDB; AAE03930.  
 XX  
 XX Nucleic acids encoding 50 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
 PT disease, botulism, cancers and Scimitar syndrome -  
 XX  
 PS Claim 1; Page 513; 614pp; English.

CC AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
 CC protein genes and AAE03998-AAE03947 represent the proteins they encode.  
 CC AAE03948-AAE03996 represent human secreted protein fragments or variants.  
 CC The genes and their secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 50 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angioecic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 XX secreted protein-encoding cDNA of the invention.

Sequence 1441 BP; 299 A; 403 C; 412 G; 283 T; 44 other;

Query Match 70.8%; Score 26.2; DB 22; Length 1441;  
 Best Local Similarity 92.6%; Pred. No. 0.072;  
 Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggactcagaatctccacagacgcgcag 37  
 Db 38 ggactcagawtctccycagacgcgcag 64  
 RESULT 4  
 AAX78122  
 ID AAX78122 standard; DNA; 39 BP.  
 XX  
 AC AAX78122;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX  
 DE HLA-B\*0702/mouse CD80 chimeric DNA PCR primer 3.  
 XX  
 KW HLA-E; human leukocyte antigen-E; interaction; natural killer cell;  
 KW NK cell; T cell; CF94/NGK2+ cell; targeted killing; CD8+ T cell; cancer;  
 KW CD94/NGK2 receptor; bone marrow transplantation; treatment; detection;  
 KW autoimmune disease; lymphoma; leukemia; infection; pregnancy; PCR primer;  
 KW transplantation; immunodeficiency; immunosuppressive; cytostatic; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9928748-A2.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 04-DEC-1998; 98WO-GB03686.  
 XX  
 PR 04-DEC-1997; 97GB-0025764.  
 XX  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX  
 XX Allan DSJ, Braud VM, McMichael AJ, O'Callaghan CA;  
 PI Ogg GS;  
 PI  
 XX WPI; 1999-385412/32.  
 DR  
 XX  
 XX Human leukocyte antigen E binding interaction with CD94/NGK2+ cells  
 Example 3; Page 29; 35pp; English.

This invention describes a novel method to identify the interaction  
 between human leukocyte antigen E (HLA-E) and natural killer (NK) cells  
 and/or a subset of T cells, and to target or isolate those cells.  
 CC Identifying the presence of, separating, killing or inactivating  
 CC CF94/NGK2+ cells comprises (a) contacting a sample with HLA-E under  
 CC binding conditions and (b) detecting binding, separating cells bound to  
 CC HLA-E or carrying out targeted killing on bound cells. The HLA-E property  
 CC of binding to CD94/NGK2 receptors on NK cells and a subset of CD8+ T  
 CC cells is useful for targeting CD94/NGK2+ cells for a variety of purposes,  
 CC such as identification, isolation, killing or inactivation. HLA-E surface  
 CC expression provides protection against killing by CD94/NGK2A+ NK cells.  
 CC Compounds, such as antibodies, that interfere with interaction of  
 CC CD94/NGK2 and HLA-E binding can be tailored for specific CD94/NGK2  
 CC receptors A, B, C and D. Therapeutic uses of antibodies that inhibit  
 CC HLA-E binding to CD94/NGK2 receptors would be useful for bone marrow  
 CC transplantation and in treatment of certain autoimmune diseases.  
 CC Detection and/or quantification of NK cells or a sub population of NK  
 CC cells, or a sub population of T cells (which may be further identified by  
 CC co-staining with anti-CD8 or anti-CD4 antibody or antibodies or ligands  
 CC to other T cell markers) will be useful for, e.g. cancer, lymphoma,  
 CC leukemia, infections, pregnancy (there is a possible role for NK cells in  
 CC the placenta), transplantation, immunodeficiency, and autoimmune  
 CC diseases, as well as monitoring secondary effects of any treatments  
 CC leading to up or down regulation of CD94/NGK2+ NK cells. The products of  
 CC the invention have immunosuppressive and cytostatic activity. This  
 CC sequence represents a PCR primer used in the construction of a chimeric  
 CC DNA containing the leader segment of human HLA-B\*0702 and the  
 CC extracellular, transmembrane and cytoplasmic domains of mouse CD80.  
 XX  
 XX Sequence 39 BP; 8 A; 14 C; 12 G; 5 T; 0 other;



Query Match 68.6%; Score 25.4; DB 20; Length 39;  
Best Local Similarity 96.3%; Pred. No. 0.092;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctccccagacgcgag 37  
Db 13 ggactcagaatctccccagacgcgag 39  
|||||

RESULT 5  
AAT74985  
ID AAT74985 standard; DNA; 707 BP.  
XX  
AC AAT74985;  
XX  
DT 09-MAR-1998 (first entry)  
XX  
DE Human HLA-A2 template for construction of a fusion protein.  
XX  
KW major histocompatibility complex; MHC; fusion protein; gene delivery;  
KW inhibit; pathogen; expression cassette; avidin; Epstein-Barr virus;  
KW EBV; human; HLA; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9724446-A2.  
XX  
PD 10-JUL-1997.  
XX  
PF 20-DEC-1996; 96WO-US020295.  
XX  
PR 29-DEC-1995; 95US-0580541.  
XX  
PR 29-DEC-1995; 95US-0009411.  
XX  
PA (CHIR ) CHIRON VIAGENE INC.  
XX  
PI Banks T, Chada S, Chang SMW, Moore M;  
XX  
DR WPI; 1997-363681/33.  
XX  
PT Fusion proteins containing non-viral cell membrane molecule - used  
PT to target gene delivery vehicles to specific cells, e.g. to inhibit  
PT pathogens

Example 2; Fig 3; 45pp; English.

This is the histocompatibility antigen (HLA-A2) template. This is fused at the amino terminus to gp350/220 peptide sequence from Epstein-Barr virus (EBV). This is used in creating a fusion protein comprising a non-virally encoded cell membrane molecule and a targeting ligand. The fusion protein usually comprises a major histocompatibility complex (MHC) class I or II molecule or beta2 microglobulin and a targeting ligand or one member of a high affinity binding pair, preferably avidin. The HLA-A2 is a MHC class I antigen. The fusion protein on the surface of a gene delivery vehicle can be used in a method for targeting such a gene delivery vehicle to a selected cell type in a warm blooded animal. The method is particularly used to inhibit or destroy a pathogenic agent in a warm blooded animal. The pathogenic agents include parasites, bacteria and viruses, cancer and tumour cells. The method can also be used to generate an immune response against an immunogenic portion of an antigen, in order to prevent or treat a disease, for suppressing graft rejection, and for suppressing an auto immune response.

Sequence 707 BP; 117 A; 221 C; 244 G; 125 T; 0 other;

Query Match 68.6%; Score 25.4; DB 18; Length 707;  
Best Local Similarity 96.3%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctccccagacgcgag 37  
|||||

Db 297.ggactcagaatctccccagacgcgag 323

RESULT 6  
AAI63980  
ID AAI63980 standard; DNA; 3357 BP.  
XX  
AC AAI63980;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 352.  
XX  
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;  
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;  
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;  
KW antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;  
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;  
KW cardiovascular disorder; neurological disease; infection; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155308-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01309.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 18-AUG-2000; 2000US-0225759.  
PR 22-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.











KW gene therapy; chromosome mapping; ss.  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 DR P-PSDB; AAG03762.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 1; SEQ ID 3766; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. An ORF has been identified within the  
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
 CC derived from 30 different tissues. EST sequences usually correspond  
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
 CC well suited for isolating cDNA sequences derived from the 5' ends of  
 CC mRNAs and even in those cases where longer cDNA sequences have been  
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
 CC gene therapy and chromosome mapping procedures. They are used to obtain  
 CC upstream regulatory sequences and to design expression and secretion  
 CC vectors.  
 XX  
 SQ Sequence 447 BP; 83 A; 150 C; 132 G; 70 T; 12 other;  
  
 Query Match 67.6%; Score 25; DB 21; Length 447;  
 Best Local Similarity 92.6%; Pred. No. 0.2;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 11 ggactcagaatctccccagacgccgag 37  
 |||||:|||||||  
 Db 34 ggactcrgattctccccagacgccgag 60  
  
 RESULT 10  
 AAC00214  
 ID AAC00214 standard; cDNA; 529 BP.  
 XX  
 AC AAC00214;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 212.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 DR P-PSDB; AAG00206.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX

PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 DR P-PSDB; AAG00208.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 1; SEQ ID 212; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. An ORF has been identified within the  
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
 CC derived from 30 different tissues. EST sequences usually correspond  
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
 CC well suited for isolating cDNA sequences derived from the 5' ends of  
 CC mRNAs and even in those cases where longer cDNA sequences have been  
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
 CC gene therapy and chromosome mapping procedures. They are used to obtain  
 CC upstream regulatory sequences and to design expression and secretion  
 CC vectors.  
 XX  
 SQ Sequence 529 BP; 97 A; 174 C; 169 G; 83 T; 6 other;  
  
 Query Match 67.6%; Score 25; DB 21; Length 529;  
 Best Local Similarity 92.6%; Pred. No. 0.2;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 11 ggactcagaatctccccagacgccgag 37  
 |||||:|||||||  
 Db 34 ggactcrgattctccccagacgccgag 60  
  
 RESULT 11  
 AAC00212  
 ID AAC00212 standard; cDNA; 432 BP.  
 XX  
 AC AAC00212;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 210.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 DR P-PSDB; AAG00206.  
 XX  
 PF New nucleic acid that is a 5' expressed sequence tag (5' EST) for



PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX Claim 1; SEQ ID 210; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. An ORF has been identified within the  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors.

XX Sequence 432 BP; 81 A; 149 C; 124 G; 62 T; 16 other;  
SQ

Query Match 66.5%; Score 24.6; DB 21; Length 432;  
Best Local Similarity 88.9%; Pred. No. 0.29;  
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagcgcgag 37  
|||||:|||||:|||||:|||||  
DB 34 ggactcrgattctcccgagcgcgag 60

RESULT 12  
AAC00213  
ID AAC00213 standard; cDNA; 358 BP.  
XX AAC00213;  
XX  
XX  
XX  
XX 06-OCT-2000 (first entry)  
XX Human secreted protein 5' EST, SEQ ID NO: 211.  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
XX Homo sapiens.  
XX  
XX EP1033401-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 21-FEB-2000; 2000EP-0200610.  
XX  
XX 26-FEB-1999; 99US-0122487.  
XX  
XX (GEST ) GENSET.  
XX  
XX Dumas Milne Edwards J, Duclert A, Giordano J;  
XX WPI; 2000-500381/45.  
XX  
XX P-PSDB; AAG00207.  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX Claim 1; SEQ ID 211; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. An ORF has been identified within the  
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
CC derived from 30 different tissues. EST sequences usually correspond  
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are

CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
CC well suited for isolating cDNA sequences derived from the 5' ends of  
CC mRNAs and even in those cases where longer cDNA sequences have been  
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
CC gene therapy and chromosome mapping procedures. They are used to obtain  
CC upstream regulatory sequences and to design expression and secretion  
CC vectors.

XX Sequence 358 BP; 65 A; 123 C; 106 G; 52 T; 12 other;  
SQ

Query Match 64.9%; Score 24; DB 21; Length 358;  
Best Local Similarity 88.9%; Pred. No. 0.51;  
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagcgcgag 37  
|||||:|||||:|||||:|||||  
DB 34 ggactcggantctcccgagcgcgag 60

RESULT 13  
AAC04279  
ID AAC04279 standard; cDNA; 527 BP.  
XX AAC04279;  
XX  
XX 06-OCT-2000 (first entry)  
XX Human secreted protein 5' EST, SEQ ID NO: 8354.  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping; ss.  
XX Homo sapiens.  
XX  
XX EP1033401-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 21-FEB-2000; 2000EP-0200610.  
XX  
XX 26-FEB-1999; 99US-0122487.  
XX  
XX (GEST ) GENSET.  
XX  
XX Dumas Milne Edwards J, Duclert A, Giordano J;  
XX WPI; 2000-500381/45.  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX Claim 1; SEQ ID 8354; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
CC identified within the present sequence. The 5' ESTs were prepared from  
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
CC derived from the 5' ends of mRNAs and even in those cases where longer  
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors.

XX Sequence 527 BP; 95 A; 176 C; 160 G; 71 T; 25 other;  
SQ



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Query Match          64.9%; Score 24; DB 21; Length 527;
Best Local Similarity 88.9%; Pred. No. 0.54;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 ggactcagaatctccacgacgcgag 37
Db 34 ggactcgantctccycagacgcgag 60

RESULT 14
AAI63981
ID AAI63981 standard; DNA; 3357 BP.
XX
AC AAI63981;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 353.
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human; ds.
XX
OS Homo sapiens.
XX
PN WO200153308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249219.  
PR 17-NOV-2000; 2000US-0249220.  
PR 17-NOV-2000; 2000US-0249221.  
PR 17-NOV-2000; 2000US-0249222.  
PR 17-NOV-2000; 2000US-0249223.  
PR 17-NOV-2000; 2000US-0249224.  
PR 17-NOV-2000; 2000US-0249225.  
PR 17-NOV-2000; 2000US-0249226.  
PR 17-NOV-2000; 2000US-0249227.  
PR 17-NOV-2000; 2000US-0249228.  
PR 17-NOV-2000; 2000US-0249229.  
PR 17-NOV-2000; 2000US-0249230.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 01-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-488781/53.  
DR  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders -  
PT  
XX  
XX Disclosure; SEQ ID NO 353; 664pp + Sequence Listing; English.  
XX  
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and  
CC the encoded proteins (AAI634497-AAI63660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 3357 BP; 645 A; 947 C; 1035 G; 730 T; 0 other;  
SQ

Query Match 64.3%; Score 23.8; DB 22; Length 3357;  
Best Local Similarity 92.6%; Pred. No. 0.86;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 11 ggactcagaatctcccgacagccgag 37  
||||||| ||||| ||||| ||||| |||||  
Db 38 ggactcagagctctctcagacgag 64

RESULT 15  
AAI63979  
ID AAI63979 standard; DNA; 3372 BP.

XX AAI63979;  
AC 22-OCT-2001 (first entry)  
XX  
DT Human polynucleotide SEQ ID NO 351.  
XX  
DE  
XX  
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;  
KW neuroprotective; anti-allergic; hepatotropic; antidiabetic;  
KW neuroinflammatory; anti-ulcer; vulnery; anticonvulsant; antibacterial;  
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;  
KW cardiovascular disorder; neurological disease; infection; human; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200155308-A2.  
PN  
XX  
XX 02-AUG-2001.  
PD  
XX  
XX 17-JAN-2001; 2001WO-US01309.  
PF  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
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PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
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PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
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PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR



PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0232403.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
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PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246529.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-488781/53.  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders -  
XX  
XX Disclosure; SEQ ID NO 351; 664pp + Sequence Listing; English.  
PS  
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and  
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 3372 BP; 663 A; 961 C; 1024 G; 724 T; 0 other;

Query Match 64.3%; Score 23.8; DB 22; Length 3372;  
Best Local Similarity 92.6%; Pred. No. 0.86;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 ggactcagaatctctccagacgcgcag 37  
||||| | |||||||  
Db 27 ggactcggattctccagacgcgcag 53

Search completed: December 6, 2001, 10:01:23  
Job time: 4267 sec



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Qy 11 ggactcagaatctccccagagcgcgag 37  
+++++  
Db 652 GGACTCAGAATCTCCTTCAGACGCCGAG 67



RESULT 2  
US-08-480-525-1  
; Sequence 1, Application US/08480525  
; Patent No. 5556754  
; GENERAL INFORMATION:  
; APPLICANT: SINGER, DINAH, S.; KOHN,  
; APPLICANT: LEONARD; MOZES, EDNA; SAJI, MOTOYASU;  
; APPLICANT: WEISSMAN, JOCELYN; NAPOLITANO, GIORGIO;  
; APPLICANT: LEDLEY, FRED, D  
; TITLE OF INVENTION: METHODS OF TREATING  
; TITLE OF INVENTION: AUTOIMMUNE DISEASES AND TRANSPLANTATION  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,525  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/073,830  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAROL M. GRUPPI  
; REGISTRATION NUMBER: P-37,341  
; REFERENCE/DOCKET NUMBER: 2026-4066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1419  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: DOUBLE  
; TOPOLOGY: UNKNOWN  
; PCT-US-08-480-525-1

Query Match 51.9%; Score 19.2; DB 1; Length 1419;  
Best Local Similarity 87.5%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 ctcagaatctccccagacgcgcag 37  
||||| ||||||||| |||||  
Db 1088 CTCAGCTCTCCCCAGACTCCGAG 1111

RESULT 3  
PCT-US94-06422-1  
; Sequence 1, Application PC/TUS9406422  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHODS OF TREATING  
; TITLE OF INVENTION: AUTOIMMUNE DISEASES AND TRANSPLANTATION  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK

COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06422  
FILING DATE: JUNE 7, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,830  
FILING DATE: 07-JUN-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4066PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1419  
TYPE: NUCLEIC ACID  
STRANDEDNESS: DOUBLE  
TOPOLOGY: UNKNOWN  
PCT-US94-06422-1

Query Match 51.9%; Score 19.2; DB 5; Length 1419;  
Best Local Similarity 87.5%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 ctcagaatctccccagacgcgcag 37  
||||| ||||||||| |||||  
Db 1088 CTCAGCTCTCCCCAGACTCCGAG 1111

RESULT 4  
PCT-US92-07103-1  
; Sequence 1, Application PC/TUS9207103  
; GENERAL INFORMATION:  
; APPLICANT: Massachusetts Institute of Technology; Forsyth Dental  
; APPLICANT: Center and Ohio State University  
; TITLE OF INVENTION: NOVEL STRAIN OF CHLAMYDIA  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: TWO MILITIA DRIVE  
; CITY: LEXINGTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07103  
; FILING DATE: 19920824  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/748,998  
; FILING DATE: 23-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: MIT-5643A PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240



```
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1510 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia sp.
; STRAIN: novel
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 165
; PUBLICATION INFORMATION:
; AUTHORS: Stills Jr., Harold F.
; TITLE: Isolation of an Intracellular Bacterium
; JOURNAL: Infect. Immun.
; VOLUME: 59
; ISSUE: 9
; DATE: August 24-1991
; PCT-US92-07103-1

Query Match 51.4%; Score 19; DB 5; Length 1510;
Best Local Similarity 62.9%; Pred. No. 28;
Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 2 ggcaagcttgactcagaatctcccagacgcga 36
| | | | | | | | | | | | | | | | | |
Db 316 GCCACACUGGACUGAGACACUGCCCGACUCCUA 350

RESULT 5
US-09-813-819-3/c
; Sequence 3, Application US/09813819
; Patent No. 6294368
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001177
; CURRENT APPLICATION NUMBER: US/09/813,819
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 17138
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(17138)
; OTHER INFORMATION: n - A,T,C or G
US-09-813-819-3

Query Match 51.4%; Score 19; DB 4; Length 17138;
Best Local Similarity 81.5%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 gcaagcttgactcagaatctcccag 29
| | | | | | | | | | | | | | | | | |
Db 3730 GCAAGTTTGGCTTCAACAATTTCCTCCAG 3704

RESULT 6
US-08-793-660B-10/c
; Sequence 10, Application US/08793660B
; Patent No. 6214614
; GENERAL INFORMATION:
; APPLICANT: MULLER, Rolf
; TITLE OF INVENTION: CELL CYCLE REGULATED REPRESSOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,660B
; FILING DATE: 09-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 96/06943
; FILING DATE: 07-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 95/06466
; FILING DATE: 29-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 94/17366
; FILING DATE: 26-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowen, Cara Z.
; REGISTRATION NUMBER: 38,227
; REFERENCE/DOCKET NUMBER: 47211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-793-660B-10

Query Match 50.8%; Score 18.8; DB 4; Length 270;
Best Local Similarity 76.7%; Pred. No. 27;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ggccaagcttgactcagaatctcccaga 30
| | | | | | | | | | | | | | | | | |
Db 170 GGCCACGTCGAGCTCAGAGTCTTCCCTGA 141

RESULT 7
US-09-039-555B-19/c
; Sequence 19, Application US/09039555B
; Patent No. 6033856
; GENERAL INFORMATION:
; APPLICANT: Koerner, Kathrin
; APPLICANT: Mueller, Rolf
; APPLICANT: Sadlacek, Hans-Harald
; TITLE OF INVENTION: PROMOTER OF THE CDC25B GENE, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/039,555B  
;; FILING DATE: 16-MAR-1998  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: DE 19710643.9  
;; FILING DATE: 14-MAR-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bent, Stephen A.  
;; REGISTRATION NUMBER: 29,768  
;; REFERENCE/DOCKET NUMBER: 016779/0131  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEFAX: (202)672-5399  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2000 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; US-09-039-555B-19

Query Match 50.8%; Score 18.8; DB 3; Length 2000;  
Best Local Similarity 76.7%; Pred. No. 36;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 999caagcttgactcagaatctcccccaga 30  
Db 1900 G6CAACGTCGACTCAGTCTCCCTGA 1871

RESULT 8  
US-09-078-459-3  
; Sequence 3, Application US/09078459  
; Patent No. 5858618  
; GENERAL INFORMATION:  
; APPLICANT: XU, SHUANG-YONG  
; APPLICANT: MAUNUS, ROBERT E.  
; APPLICANT: LUNNEN, KEITH D.  
; APPLICANT: ALLEN, RACHEL  
; TITLE OF INVENTION: METHOD FOR CLONING  
; TITLE OF INVENTION: AND PRODUCING THE AgeI RESTRICTION  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: New England Biolabs, Inc.  
; STREET: 32 Tozer Road  
; CITY: Beverly  
; STATE: MA  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/078,459  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams, Gregory D  
; REGISTRATION NUMBER: 30901

;; REFERENCE/DOCKET NUMBER: NEB-136  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 978-927-5054  
;; TELEFAX: 978-927-1705  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 852 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: Coding Sequence  
;; LOCATION: 1...849  
;; OTHER INFORMATION:  
;; US-09-078-459-3

Query Match 50.3%; Score 18.6; DB 2; Length 852;  
Best Local Similarity 72.7%; Pred. No. 38;  
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 5 aagcttgactcagaatctcccccagagccag 37  
Db 472 AAGCAGGAGGCGACGCTCTCCGCGCCGAG 504

RESULT 9  
US-08-678-039A-41  
; Sequence 41, Application US/08678039A  
; Patent No. 5858662  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Morris, Colleen A.  
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and  
; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the  
; TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
; STREET: 555 Thirteenth Street, N.W., Suite 701 East  
; STREET: Tower  
; CITY: Washington  
; STATE: DC  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/678,039A  
; FILING DATE: 10-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Stephen A.  
; REGISTRATION NUMBER: 38,609  
; REFERENCE/DOCKET NUMBER: 2323-120A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-624-1589  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3262 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:



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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 96..2036
; US-08-678-039A-41

Query Match          50.3%; Score 18.6; DB 2; Length 3262;
Best Local Similarity 72.7%; Pred. No. 46;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 ggcaagcttgagctcagaatctccccagccg 34
    ||||| ||||| | ||||| |||||
Db 615 GGCAAGCGTGGACTTTCAGCTCCTCCATGACCC 647

RESULT 10
US-09-102-204-3
; Sequence 3, Application US/09102204
; Patent No. 6190899
; GENERAL INFORMATION:
; APPLICANT: Jones, Brian E.
; APPLICANT: Van Der Kleij, Wilhelmus A.H.
; APPLICANT: Van Solingen, Piet
; APPLICANT: Weyler, Walter
; TITLE OF INVENTION: No. 6190899el Cellulase Producing Actinomycetes,
; TITLE OF INVENTION: Cellulase Produced Therefrom
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,204
; FILING DATE: 22-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,041
; FILING DATE: 19-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher L.
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC539
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-6504
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-102-204-3

Query Match          49.7%; Score 18.4; DB 4; Length 421;
Best Local Similarity 69.4%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 gggaagcttgagctcagaatctccccagccg 36
    ||||| ||||| || ||||| ||||| |||||
Db 289 GGCCACTGGGACTGAGACAGGCCCCAGACTCCTA 324

RESULT 11
US-09-104-308-3
; Sequence 3, Application US/09321981
; Patent No. 6287839
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
; TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing Same
; FILE REFERENCE: GC540-2
; CURRENT APPLICATION NUMBER: US/09/321,981
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: PCT/US99/11971
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 09/104,308
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 08/974,042
; PRIOR FILING DATE: 1997-11-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3

Query Match          49.7%; Score 18.4; DB 4; Length 463;
Best Local Similarity 69.4%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 gggaagcttgagctcagaatctccccagccg 36
    ||||| ||||| || ||||| ||||| |||||
Db 274 GGCCACTGGGACTGAGACAGGCCCCAGACTCCTA 309

RESULT 12
US-09-321-981-3
; Sequence 3, Application US/09321981
; Patent No. 6287839
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: No. 6287839el Cellulase Producing Actinomycetes,
; TITLE OF INVENTION: Cellulase Produced Therefrom and Method of Producing Same
; FILE REFERENCE: GC540-2
; CURRENT APPLICATION NUMBER: US/09/321,981
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: PCT/US99/11971
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 09/104,308
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 08/974,042
; PRIOR FILING DATE: 1997-11-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
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**Qy** 1 ggcaagcttgactcagaatctccacagacgcga 36  
||| ||| ||| ||| ||| ||| ||| |||  
**Pb** 291 ggcacactggactgagacacggcccagactcta 326



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2001, 08:50:16 : Search time 2220.1 seconds  
(without alignments)  
179.088 Million cell updates/sec

Title: US-09-673-795-3

Perfect score: 37

Sequence: 1 gggcaagcttgactcagaatctccccagacgcgag 37

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_estl:*
11: gb_estc:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pin:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.8	69.7	719	11	BG721571
2	25.4	68.6	50	10	AU106142
3	25.4	68.6	50	10	AU106167
4	25.4	68.6	185	11	BF170215
5	25.4	68.6	315	11	BF806991
6	25.4	68.6	490	11	BG537751
7	25.4	68.6	550	11	BF724208
8	25.4	68.6	552	11	BG108345
9	25.4	68.6	721	11	BG325639
10	25.4	68.6	763	11	BF969741
11	25.4	68.6	802	10	AL549560
12	25.4	68.6	891	10	AL537221

13	25.4	68.6	962	11	BG775632
14	25.4	68.6	1139	11	BE894912
c 15	24.8	67.0	486	10	AU088719
c 16	24.8	67.0	741	11	BG476157
17	24.6	66.5	257	10	BE476868
18	24.4	65.9	722	11	BG536621
19	23.8	64.3	419	10	AA102697
20	23.8	64.3	519	11	BG340457
21	23.8	64.3	575	11	BG546413
22	23.8	64.3	698	11	BG751030
23	23.8	64.3	718	11	BG755440
24	23.8	64.3	733	11	BF568512
c 25	23.8	64.3	768	11	BG476149
26	23.8	64.3	786	11	BG830531
27	23.8	64.3	795	11	BG884727
28	23.4	63.2	965	10	AL533479
29	23	62.2	415	11	BG693832
30	23	62.2	636	11	BG691647
31	22.8	61.6	50	10	AU106135
32	22.4	60.5	752	11	BF579406
33	22.2	60.0	50	10	AU106243
34	22.2	60.0	50	10	AU106245
35	22.2	60.0	400	11	BG818707
36	22.2	60.0	812	11	BG718363
37	22	59.5	244	10	BE486369
38	21.6	58.4	593	13	CNS01PXO
39	21.4	57.8	50	10	AU106172
40	21.4	57.8	50	10	AU106177
41	21.4	57.8	50	10	AU106184
42	21.4	57.8	50	10	AU106191
43	21.4	57.8	50	10	AU106195
44	21.4	57.8	50	10	AU106208
45	21.4	57.8	50	10	AU106215

#### ALIGNMENTS

```
RESULT 1
BG721571 719 bp mRNA EST 08-MAY-2001
LOCUS 602695180F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4827499 5',
DEFINITION mRNA sequence.
ACCESSION BG721571.1 GI:14000758
VERSION BG721571.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 719)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps@email.nih.gov
Tissue procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10743 row: 0 column: 20
High quality sequence stop: 719.
FEATURES
Location/Qualifiers
1..719
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4827499"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
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RESULT	3
AU106167	
LOCUS	AU106167
DEFINITION	50 bp mRNA EST
	AU106167 Sugano Homo sapiens cdna library Homo sapiens CDNA clone
	HRC09410, mRNA sequence.
	05-APR-2001

```
1. .10J
/organism="Homo sapiens"
/db_xref="taxon:9606"
```



```

/clone_lib="Myeloma (PCL) cDNA library"
/sex="male"
/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="Plasma cell leukemia"
/notes="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from plasma cell leukemia
patient's peripheral blood containing >95% myeloma. An
oligo d(T)18 primer containing XhoI restriction site was
used to prime first strand synthesis using M-MLV reverse
transcriptase. To protect the cDNAs from XhoI digestion in
subsequent cloning step, the nucleotide analogue
5-methyl-dCTP was added to the nucleotide mixture and
la-32P dATP was added to monitor the quantity and quality
of first strand synthesis. After second-strand synthesis
and blunting of cDNA termini, EcoRI adapters were ligated
, followed by kinase treatment and digestion with XhoI.
The cDNAs were then size-fractionated using Sephacryl
S-500 column and then ligated into EcoRI and XhoI digested
Lambda Zap Express vector. The ligation product was
packaged using Gigapack II packaging extract. The library
had primary titre of approx. 1x106. Clones from the
primary library were randomly selected for single pass
sequencing."
BASE COUNT      27 a      71 c      55 g      32 t
ORIGIN

Query Match      68.6%; Score 25.4; DB 11; Length 185;
Best Local Similarity 96.3%; Pred. No. 5.4;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccccagacgcgcag 37
|||||
Db 7 GGACTCAGAATCTCCCTCAGACGCCGAG 33

RESULT 5
BF806991
LOCUS      BF806991      315 bp      mRNA      EST      12-JAN-2001
DEFINITION QV4-C10151-091100-522-h06 C10151 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF806991
VERSION     BF806991.1 GI:12135980
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 315)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-C10151-
            091100-522-h06&t3=2000-11-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 315.

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```

FEATURES
source
Location/Qualifiers
1..315
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="C10151"
/dev_stage="Adult"
/notes="Organ: colon_ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      52 a      102 c      110 g      51 t
ORIGIN

Query Match      68.6%; Score 25.4; DB 11; Length 315;
Best Local Similarity 96.3%; Pred. No. 5.9;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccccagacgcgcag 37
|||||
Db 122 GGACTCAGAATCTCCCTCAGACGCCGAG 148

RESULT 6
BG537751
LOCUS      BG537751      490 bp      mRNA      EST      03-APR-2001
DEFINITION G02566102F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4690512 5',
            mRNA sequence.
ACCESSION  BG537751
VERSION     BG537751.1 GI:13529983
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 490)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1508 row: d column: 01
            High quality sequence stop: 462.
            Location/Qualifiers
            1..490
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="NIH_MGC_77"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
            SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCCGCGCCGACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.9
            kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH_MGC Library."
BASE COUNT      94 a      158 c      159 g      79 t
ORIGIN

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```

Query Match      68.6%; Score 25.4; DB 11; Length 490;
Best Local Similarity 96.3%; Pred. No. 6.3;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagcgcgag 37
||||| ||||| ||||| ||||| |||||
Db 1 GGACTCAGATTCTCCCGAGCGCGGAG 27

RESULT 7
BF724208
LOCUS
DEFINITION
  bx02b09.y1 Human Iris cDNA (Un-normalized, unamplified): Bx Homo sapiens cDNA clone bx02b09 5', mRNA sequence.
ACCESSION
  BF724208
VERSION
  BF724208.1 GI:12040117
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
AUTHORS
  Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE
  NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL
  Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT
  Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 02 row: b column: 09
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
  source
    1..550
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="bx02b09"
      /tissue_type="Human Iris cDNA (Un-normalized, unamplified): Bx"
      /tissue_type="Iris"
      /dev_stage="Adult"
      /lab_host="EMDH10B"
      /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTCTAGATCGGCGGCCG(T)15-3' 1. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."]
BASE COUNT      111 a 190 c 172 g 76 t 1 others
ORIGIN

Query Match      68.6%; Score 25.4; DB 11; Length 550;
Best Local Similarity 96.3%; Pred. No. 6.4;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagcgcgag 37
||||| ||||| ||||| ||||| |||||
Db 12 GGACTCAGAAATCTCTCAGACGCCGAG 38

```

```

RESULT 8
BG108345
LOCUS
DEFINITION
  602280354F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368132 5', mRNA sequence.
ACCESSION
  BG108345
VERSION
  BG108345.1 GI:12602191
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 652)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaabs-r@mail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM10021 row: k column: 13
  High quality sequence stop: 649.
FEATURES
  Location/Qualifiers
    1..652
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:4368132"
      /clone_lib="NIH_MGC_86"
      /tissue_type="osteosarcoma, cell line"
      /lab_host="DH10B (phage-resistant)"
      /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."
BASE COUNT      133 a 215 c 217 g 87 t
ORIGIN

Query Match      68.6%; Score 25.4; DB 11; Length 652;
Best Local Similarity 96.3%; Pred. No. 6.6;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagcgcgag 37
||||| ||||| ||||| ||||| |||||
Db 23 GGACTCAGAAATCTCTCAGACGCCGAG 49

RESULT 9
BG325639
LOCUS
DEFINITION
  602424355F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4562485 5', mRNA sequence.
ACCESSION
  BG325639
VERSION
  BG325639.1 GI:13132076
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 721)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaabs-r@mail.nih.gov
  Tissue Procurement: DCTD/DTP
  cDNA Library Preparation: Ling Hong/Rubin Laboratory

```







KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 891)

TITLE Li.W.B., Gruber.C., Jessee,J. and Polayes.D.

JOURNAL Full-length cDNA libraries and normalization

COMMENT Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES location/Qualifiers  
Source 1. .891  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DF019YC10"  
/clone\_lib="LTI\_FL013\_FBrn1"  
/dev\_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"  
/lab\_host="DH10B"  
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 182 a 282 c 238 g 129 t

LOCUS BE894912

DEFINITION BE894912 1139 bp mRNA EST 20-OCT-2000

ACCESSION BE894912

VERSION BE894912.1 GI:10357776

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 962)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCFD/DTP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9753 row: h column: 01  
High quality sequence stop: 432.

FEATURES location/Qualifiers  
Source 1. .1139  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3921072"  
/clone\_lib="NIH\_MGC\_40"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 181 a 585 c 268 g 104 t

ORIGIN

Query Match 68.6%; Score 25.4; DB 11; Length 962;  
Best Local Similarity 96.3%; Pred. No. 7;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagccgag 37  
||||||| ||||||| ||||||| |||||||

Db 32 GGACTCAGATTCCTCCCGAGCGCGAG 58

RESULT 13

LOCUS BG775632

DEFINITION BG775632 962 bp mRNA EST 15-MAY-2001

ACCESSION BG775632

VERSION BG775632.1 GI:14045949

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 962)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCMI613 row: j column: 17  
High quality sequence stop: 837.

FEATURES location/Qualifiers

source 1. .962  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4761328"  
/clone\_lib="NIH\_MGC\_40"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 188 a 304 c 322 g 148 t

ORIGIN

Query Match 68.6%; Score 25.4; DB 11; Length 962;  
Best Local Similarity 96.3%; Pred. No. 7;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ggactcagaatctcccgagccgag 37  
||||||| ||||||| ||||||| |||||||

Db 32 GGACTCAGATTCCTCCCGAGCGCGAG 58

RESULT 14

LOCUS BE894912

DEFINITION BE894912 1139 bp mRNA EST 20-OCT-2000

ACCESSION BE894912

VERSION BE894912.1 GI:10357776

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 1139)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCFD/DTP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9753 row: h column: 01  
High quality sequence stop: 432.

FEATURES location/Qualifiers  
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/clone\_lib="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 181 a 585 c 268 g 104 t

ORIGIN

Query Match 68.6%; Score 25.4; DB 11; Length 1139;  
Best Local Similarity 96.3%; Pred. No. 7.2;



Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 ggaactcagaatctccccagacgccgag 37  
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Db 1 GGACTCAGATTCTCCCCAGACGCCGAG 27

RESULT 15  
AU088719/c  
LOCUS AU088719 486 bp mRNA EST 31-MAR-2000  
DEFINITION AU088719 Rice shoot Oryza sativa cDNA clone S4716, mRNA sequence.  
ACCESSION AU088719  
VERSION AU088719.1 GI:7378448  
KEYWORDS EST.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 486)  
Sasaki, T. and Yamamoto, K.  
Rice cDNA from etiolated shoot (2000)  
UNPUBLISHED (2000)  
Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
305-8602, Japan  
Tel: 81-298-38-7441  
Fax: 81-298-38-7468  
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
PROJECT = 'RGP'.  
S4716\_10Z.

FEATURES  
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BASE COUNT 116 a 91 c 105 g 170 t 4 others  
ORIGIN

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Best Local Similarity 80.6%; Pred. No. 11;  
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ggggaagcttggaatctccccagacgccga 36  
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Db 93 GGACAGAGCTGGGACTCAGAAAAATCACCAGAGCCGA 58

Search completed: December 6, 2001, 09:29:42  
Job time: 2366 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2001, 09:57:28 ; Search time 1647.92 Seconds  
(without alignments)  
360.393 Million cell updates/sec

Title: US-09-673-795-4

Perfect score: 36

Sequence: 1 gccctcagatctcagtcctccacaaagcgagctgctc 36

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_om:\*

20: em\_or:\*

21: em\_ov:\*

22: em\_pat:\*

23: em\_ph:\*

24: em\_pl:\*

25: em\_ro:\*

26: em\_sts:\*

27: em\_sy:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htgo\_hum:\*

31: em\_htgo\_inv:\*

32: em\_htgo\_rod:\*

33: em\_htg\_hum:\*

34: em\_htg\_inv:\*

35: em\_htg\_rod:\*

36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	100.0	36	6	AX012956	AX012956 Sequence
c 2	27.2	75.6	1347	9	CHPMHCAE	M24048 Chimpanzee
c 3	27.2	75.6	1359	9	CHPMHCA	M24044 Chimpanzee
c 4	27.2	75.6	1516	9	PTCHLAB2	X13116 Chimpanzee
c 5	27.2	75.6	1517	9	CHPMHCRAB	M30679 Pan troglod
c 6	26.4	73.3	39	6	AR073931	AR073931 Sequence
c 7	26.4	73.3	39	6	AR075099	AR075099 Sequence
c 8	26.2	72.8	427	11	G07078	G07078 human STS W
c 9	26.2	72.8	1270	9	HSHLA35A	Z22651 H.sapiens H
c 10	26.2	72.8	1270	9	HUMHLAB44A	L42345 Homo sapien
c 11	26.2	72.8	1272	9	HSHLAB27X	Z33453 H.sapiens m
c 12	26.2	72.8	1273	9	GGBO201	X60253 G.gorilla M
c 13	26.2	72.8	1273	9	AF157406	AF157406 Gorilla g
c 14	26.2	72.8	1323	9	HUMHBIATW3	M27540 Human MHC c
c 15	26.2	72.8	1357	9	HUMHLABH	L42024 Homo sapien
c 16	26.2	72.8	1479	9	HUMHMB82	M28204 Homo sapien
c 17	26.2	72.8	1500	9	HUMHMB44	M15470 Human MHC c
c 18	26.2	72.8	1504	9	D87665	D87665 Human heart
c 19	26.2	72.8	1507	9	HUMHMB27A	M12678 Human HLA-B
c 20	26.2	72.8	1507	9	PTCHLAB1	X13115 Chimpanzee
c 21	26.2	72.8	1521	9	HUMHMB7A	M16102 Human MHC H
c 22	26.2	72.8	1535	9	BC007243	BC007243 Homo sapi
c 23	26.2	72.8	1537	9	CHPMHCAA	M24045 Chimpanzee
c 24	26.2	72.8	1550	9	AY007140	AY007140 Homo sapi
c 25	26.2	72.8	1639	9	HSHLAK2	X03667 Human class
c 26	26.2	72.8	1639	9	HSHLAW2	X03666 Human class
c 27	26.2	72.8	3019	9	HSAL33267	AJ133267 Homo sapi
c 28	26.2	72.8	3027	9	HSU56246	U56246 Human MHC c
c 29	26.2	72.8	3036	9	HSJ294938	AJ294938 Homo sapi
c 30	26.2	72.8	3036	9	HSJ294939	AJ294939 Homo sapi
c 31	26.2	72.8	3039	9	HSJ309047	AJ309047 Homo sapi
c 32	26.2	72.8	3135	9	HSJ297317	AJ297317 Homo sapi
c 33	26.2	72.8	3139	9	HSJ292253	AJ292253 Homo sapi
c 34	26.2	72.8	3170	9	HSJ308398	AJ308398 Homo sapi
c 35	26.2	72.8	3180	9	HSJ278903	AJ278903 Homo sapi
c 36	26.2	72.8	3187	9	HSJ245869	AJ245869 Homo sapi
c 37	26.2	72.8	3190	9	HSJ295141	AJ295141 Homo sapi
c 38	26.2	72.8	3190	9	HSJ300180	AJ300180 Homo sapi
c 39	26.2	72.8	3337	9	HSJ309193	AJ309193 Homo sapi
c 40	26.2	72.8	3350	9	HSJ309936	AJ309936 Homo sapi
c 41	26.2	72.8	3350	9	HSJ309937	AJ309937 Homo sapi
c 42	26.2	72.8	3370	9	HSJ310358	AJ310358 Homo sapi
c 43	26.2	72.8	3375	9	HSJ278944	AJ278944 Homo sapi
c 44	26.2	72.8	3437	9	HSJ301657	AJ301657 Homo sapi
c 45	26.2	72.8	3445	9	HSJ311601	AJ311601 Homo sapi

#### ALIGNMENTS

RESULT	1					
LOCUS	AX012956	36 bp	DNA	PAT	07-SEP-2000	
DEFINITION	Sequence 4 from Patent WO9954464.					
ACCESSION	AX012956					
VERSION	AX012956.1	GI:10040206				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	1 (bases 1 to 36)					
TITLE	Gaudin,C. and Triebel,F.					
JOURNAL	Mutated peptide compounds, derived from hsp70, useful in cancer immunotherapy					
FEATURES	Patent: WO 9954464-A 4 28-OCT-1999; ROUSSY INST GUSTAVE (FR); GAUDIN CATHERINE (FR); TRIEBEL FREDERIC (FR)					
source	Location/Qualifiers					
	1..36					



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/db_xref="taxon:9606"
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BASE COUNT 7 a 14 c 7 g 8 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcccttagatctcagtcctcacaagcagctgtc 36
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Db 1 gcccttagatctcagtcctcacaagcagctgtc 36

RESULT 2
CHPMHCAE/c
LOCUS CHPMHCAE 1347 bp mRNA PRI 27-SEP-1993
DEFINITION Chimpanzee MHC class I ChIA chain mRNA, complete cds, clone 18.
ACCESSION M24048 M24029
VERSION M24048.1 GI:176820
KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene;
Integral membrane protein; major histocompatibility complex.
SOURCE Chimpanzee (Tank) EBV-transformed B lymphoblastoid cell, CDNA to
mRNA, clone 18.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 918; 919 to 1347)
AUTHORS Parham,P., Lawlor,D.A., Lomen,C.E. and Ennis,P.D.
TITLE Diversity and diversification of HLA class I alleles
JOURNAL J. Immunol. 142, 3937-3950 (1989)
MEDLINE 89235215
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by P.D.Ennis, 14-APR-1989.
FEATURES
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Location/Qualifiers
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ISDHEATLRWALGFYPAETLTWQDGEDQTDTELVEPRPAGDRTFOKWAAYVPS
GEQRYTCHVOHEGLPKPLTLRWEPSSQSTIPIVIGVAGLAVLVVIGAVVAVMCR
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369 a 369 g 400 g 278 t
BASE COUNT 300 a 369 g 400 g 278 t
ORIGIN

Query Match 75.6%; Score 27.2; DB 9; Length 1347;
Best Local Similarity 90.6%; Pred. No. 0.11;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 tctagatctcagtcctcacaagcagctgtc 36
|||||
Db 959 TCTGCATCTCAGTCCTCACAAGCAGCTGTC 928

RESULT 3
CHPMHCA/c
LOCUS CHPMHCA 1359 bp mRNA PRI 27-SEP-1993
DEFINITION Chimpanzee MHC class I ChIA chain mRNA, partial cds, clone 7.
ACCESSION M24044 M24029
VERSION M24044.1 GI:176812
KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene;

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integral membrane protein; major histocompatibility complex.
Chimpanzee (Kasey) EBV transformed B lymphoblastoid cell, CDNA to
mRNA, clone 7.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 929; 930 to 1359)
AUTHORS Parham,P., Lawlor,D.A., Lomen,C.E. and Ennis,P.D.
TITLE Diversity and diversification of HLA class I alleles
JOURNAL J. Immunol. 142, 3937-3950 (1989)
MEDLINE 89235215
COMMENT Computer-readable copy of sequence [1] kindly submitted by
P.D.Ennis 14-APR-1989.
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VPSGEQRYTCHVOHEGLPKPLTLRWEPSSQSTIPIVIGVAGLAVLVVIGAVVAAV
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308 a 372 c 401 g 278 t
BASE COUNT 308 a 372 c 401 g 278 t
ORIGIN

Query Match 75.6%; Score 27.2; DB 9; Length 1359;
Best Local Similarity 90.6%; Pred. No. 0.11;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 tctagatctcagtcctcacaagcagctgtc 36
|||||
Db 970 TCTGCATCTCAGTCCTCACAAGCAGCTGTC 939

RESULT 4
PTCHLAB2/c
LOCUS PTCHLAB2 1516 bp mRNA PRI 27-MAR-1995
DEFINITION Chimpanzee mRNA for class I antigen ChLA-B2.
ACCESSION X13116 X12781
VERSION X13116.1 GI:38208
KEYWORDS antigen; cell surface glycoprotein; class I antigen; major
histocompatibility complex; surface antigen.
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 11 to 1516)
AUTHORS Mayer,W.E.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1988) W.E. Mayer, Stanford University, Dept. of
Biological Sciences, Stanford, CA 94305-5020, USA
REFERENCE 2 (bases 11 to 1516)
AUTHORS Mayer,W.E., Jonker,M., Klein,D., Ivanyi,P., van Seventer,G. and
Klein,J.
TITLE Nucleotide sequences of chimpanzee MHC class I alleles: evidence
for trans-species mode of evolution
JOURNAL EMBO J. 7 (9), 2765-2774 (1988)
MEDLINE 89030641
REFERENCE 3 (bases 1 to 1516)
AUTHORS Mayer,W.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1989) to the EMBL/GenBank/DBJ databases
POSITION 617 is c in [1], [3] and u in [2].

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QY 1 gccctctagatctcagtcctcctcacaggcagctgtc 36  
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 Db 4 GCCCGAATTCCTCAGTCCTCCTCACAGGCGAGCTGTC 39

RESULT 7  
 AR075099  
 LOCUS AR075099 39 bp DNA PAT 28-AUG-2000  
 DEFINITION Sequence 4 from patent US 5955313.  
 ACCESSION AR075099  
 VERSION AR075099.1 GI:10001851  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 39)  
 AUTHORS van der Bruggen, P., Mandruzzato, S. and Boon-Falleur, T.  
 TITLE Nucleic acid molecule encoding a bifunctional protein, the protein  
 so encoded uses thereof  
 JOURNAL Patent: US 5955313-A 4 21-SEP-1999;  
 FEATURES Location/Qualifiers  
 source 1..39  
 BASE COUNT 8 a 15 c 7 g 9 t  
 ORIGIN

Query Match 73.3%; Score 26.4; DB 6; Length 39;  
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 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctagatctcagtcctcctcacaggcagctgtc 36  
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 Db 4 GCCCGAATTCCTCAGTCCTCCTCACAGGCGAGCTGTC 39

RESULT 8  
 LOCUS G07078/c 427 bp DNA STS 19-OCT-1995  
 DEFINITION human STS WI-9014.  
 ACCESSION G07078  
 VERSION G07078.1 GI:860323  
 KEYWORDS STS sequence; primer; sequence tagged site.  
 SOURCE human STS derived from sequences in dbEST and the Unigene collection.

ORGANISM Homo sapiens  
 Eukaryota; Eukaryota; Chordata; Chordata; Vertebrata; Mammalia; Mammalia; Eutheria; Eutheria; Theria; Archonta; Primates; Tetrapoda; Amniota; Mammalia; Theria; Archonta; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 427)  
 AUTHORS Hudson, T.  
 TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
 Mapped ESTs  
 JOURNAL Unpublished (1995)

COMMENT  
 Contact: Thomas Hudson  
 Whitehead Institute/MIT Center for Genome Research  
 Whitehead Institute for Biomedical Research  
 9 Cambridge center, Cambridge MA 02142 USA  
 Tel: 617 252 1900  
 Fax: 617 252 1902  
 Email: thudson@genome.wi.mit.edu

Primer A: CCCTGTCCTCCATGCTGAC  
 Primer B: AGAGTTGCGAGCTCAGTGCA  
 STS size: 115  
 PCR profile:  
 Presoak:  
 Denaturation:  
 Annealing: 56 degrees C  
 Polymerization:

PCR Cycles: 35  
 Thermal Cycler:  
 Protocol:  
 Template: 10 ng  
 Primer: each 5 pM  
 dNTPs: each 4 mM  
 Taq Polymerase: 0.025 units/ul  
 Total Vol: 20 ul

Buffer:  
 MgCl2: 1.5 mM  
 KCl: 50 mM  
 Tris-HCl: 10 mM  
 pH: 9.3

Prepared with primer pairs derived from MI2678 -- Unigene.

FEATURES  
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 Best Local Similarity 90.3%; Pred. No. 0.35;  
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctgatatctcagtcctcctcacaggcagctgtc 36  
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 Db 40 CTGATCTCAGTCCTCCTCACAGGCGAGCTGTC 10

RESULT 9  
 LOCUS HSHLA35A/c  
 DEFINITION H. sapiens HLA-B35 mRNA.  
 ACCESSION 222651  
 VERSION 222651.1 GI:297142  
 KEYWORDS HLA-B35.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1270)  
 AUTHORS Steinle, A., Reinhardt, C., Nossner, E., Uchanska-Ziegler, B., Ziegler, A., and Schendel, D.J.  
 TITLE Microheterogeneity in HLA-B35 alleles influences peptide-dependent allorecognition by cytotoxic T cells but not binding of a peptide-restricted monoclonal antibody  
 JOURNAL Hum. Immunol. 38 (4), 261-269 (1993)  
 MEDLINE 94186367  
 REFERENCE 2 (bases 1 to 1270)  
 AUTHORS Steinle, A.

COMMENT  
 Direct Submission  
 Submitted (27-APR-1993) Steinle A., University of Munich, Institute  
 of Immunology, Goethestrasse 31, W-8000 MUENCHEN 2, GERMANY  
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 /db\_xref="taxon:9606"  
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Best Local Similarity 90.3%; Pred. No. 0.32;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctgatatcagtcctccacaaaggcagctgtc 36
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Db 1129 CTCATCTCAGTCCCTCACAGACAGCTGTC 1099

RESULT 10
HUMHLAB44A/c 1270 bp mRNA PRI 18-JAN-1996
LOCUS Homo sapiens lymphocyte antigen HLA-B*4402 and HLA-B*5101 mRNA,
exons 1-7, complete cds.
ACCESSION L42345
VERSION L42345.1 GI:1160933
KEYWORDS HLA-B*4402 gene; HLA-B*5101 gene; HLA-B-51x44 gene; lymphocyte
antigen.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1270)
AUTHORS Zhao, W., Fernandez-Vina, M.A. and Stastny, P.
TITLE Novel HLA-B allele part B*5101 and part B*4402
JOURNAL Unpublished (1995)
FEATURES
Location/Qualifiers
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DTAAQITORKWEAARVAQRDAYLEGLCVESLRRLYENKGTFLORADPPKTHVTHPI
SDHEATLRCWALGFFPAEITLWQRDGEDQTDTELVTFRPAGDRTFQKMAAVVPSG
BEQRYTCHVQHGELPKPLTLRWEPSSQSTPIPIVIGAVLAVLVAVVIGAAVAVMCCR
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206
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213
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/replace="c"
259..261
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/replace="aac"
272
/gene="HLA-B*4402"
/replace="t"
309..311
/gene="HLA-B*4402"
/replace="gat"
344..619
/number=3
620..895
/number=4
896..1012
/number=5
1013..1045
/number=6
1046..1089
/number=7
1090..1270
3'UTR 259 a 386 c 406 g 219 t
BASE COUNT
ORIGIN

Query Match 72.8%; Score 26.2; DB 9; Length 1270;
Best Local Similarity 90.3%; Pred. No. 0.32;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctgatatcagtcctccacaaaggcagctgtc 36
|| ||||| ||||| ||||| ||||| |||||
Db 1129 CTCATCTCAGTCCCTCACAGACAGCTGTC 1099

RESULT 11
HSHLAB27X/c 1272 bp mRNA PRI 02-FEB-1995
LOCUS H.sapiens mRNA for human leukocyte antigen HLA-B27.
DEFINITION H.sapiens mRNA for human leukocyte antigen HLA-B27.
ACCESSION Z33453
VERSION Z33453.1 GI:486652
KEYWORDS HLA-B27 antigen; human leukocyte antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1272)
AUTHORS Del Porto, P., D'Amato, M., Fiorillo, M.T., Tuosto, L., Piccolella, E.
and Sorrentino, R.
TITLE Identification of a novel HLA-B27 subtype by restriction analysis
of a cytotoxic gamma delta T cell clone
JOURNAL J. Immunol. 153 (7), 3093-3100 (1994)
MEDLINE 94375872
REFERENCE 2 (bases 1 to 1272)
AUTHORS D'Amato, M.
DIRECT SUBMISSION Direct Submission
TITLE Submitted (10-MAY-1994) D'Amato M., Institute of Cell Biology-CNR,
JOURNAL Immunobiology, Viale Marx 43, Rome, Italy, 00143
FEATURES
Location/Qualifiers
source
1..1272
/organism="Homo sapiens"
/isolate="Ci"
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```

/db_xref="taxon:9606"
/chromosome="6"
/haplotype="HLA-A2/-A10/-B16/-B27/-Cw1"
/sex="Male"
/clone="M13Ci"
/dev_stage="Adult"
/tissue_type="blood"
/cell_type="B-cell"
/cell_line="Ci"
2..1090
/codon_start=1
/product="human lymphocyte antigen HLA-B27"
/protein_id="CAA83876.1"
/db_xref="GI:486653"
/db_xref="SPTREMBL:Q29846"
/translation="NRVTPAPRTLLLLGAVALTETWAGSHSMRYFHTSVSRPGRGEP
RITVGVYDDTQFVFDSDAASPKEPRTPIEIOEGPEYWDRETOICKAKADTDSREDL
RILLRYNQSAGSTLQNMVCDVPGDGLRGYHGHAYDKGDKYLALNEDLSSTAA
DTAAQITQRKWAARVAEQRLAYLEGCVEWLRRLYENKGLQRLADPKTHVTHPI
SDHEATLRCWALGFYPAEITLTWRDGEDQTDTELVEVTRPAGDRFTFKWAAVVVPSG
REQRYTCRVQHEGLPKPLTRWEPSSQSTPIVIGIVAGLAVLVVTVAVVAAMVCR
KSSGGKGSYSQAASDSQAQSDVSLTA"
BASE COUNT      253 a   386 c   415 g   218 t
ORIGIN
Query Match      72.8%; Score 26.2; DB 9; Length 1272;
Best Local Similarity 90.3%; Pred. No. 0.32;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctgatatcagtcctcacaggcagctgtc 36
|| ||||| ||||| ||||| ||||| |||||
Db 1130 CTGATCTCAGTCCTCACAGACAGCTGTC 1100

RESULT 12
GGB0201/c      1273 bp      mRNA      PRI      07-FEB-1992
LOCUS      G.gorilla MhcGogo-B0201 gene for Mhc class I heavy chain.
DEFINITION      X60253
ACCESSION      X60253
VERSION      X60253.1 GI:22871
KEYWORDS      B locus allele; Class I major histocompatibility gene; heavy chain;
major histocompatibility gene; peptide binding protein;
transplantation antigen.
SOURCE      gorilla.
ORGANISM      Gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
Lawlor,D.A.
Direct Submission
Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of
Medicine, Dept of Cell Biology, Stanford CA 94305, USA
2 (bases 1 to 1092)
Lawlor,D.A., Warren,E., Taylor,P. and Parham,P.
Gorilla class I major histocompatibility complex alleles:
comparison to human and chimpanzee class I
J. Exp. Med. 174 (6), 1491-1509 (1991)
92078860
MEDLINE
COMMENT      See X60248-59 & X60692-3.
FEATURES
source
1..1273
Location/Qualifiers
/organism="Gorilla gorilla"
/isolate="Oko"
/db_xref="taxon:9593"
/cell_type="lymphoblast"
/cell_line="Oko B lymphoblastoid cell line"
/clone_lib="OKB192"
1..1092
/gene="MhcGogo-B0201"
1..73
/gene="MhcGogo-B0201"
/number=1

gene
exon
1..73
/number=1

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/gene="HLA-B39"
/number=2
/product="major histocompatibility complex"
431..706
/gene="HLA-B39"
/number=3
441..449
/gene="HLA-B39"
/replace="cctccagag"
707..982
/gene="HLA-B39"
/standard_name="4e"
/number=4
983..1099
/gene="HLA-B39"
/number=5
1100..1132
/gene="HLA-B39"
/number=6
1133..1176
/gene="HLA-B39"
/number=7
1177..>1357
/gene="HLA-B39"
279 a 415 c 428 g 235 t
BASE COUNT
ORIGIN
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Query Match 72.8%; Score 26.2; DB 9; Length 1357;
Best Local Similarity 90.3%; Pred. No. 0.32;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 6 ctagatctcagtcctccacaagcagctgtc 36
|| ||||| ||||| ||||| |||||
Db 1216 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 1186
```

Search completed: December 6, 2001, 09:57:30  
Job time: 4034 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2001, 10:01:23 ; Search time 230.64 Seconds  
(without alignments)  
133.818 Million cell updates/sec

Title: US-09-673-795-4  
Perfect score: 36  
Sequence: 1 gccctcgtatctcagtcctccacagcgagctgtc 36

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues  
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_1101.\*  
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2: /SIDS8/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/NA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/NA1983.DAT.\*  
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22: /SIDS8/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	100.0	36	21	AAZ22706 Human HLA allele a
2	26.4	73.3	39	19	AAV21517 HLA-B35 cDNA antis
3	26.2	72.8	1441	22	AAO08377 Human secreted pro
4	26.2	72.8	3357	22	AAI63980 Human polynucleoti
5	26.2	72.8	3357	22	AAI63981 Human polynucleoti
6	26.2	72.8	3874	8	AAW02225 Sequence of genom
7	26.2	72.8	4059	16	AAQ75974 pHLA-B7 expression
8	26.2	72.8	4965	16	AAQ75973 pHLA-B7/beta-2 mic
9	26.2	72.8	6553	18	AAI61639 HLA B27 consensus
10	25.4	70.6	509	22	AAI44886 Human breast cance
11	25.2	70.0	456	21	AAZ38041 T lymphocyte cDNA

C 12	69.4	25	439	21	AAO07491 Human secreted pro
C 13	69.4	25	1817	22	AAH02916 Human shear stress
C 14	69.4	25	4756	22	AAI63974 Human polynucleoti
C 15	69.4	25	4756	22	AAI63975 Human polynucleoti
C 16	24.4	67.8	452	16	AAI20964 Human gene signatu
C 17	24.4	67.8	828	22	AAI61063 Human polynucleoti
C 18	24.4	67.8	943	22	AAI59277 Human polynucleoti
C 19	24.4	67.8	1567	22	AAH98676 Human EST-derived
C 20	20.8	57.8	70	20	AAZ25761 Human oligonucleot
C 21	20.8	57.8	137	20	AAZ25752 Human HLA-G gene e
C 22	20.8	57.8	151	20	AAZ25751 Human HLA-G gene e
C 23	20.8	57.8	443	16	AAO03428 HLA-G 3-5 from whi
C 24	20.8	57.8	2441	20	AAZ25757 Human HLA-G gene D
C 25	20.8	57.8	2441	20	AAZ25758 Human HLA-G gene D
C 26	20.8	57.8	2442	20	AAZ25755 Human HLA-G gene I
C 27	20.8	57.8	2442	20	AAZ25756 Human HLA-G gene I
C 28	20	55.6	1129	21	AAO79821 Human secreted pro
C 29	19.6	54.4	280	16	AAO24989 Human gene signatu
C 30	19.6	54.4	3622	22	AAH89966 Human bone marrow
C 31	19.4	53.9	150	19	AAI12144 Human biallelic po
C 32	19.2	53.3	253	21	AAH76194 Human sulfonyleurea
C 33	19.2	53.3	333	21	AAO74628 Human ORFX ORP183
C 34	19.2	53.3	1928	22	AAO29743 Castor bean calret
C 35	19.2	53.3	3517	21	AAI14339 cDNA encoding muri
C 36	19.2	53.3	3517	21	AAI13378 Mouse MT4-MMP (2)
C 37	19.2	53.3	3551	22	AAH18414 Human cDNA sequenc
C 38	19.2	53.3	103929	21	AAO22287 BAC containing rep
C 39	19	52.8	19	21	AAO47587 Primer for amplif
C 40	19	52.8	660	21	AAO18009 Lung cancer associ
C 41	19	52.8	908	22	AAO09957 DNA encoding human
C 42	19	52.8	926	21	AAO12553 Aspergillus oryzae
C 43	19	52.8	966	22	AAH31904 Human olfactory re
C 44	19	52.8	996	22	AAH31616 Human olfactory re
C 45	19	52.8	1638	22	AAO74495 Clone 16467945.0.8

ALIGNMENTS

RESULT 1  
AAZ22706  
ID AAZ22706 standard; DNA; 36 BP.  
XX  
AC AAZ22706;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Human HLA allele amplification primer 3P2-X.  
XX  
DE Human; heat shock protein 70; hsp70; identification; tumour; mutation;  
KW T cell response; amplification; vector; bacterium; cancer; allele;  
KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;  
KW Immune defence; immunogenicity; specificity; human leucocyte antigen;  
KW PCR; primer; amplification; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
PN WO954464-A1.  
XX  
XX 28-OCT-1999.  
PD  
XX  
PF 22-APR-1999; 99WO-FR00957.  
XX  
PR 22-APR-1998; 98FR-0005033.  
XX  
PA (INSR ) INST ROUSSY GUSTAVE.  
XX  
PI Triebel F, Gaudin C;  
DR WPI; 2000-013251/01.  
XX  
PT Identifying mutant peptides from heat-shock protein 70, for treatment



PT of cancer -

XX Example 7; Page 24; 56pp; French.

XX The invention relates to a method of identifying peptides, derived from  
 CC hsp70 that stimulate a tumour-specific T cell response (e.g. AAY44199  
 CC and AAY4200). Identification of the hsp70 peptides that have at least  
 CC one mutation or alteration compared with the native sequence, and induce  
 CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70  
 CC encoding DNA from one or more tumours; (ii) cloning the amplified  
 CC sequences into a vector that can be replicated in bacteria; (iii)  
 CC sequencing fragments in each cultured bacterial colony to identify any  
 CC hsp70 mutations; and (iv) determining the immunogenicity of the mutant  
 CC peptides identified. The peptides, optionally formulated with an agent  
 CC that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic T  
 CC lymphocytes in a cell culture and/or induce these cells to secrete  
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
 CC tumour necrosis factor), particularly where the cells are used to  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles. The primers AAZ22705-22706 were used to PCR amplify  
 CC HLA alleles for the method of the invention.

SQ Sequence 36 BP; 7 A; 14 C; 7 G; 8 T; 0 other;

Query Match 100.0%; Score 36; DB 21; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcccttagatctcagtcctccacaaaggcagctgctc 36  
 Db 1 gcccttagatctcagtcctccacaaaggcagctgctc 36

RESULT 2

AAV21517  
 ID AAV21517 standard; DNA; 39 BP.

XX AAV21517;

XX 14-SEP-1998 (first entry)

DE HLA-B35 cDNA antisense primer.

KW Tumour rejection antigen; HLA-B35; cysteine protease; apoptosis;  
 KW diagnosis; therapy; human; PCR; primer; ss.

OS Synthetic.  
 OS Homo sapiens.

XX WO9813374-A1.

XX 02-APR-1998.

XX 09-JUL-1997; 97WO-US12431.

XX 26-SEP-1996; 96US-0718964.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon-Falleur T, Mandruzzato S, Van Der Bruggen P;  
 PI WPI; 1998-230629/20.

XX New tumour rejection antigen - used to develop products for the  
 PT diagnosis and treatment of conditions characterised by HLA-B35  
 PT positive cells

XX Example 5; Page 8; 30pp; English.

XX

CC This antisense primer and a sense primer (see AAV21516) were  
 CC designed for the PCR amplification of HLA-B35 cDNA. The PCR  
 CC product was cloned into pCDNA3, and used with plasmids containing  
 CC cDNA from BB49-SCCHN head and neck squamous cell carcinoma cells to  
 CC cotransfect COS-7 cells. Transfectants were tested to determine if  
 CC they could stimulate tumour necrosis factor production by CTL  
 CC clones 328a/69 and 328a/121. A 2649 bp cDNA clone (see AAV21515)  
 CC was obtained that codes for a novel tumour rejection antigen  
 CC precursor that is processed to an antigenic peptide (see AAW54237)  
 CC that can be used to develop products for the diagnosis and  
 CC treatment of conditions characterised by HLA-B35 positive cells,  
 CC e.g. tumours.

XX Sequence 39 BP; 8 A; 15 C; 7 G; 9 T; 0 other;

Query Match 73.3%; Score 26.4; DB 19; Length 39;  
 Best Local Similarity 83.3%; Pred. No. 0.028;  
 Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 gcccttagatctcagtcctccacaaaggcagctgctc 36  
 Db 4 gcccgaaattctcagtcctccacaaaggcagctgctc 39

RESULT 3

AAAD08377/c

ID AAD08377 standard; cDNA; 1441 BP.

XX AAD08377;

XX 09-AUG-2001 (first entry)

DE Human, secreted protein-encoding gene 33 cDNA clone HTXDC77, SEQ ID NO:43.

KW Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnerability;  
 KW cell culture; chemotaxis; food additive; gene therapy;  
 KW binding partner identification; ss.

XX Homo sapiens.

XX Key

FT CDS Location/Qualifiers

FT 65..520  
 FT /\*tag= a  
 FT /product= "Human secreted protein precursor"  
 FT /transl\_except= (pos:74..76, aa:Xaa)  
 FT /transl\_except= (pos:89..91, aa:Xaa)  
 FT /transl\_except= (pos:104..106, aa:Xaa)  
 FT /transl\_except= (pos:113..115, aa:Xaa)  
 FT /transl\_except= (pos:170..172, aa:Xaa)  
 FT /transl\_except= (pos:269..271, aa:Xaa)  
 FT /transl\_except= (pos:275..277, aa:Xaa)  
 FT /transl\_except= (pos:323..325, aa:Xaa)  
 FT /transl\_except= (pos:338..340, aa:Xaa)  
 FT /transl\_except= (pos:347..349, aa:Xaa)  
 FT /transl\_except= (pos:386..388, aa:Xaa)  
 FT /transl\_except= (pos:419..421, aa:Xaa)  
 FT /transl\_except= (pos:512..514, aa:Xaa)  
 FT /note= "Xaa equals any of the naturally occurring  
 FT L-amino acids"  
 FT 65..118

FT sig\_peptide /\*tag= b

FT mat\_peptide 119..517  
 FT /\*tag= c



FT /product= "Mature human secreted protein"

XX W0200077022-A1.

PN 21-DEC-2000.

PD 01-JUN-2000; 2000WO-US15136.

XX 11-JUN-1999; 99US-0138629.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM, Komatsoulis GA;

PI WPI; 2001-367020/38.

XX P-PSDB; AAE03930.

DR Nucleic acids encoding 50 human secreted polypeptides, useful for

DR preventing, diagnosing and/or treating diseases, e.g. Parkinson's

XX disease, botulism, cancers and Scimitar syndrome -

PS Claim 1; Page 513; 614pp; English.

XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted

CC protein genes and AAE03898-AAE03947 represent the proteins they encode.

CC AAE03948-AAE03996 represent human secreted protein fragments or variants.

CC The genes and their secreted proteins are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Pathological conditions can be diagnosed by determining the

CC amount of the new protein in a sample or by determining the presence of

CC mutations in the new genes. Specific uses are described for each of the

CC 50 genes, based on the tissues in which they are most highly expressed,

CC and include developing products for the diagnosis or treatment of

CC proliferative disorders, cancer, tumours, foetal and developmental

CC abnormalities, haematopoietic disorders, diseases of the immune system,

CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,

CC allergies, neurological disorders (e.g., Alzheimer's disease,

CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,

CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,

CC cardiovascular disorders, angiogenic disorders, kidney disorders,

CC gastrointestinal disorders, pregnancy-related disorders, endocrine

CC disorders, and infections. The proteins can also be used to aid wound

CC healing and epithelial cell proliferation, to prevent skin aging due to

CC sunburn, to maintain organs before transplantation, for supporting cell

CC culture of primary tissues, to regenerate tissues, to identify their

CC cognate ligands or binding partners, and in chemotaxis, and can be used

CC as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in

CC alleviating symptoms associated with the disorders mentioned above, and

CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked

CC immunosorbent assay (ELISA). The present sequence represents a human

CC secreted protein-encoding cDNA of the invention.

XX Sequence 1441 BP; 299 A; 403 C; 412 G; 283 T; 44 other;

SQ

Query Match 72.8%; Score 26.2; DB 22; Length 1441;

Best Local Similarity 90.3%; Pred. No. 0.065; Indels 0; Gaps 0;

Matches 28; Conservative 0; Mismatches 3;

Qy 6 ctgagctcagtcacctcacaagcgagctgctc 36

II |||||

Db 990 CTGCATCTCAGTCCCTCACAGACAGCTGTC 960

RESULT 4

ID AAI63980/c

XX AAI63980 standard; DNA; 3357 BP.

AC AAI63980;

XX 22-OCT-2001 (first entry)

DT

XX

DE Human polynucleotide SEQ ID NO 352.

XX Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;

KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;

KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;

KW neuroprotective; antiallergic; hepatotropic; antidiabetic;

KW antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;

KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;

KW cardiovascular disorder; neurological disease; infection; human; ds.

XX Homo sapiens.

OS

XX W0200155308-A2.

PN 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01309.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 06-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.

PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.



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PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241121.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0246177.
PR 01-NOV-2000; 2000US-0246178.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488781/53.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating and/or preventing human diseases and disorders -
XX
XX Disclosure; SEQ ID NO 352; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
XX the encoded proteins (AAI634497-AAI63660) useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. The
XX genes were isolated from a range of human tissues disclosed in the
XX specification. The nucleic acids, proteins, antibodies and (ant)agonists
XX are useful in the diagnosis, treatment and prevention of: (a) cancer,
XX e.g. breast and ovarian cancer and other cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
XX urogenital; (b) immune disorders e.g. Addison's disease, allergies,
XX autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.
XX
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3357 BP; 647 A; 949 C; 1036 G; 725 T; 0 other;

Query Match 72.8%; Score 26.2; DB 22; Length 3357;
Best Local Similarity 90.3%; Pred. No. 0.075;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctgagatctcagtcctccacagcagctgtc 36
Db 2962 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 2932

RESULT 5
AAI63981/C
ID AAI63981 standard; DNA; 3357 BP.
XX
XX AAI63981;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 353.
XX
XX Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; cytostatic; immunosuppressive; neurotropic;
XX neuroprotective; anti-allergic; hepatotropic; antidiabetic;
XX anti-inflammatory; anti-ulcer; vulnerable; anticonvulsant; antibacterial;
XX antiparasitic; cardiac; gene therapy; cancer; immune disorder;
XX cardiovascular disorder; neurological disease; infection; human; ds.
XX
XX Homo sapiens.
XX
XX WO200155308-A2.
XX
```







XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
 PT treating and/or preventing human diseases and disorders -  
 XX  
 PS Disclosure; SEQ ID NO 353; 664pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AAI63803-AAI64012) and  
 CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating  
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
 CC genes were isolated from a range of human tissues disclosed in the  
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 3357 BP; 645 A; 947 C; 1035 G; 730 T; 0 other;

Query Match 72.8%; Score 26.2; DB 22; Length 3357;  
 Best Local Similarity 90.3%; Pred. No. 0.075;  
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctatgattcagtcctccacagcagctgtc 36  
 || |||||

Db 2962 CTGCATCTCAGTCCCTCACAGACAGCTGTC 2932

RESULT 6  
 ID AAN70225/c  
 XX AAN70225 standard; DNA; 3874 BP.  
 AC AAN70225;  
 XX  
 DT 03-APR-1991 (first entry)  
 XX  
 DE Sequence of genomic DNA encoding human histocompatibility antigen  
 DE HLA-B 27.  
 XX  
 KW Ankylosing spondylitis; rheumatic disorder; diagnosis; ss.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT intron 518..590  
 FT intron /\*tag= a  
 FT intron 720..989  
 FT intron /\*tag= b  
 FT intron 1090..1506  
 FT intron /\*tag= c  
 FT intron 1932..2357  
 FT intron /\*tag= d  
 FT intron 2450..2566  
 FT intron /\*tag= e  
 FT intron 3009..3041  
 FT intron /\*tag= f  
 FT intron 3148..3191  
 FT intron /\*tag= g

XX EP226069-A.

XX 24-JUN-1987.

XX 21-NOV-1986; 86EP-0116139.

XX 21-DEC-1985; 85DE-3545576.  
 PR 01-JAN-1985; 85DE-3542024.  
 XX  
 PA (BEHW) BEHRINGER AG.  
 XX  
 PI Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G;  
 XX  
 DR WPI; 1987-171469/25.  
 DR P-PSDB; AAP70155.  
 XX  
 PT DNA coding for human histocompatibility antigen HLA-B 27 - useful  
 PT for diagnosis and antigen and antibody prodn.  
 XX  
 PS Claim 1; p6; 13pp; German.  
 XX  
 CC The DNA may be used to detect the HLA-B 27 gene (opt. mutated) in  
 CC human genetic material. The HLA-B 27 may be used to detect anti-HLA-  
 CC B 27 antibodies in human serum. The antibodies may be used to  
 CC determine HLA-B 27 levels in human serum, e.g. for diagnosis of  
 CC rheumatic disorders, esp. ankylosing spondylitis.  
 XX  
 SQ Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T; 0 other;

Query Match 72.8%; Score 26.2; DB 8; Length 3874;  
 Best Local Similarity 90.3%; Pred. No. 0.077;  
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctatgattcagtcctccacagcagctgtc 36  
 || |||||

Db 3272 CTGCATCTCAGTCCCTCACAGACAGCTGTC 3242

RESULT 7  
 ID AAO75974  
 XX AAO75974 standard; cDNA; 4059 BP.  
 AC AAO75974;  
 XX  
 DT 23-AUG-1995 (first entry)  
 XX  
 DE pHLA-B7 expression vector.  
 XX  
 KW expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;  
 KW light beta-2 microglobulin; class I major histocompatibility complex;  
 KW MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..354  
 FT /\*tag= a  
 FT /\*note= "pBR322 backbone contg. bacterial origin of  
 FT replication"  
 FT CDS 355..1170  
 FT /\*tag= b  
 FT /\*note= "kanamycin resistance gene open reading frame;  
 FT the gene is taken from the transposable element  
 FT Tn903"  
 FT polyA\_signal complement (1410..1177)  
 FT /\*tag= c  
 FT /\*note= "SV40 polyA signal sequence"  
 FT intron complement (1412..1560)  
 FT /\*tag= d  
 FT /\*note= "SV40 small t intron"  
 FT 3'UTR complement (1561..1794)  
 FT /\*tag= e  
 FT /\*note= "3' untranslated region of HLA-B7  
 FT heavy chain mRNA"  
 FT CDS complement (1795..2880)  
 FT /\*tag= f  
 FT /\*note= "HLA-B7 open reading frame"



```
FT LTR complement (2886..3415)
FT /*tag= g
FT /note= "Rous sarcoma virus 3' LTR promoter region"
FT misc_feature 3416..4059
FT /*tag= h
FT /note= "pBR322 backbone"
FT XX
FT PN W09429469-A.
FT XX
FT PD 22-DEC-1994.
FT XX
FT PF 27-MAY-1994; 94WO-US06069.
FT XX
FT PR 07-JUN-1993; 93US-0074344.
FT XX
FT PA (UNMI ) UNIV MICHIGAN.
FT PA (VICA-) VICAL INC.
FT XX
FT PI Lew D, Marquet M, Nabel EG, Nabel GJ;
FT XX
FT DR WPI; 1995-036494/05.
FT XX
FT PT New vectors for gene therapy, partic for tumours - comprising
FT PT genetic material encoding one or more cistron(s) which express
FT PT immunogenic or therapeutic peptide(s)
FT XX
FT PS Claim 9; Page 42-43; 50pp; English.
FT XX
FT CC This HLA-B7 antigen encoding plasmid was developed to incorporate many
FT CC advantageous features, eg. the kanamycin resistance gene. The
FT CC eradication of two open reading frames encoding portions of SV40 viral
FT CC proteins lowers the risk of tumorigenicity. The vector may also operate
FT CC as a cassette into which cistrons may be inserted and removed at will
FT CC for the transcription and subsequent translation of peptides of interest.
FT CC The vector is used partic. for the treatment of neoplastic disease,
FT CC eg. melanoma, and provides enhanced gene delivery and expression
FT CC in vivo.
FT XX
FT SQ Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 other;

Query Match 72.8%; Score 26.2; DB 16; Length 4059;
Best Local Similarity 90.3%; Pred. No. 0.078;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctatgctcagtcctccacaaagcagctgctc 36
   || ||||| ||||| ||||| ||||| |||||
Db 1755 ctgcatctcagtcctccacaaagcagctgctc 1785

RESULT 8
AAQ75973/c
ID AAQ75973 standard; cDNA: 4965 BP.
XX
AC AAQ75973;
XX
DT 23-AUG-1995 (first entry)
XX
DE pHLA-B7/beta-2 microglobulin expression vector.
XX
KW expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
KW light beta-2 microglobulin; class I major histocompatibility complex;
KW MHC; bicistronic mRNA; human leukocyte antigen; HLA;
KW covalently closed circular DNA; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT LTR 1..529
FT /*tag= a
FT /note= "Rous sarcoma virus LTR promoter domain, derived
FT for the Schmidt-Rupin strain nucleotides
FT 8673-9146. This region also includes a 56 bp
FT XX
```

```
FT region of a synthetic oligonucleotide which
FT modifies this regulatory sequence to effect a
FT higher level of expression of downstream
FT sequences. The oligonucleotide removes a
FT polyadenylation signal sequence originally found
FT in the RSV DNA sequence."
FT misc_signal 531..534
FT /*tag= b
FT /label= consensus_Kozak_signal_sequence
FT 535..1620
FT /*tag= c
FT /note= "HLA-B7 heavy chain open reading frame"
FT 535..606
FT /*tag= d
FT /note= "encodes putative signal peptide of the
FT HLA-B7 heavy chain"
FT 607..1620
FT /*tag= e
FT /note= "encodes putative HLA-B7 heavy chain mature
FT peptide"
FT 1621..1853
FT /*tag= f
FT /note= "3' untranslated sequence of HLA-B7 heavy
FT chain mRNA"
FT 1854..1888
FT /*tag= g
FT /note= "multiple cloning site, forms a junction
FT between the HLA-B7 sequence and the EMCV-CITE"
FT sequence, and is used to facilitate subcloning"
FT 1889..2479
FT /*tag= h
FT /note= "murine encephalomyocarditis CAP-independent
FT translational enhancer (EMCV-CITE); taken from
FT nucleotides 255-843 of cloned EMCV genomic DNA.
FT It is a non-coding regulatory sequence functioning
FT as an internal entry point for the eukaryotic
FT ribosomal subunits when located within a mRNA
FT mol.. It enables the translational start codon of
FT the beta-2 microglobulin, downstream of the HLA-B7
FT stop codon on this bicistronic mRNA to be
FT recognised by the ribosome"
FT 2480..2839
FT /*tag= i
FT /note= "encodes beta-2 microglobulin; this cDNA is
FT deriv. from chimpanzee (differs to the human
FT cDNA by only 4 bases)"
FT 2840..2846
FT /*tag= j
FT /note= "3' untranslated region of the beta-2
FT microglobulin mRNA"
FT 2847..2870
FT /*tag= k
FT /note= "synthetic linker"
FT ..3111
FT /*tag= l
FT /note= "bovine growth hormone 3'UTR and transcriptional
FT terminator; it starts at a blunt-ended BglI site
FT within the 3'UTR of the mRNA coding sequence"
FT 2979..2984
FT /*tag= m
FT 3112..3151
FT /*tag= n
FT /note= "synthetic linker to facilitate cloning"
FT complement (3151..3967)
FT /*tag= o
FT /note= "kanamycin resistance gene open reading frame;
FT the gene is taken from the transposable element
FT Tn903"
FT 4014..4965
FT /*tag= p
FT /note= "pBR322 backbone contg. bacterial origin of
FT replication, it represents nucleotides 2244-3193"
FT XX
```



PN WO9429469-A.  
 XX 22-DEC-1994.  
 XX 27-MAY-1994; 94WO-US06069.  
 XX 07-JUN-1993; 93US-0074344.  
 XX (UNMI ) UNIV MICHIGAN.  
 PA (VICA-) VICAL INC.  
 XX Lew D, Marquet M, Nabel EG, Nabel GJ;  
 XX WPI; 1995-036494/05.  
 XX New vectors for gene therapy, partic for tumours - comprising  
 FT genetic material encoding one or more cistron(s) which express  
 PT immunogenic or therapeutic peptide(s)  
 XX Claim 8; Page 41-42; 50pp; English.  
 XX The pHLA-B7/beta-2 microglobulin plasmid expression vector, in addition  
 CC to the kanamycin resistance gene, contains the plasmid DNA encoding the  
 CC heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a  
 CC class I major histocompatibility complex (MHC) antigen. The plasmid is  
 CC designed to express these two proteins via a bicistronic mRNA in  
 CC eukaryotic cells. Initiation of transcription of the mRNA is dependent  
 CC on a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long  
 CC terminal repeat. Termination of transcription is dependent upon the  
 CC polyadenylation signal sequence deriv. from the bovine growth hormone  
 CC gene. Eukaryotic cell translation of the heavy chain is regulated by the  
 CC 5' cap-dependent protein start site. Translation of the light chain is  
 CC controlled by the CITE. Finally the replication of the plasmid in  
 CC bacterial cells is controlled by the presence of a bacterial origin of  
 CC replication. The vector is used partic. for the treatment of neoplastic  
 CC disease, eg. melanoma, and provides enhanced gene delivery and expression  
 CC in vivo.  
 XX Sequence 4965 BP; 1171 A; 1293 C; 1338 G; 1163 T; 0 other;  
 SQ

Query Match 72.8%; Score 26.2; DB 16; Length 4965;  
 Best Local Similarity 90.3%; Pred. NO. 0.081;  
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctatgatctcagtcctccacaaagcagctgtc 36  
 || |||||  
 Db 1663 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 1633

RESULT 9  
 AAT61639/c  
 ID AAT61639 standard; DNA; 6553 BP.  
 XX AAT61639;  
 AC  
 XX 05-JUN-1997 (first entry)  
 DT  
 XX HLA B27 consensus sequence.  
 DE  
 XX HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;  
 KW Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;  
 KW ss; ds.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 3968..6653  
 FT mRNA /\*tag= a  
 FT /\*note= "HLA-B27 3' flanking region, downstream of  
 FT 3' untranslated region"  
 FT mRNA 4112..4556  
 FT /\*tag= b

FT /note= "3' flanking region diagnostic for genetic  
 FT predisposition to SNSA"  
 FT 4270..4556  
 FT /\*tag= b  
 FT /note= "3' flanking region diagnostic for genetic  
 FT predisposition to SNSA"  
 FT misc\_difference 4495  
 FT /\*tag= d  
 FT /note= "absence of cytosine at this site is  
 FT indicative of a predisposition to SNSA"  
 XX  
 XX WO9709450-A1.  
 PN 13-MAR-1997.  
 PD  
 XX 16-AUG-1996; 96WO-US13256.  
 PF  
 XX 01-SEP-1995; 95US-0522942.  
 PR  
 XX (CEDA-) CEDARS SINAI MEDICAL CENT.  
 PA  
 XX Tyan DB;  
 PI  
 XX WPI; 1997-192924/17.  
 DR  
 XX Detecting pre-disposition to seronegative spondylarthropathies -  
 FT from the absence of a C residue at a specific position in the  
 PT 3'-flanking region of the HLA B27 allele  
 XX Claim 1; Page 52-56; 68pp; English.  
 PS  
 XX Genetic predisposition to seronegative spondylarthropathies (SNSA)  
 CC is detected by determining the absence of a cytosine nucleotide in  
 CC the 3' flanking region (see also AAT61647-48) of an HLA-B gene at a  
 CC position corresponding to nucleotide 4495 of the HLA-B27 consensus  
 CC sequence given in AAT61639. Probes and primers (see also AAT61640-46)  
 CC based on this region can be used in diagnostic assays to detect the  
 CC genetic predisposition to SNSA, and permit the distinction of B27+  
 CC individuals who are resistant to SNSA from B27+ normal individuals  
 CC who are susceptible (but as yet unaffected) to such diseases.  
 XX  
 SQ Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T; 0 other;

Query Match 72.8%; Score 26.2; DB 18; Length 6553;  
 Best Local Similarity 90.3%; Pred. No. 0.085;  
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ctatgatctcagtcctccacaaagcagctgtc 36  
 || |||||  
 Db 3579 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 3549

RESULT 10  
 AAF44886/c  
 ID AAF44886 standard; cDNA; 509 BP.  
 XX AAF44886;  
 AC  
 XX 28-MAR-2001 (first entry)  
 DT  
 XX Human breast cancer related protein coding sequence SEQ ID NO: 42.  
 DE  
 XX Human; breast cancer; diagnosis; therapy; vaccine; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200078960-A2.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 23-JUN-2000; 2000WO-US17536.  
 PF  
 XX



PR 23-JUN-1999; 99US-0140903.  
 PR 12-OCT-1999; 99US-0158980.  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Yuqiu J, Mitcham JL;  
 DR WPI; 2001-041426/05.  
 XX  
 PT New polynucleotides encoding breast tumor specific proteins, useful for  
 PT prevention, treatment and diagnosis of breast cancer -  
 PS Claim 25; Page 132-133; 165pp; English.  
 XX  
 CC The present invention provides the coding sequences for a number of  
 CC breast cancer related proteins. These can be used in vaccinations  
 CC against, diagnosis of and treatment of cancer, particularly breast  
 CC cancer.  
 XX  
 SQ Sequence 509 BP; 120 A; 124 C; 119 G; 146 T; 0 other;  
 SQ  
 Query Match 70.6%; Score 25.4; DB 22; Length 509;  
 Best Local Similarity 96.3%; Pred. No. 0.12;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 atctcagtcctccacaaagcagctgtc 36  
 DB 118 ATCTCAGTCCCTCACAAGACAGCTGTC 92  
 RESULT 11  
 AAZ38041/C  
 ID AAZ38041 standard; cDNA; 456 BP.  
 XX  
 AC AAZ38041;  
 XX  
 DT 07-FEB-2000 (first entry)  
 XX  
 DE T lymphocyte cDNA sequence ID No: 29 of WO9957130.  
 XX  
 KW T lymphocyte; sterile inflammatory disease; autoimmune disorder; GVHD;  
 KW immunodeficiency disease; cancer; graft-versus-host-disease; psoriasis;  
 KW rheumatoid arthritis; asthma; genetic disease; cytokine gene; Jurkat; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9957130-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 05-MAY-1999; 99WO-US09761.  
 XX  
 PR 05-MAY-1998; 98US-0084329.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Prashar Y, Weissman S;  
 XX  
 DR WPI; 2000-023547/02.  
 XX  
 PT Studying changes in gene expression in T lymphocytes used to identify  
 PT therapeutic or prophylactic agents which modulate T lymphocyte  
 PT populations -  
 XX  
 PS Disclosure; Page 74; 78pp; English.  
 XX  
 CC The invention provides methods to identify a therapeutic or prophylactic  
 CC agent that modulates a T lymphocyte population found in a subject having  
 CC a sterile inflammatory disease, autoimmune disorder, immunodeficiency  
 CC disease, cancer or graft-versus-host-disease (GVHD). The methods can be  
 CC used to identify therapeutic or prophylactic agents that modulate T  
 CC lymphocyte populations in subjects having a sterile inflammatory disease

CC (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma,  
 CC allergic rhinitis, cardiac and renal reperfusion injury, thrombosis,  
 CC adult respiratory distress syndrome, inflammatory bowel disease, Crohn's  
 CC disease, ulcerative colitis, periodontal disease, lymphocytopenias,  
 CC autoimmune lymphoproliferative syndrome, synovitis, sarcoidosis,  
 CC DiGeorge's syndrome, Nezelof syndrome, Ataxia-telangiectasia, Cartilage-  
 CC syndromes, Wiskott-Aldrich syndrome, severe combined immunodeficiency  
 CC hair hypoplasia, immunodeficiency with thymoma and leukocyte adhesion  
 CC deficiency 1), cancer (15 T lymphocyte leukemia/lymphoma's are listed in  
 CC the specification), immunodeficiency disease, autoimmune disorder (20  
 CC listed in the specification) or a genetic disease. The methods can also  
 CC be used to identify an agent that induces the differentiation of  
 CC quiescent pre-, cortical or medullary T lymphocytes into a  
 CC differentiated T lymphocyte subpopulation. The methods are especially  
 CC useful for identifying cytokine genes, genes encoding cell surface  
 CC receptors and genes encoding intermediary signaling molecules. Sequences  
 CC AAZ38026-37 represent T lymphocyte cDNA sequences.  
 XX  
 SQ Sequence 456 BP; 94 A; 109 C; 99 G; 136 T; 18 other;  
 SQ  
 Query Match 70.0%; Score 25.2; DB 21; Length 456;  
 Best Local Similarity 90.0%; Pred. No. 0.14;  
 Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 ctagatctcagtcctccacaaagcagctgt 35  
 DB 80 CTGCATCTCAGTCCCTCACAAGACAGCTGT 51  
 RESULT 12  
 AAC07491/C  
 ID AAC07491 standard; cDNA; 439 BP.  
 XX  
 AC AAC07491;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 11566.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 1; SEQ ID 11566; 71pp + CD-ROM; English.  
 XX  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer



CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.

SQ Sequence 439 BP; 93 A; 110 C; 147 G; 85 T; 4 other;

Query Match 69.4%; Score 25; DB 21; Length 439;  
 Best Local Similarity 84.8%; Pred. No. 0.17;  
 Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ctctagatctcagtcctcacaaggcagctgtc 36  
 ||| | ||||| | ||||| |||||  
 Db 422 CTGTGCATCTCAGTCGCACACAAAGGCAGCTGTC 390

RESULT 13

AAH02916/c

ID AAH02916 standard; DNA; 1817 BP.

XX AC AAH02916;

XX AC AAH02916;

XX DT 15-JUN-2001 (first entry)

XX DE Human shear stress-response coding sequence SEQ ID NO: 85.

XX KW Human; shear stress-response protein; vascular disease;

XX KW arteriosclerosis; ds.

XX OS Homo sapiens.

XX XX WO200125427-A1.

XX XX 12-APR-2001.

XX XX 02-OCT-2000; 2000WO-JP06840.

XX XX 01-OCT-1999; 99JP-0280976.

XX XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX XX (NOJI/) NOJIMA H.

XX XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;

XX XX Kuga T, Sekine S, Nakamura Y, Sugano S;

XX XX WPI; 2001-266308/27.

XX XX P-PSDB; AAB90793.

XX XX DNA sequences, proteins encoded by them and antibodies against them

XX XX useful in diagnosis and treatment of vascular disease caused by

XX XX arteriosclerosis -

XX XX Claim 20; Page 469-471; 678pp; Japanese.

XX XX The present invention provides the protein and coding sequences of a

XX XX number of human shear stress response proteins. These are useful in the

XX XX diagnosis, treatment and screening of vascular diseases caused by

XX XX arteriosclerosis, including heart failure, post-PTCA restenosis and

XX XX hypertension.

XX XX Sequence 1817 BP; 465 A; 449 C; 489 G; 414 T; 0 other;

SQ

Query Match

Best Local Similarity 69.4%; Score 25; DB 22; Length 1817;

Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ctctagatctcagtcctcacaaggcagctgtc 36  
 ||| | ||||| | ||||| |||||

Db 404 CTGTGCATCTCAGTCGCACACAAAGGCAGCTGTC 372

RESULT 14

AAI63974/c

ID AAI63974 standard; DNA; 4756 BP.

XX AC AAI63974;

XX AC AAI63974;

XX DT 22-OCT-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 346.

XX XX Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;

XX KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;

XX KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;

XX KW neuroprotective; antiallergic; hepatotropic; antidiabetic;

XX KW antiinflammatory; antitumor; anticonvulsant; antibacterial;

XX KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;

XX KW cardiovascular disorder; neurological disease; infection; human; ds.

XX OS Homo sapiens.

XX XX WO200155308-A2.

XX XX 02-AUG-2001.

XX XX 17-JAN-2001; 2001WO-US01309.

XX XX 31-JAN-2000; 2000US-0179065.

XX XX 04-FEB-2000; 2000US-0180628.

XX XX 24-FEB-2000; 2000US-0184664.

XX XX 02-MAR-2000; 2000US-0186350.

XX XX 16-MAR-2000; 2000US-0189874.

XX XX 17-MAR-2000; 2000US-0190076.

XX XX 18-APR-2000; 2000US-0198123.

XX XX 19-MAY-2000; 2000US-0205515.

XX XX 07-JUN-2000; 2000US-0209467.

XX XX 28-JUN-2000; 2000US-0214886.

XX XX 30-JUN-2000; 2000US-0215135.

XX XX 07-JUL-2000; 2000US-0216647.

XX XX 07-JUL-2000; 2000US-0216880.

XX XX 11-JUL-2000; 2000US-0217487.

XX XX 14-JUL-2000; 2000US-0218290.

XX XX 26-JUL-2000; 2000US-0220963.

XX XX 26-JUL-2000; 2000US-0220964.

XX XX 14-AUG-2000; 2000US-0224518.

XX XX 14-AUG-2000; 2000US-0224519.

XX XX 14-AUG-2000; 2000US-0225213.

XX XX 14-AUG-2000; 2000US-0225214.

XX XX 14-AUG-2000; 2000US-0225266.

XX XX 14-AUG-2000; 2000US-0225267.

XX XX 14-AUG-2000; 2000US-0225268.

XX XX 14-AUG-2000; 2000US-0225270.

XX XX 14-AUG-2000; 2000US-0225447.

XX XX 14-AUG-2000; 2000US-0225757.

XX XX 14-AUG-2000; 2000US-0225758.

XX XX 18-AUG-2000; 2000US-0225759.

XX XX 22-AUG-2000; 2000US-0226279.

XX XX 22-AUG-2000; 2000US-0226681.

XX XX 22-AUG-2000; 2000US-0226868.

XX XX 22-AUG-2000; 2000US-0227182.

XX XX 23-AUG-2000; 2000US-0227009.

XX XX 30-AUG-2000; 2000US-022824.

XX XX 01-SEP-2000; 2000US-0229287.

XX XX 01-SEP-2000; 2000US-0229343.

XX XX 01-SEP-2000; 2000US-0229344.

XX XX 05-SEP-2000; 2000US-0229345.

XX XX 05-SEP-2000; 2000US-0229509.

XX XX 06-SEP-2000; 2000US-0229513.

XX XX 06-SEP-2000; 2000US-0230437.

XX XX 08-SEP-2000; 2000US-0230438.

XX XX 08-SEP-2000; 2000US-0231242.



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PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231245.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231415.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.

PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488781/53.
XX
DR New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
XX Disclosure; SEQ ID NO 346; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4756 BP; 1043 A; 1299 C; 1340 G; 1074 T; 0 other;

Query Match 69.4%; Score 25; DB 22; Length 4756;
Best Local Similarity 84.8%; Pred. No. 0.26;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ctctagatctcagtcctcctcaaggcagctgtc 36
||| | ||||| ||||| ||||| |||||
Db 3337 CTGTGCATCTCAGTCGCACACAAAGGCAGCTGTC 3305

RESULT 15
AAI63975/C.
ID AAI63975 standard; DNA; 4756 BP.
XX
AC AAI63975;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 347.
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
```



KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;  
KW neuroprotective; anti-allergic; hepatotropic; antidiabetic;  
KW antiinflammatory; antitumor; vulnary; anticonvulsant; antibacterial;  
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;  
XX cardiovascular disorder; neurological disease; infection; human; ds.  
OS Homo sapiens.  
XX XX  
PN WO200155308-A2.  
XX XX  
PD 02-AUG-2001.  
XX XX  
XX 17-JAN-2001; 2001WO-US01309.

PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189674.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
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PR 11-JUL-2000; 2000US-0217487.  
PR 14-JUL-2000; 2000US-0217496.  
PR 26-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 14-AUG-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
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PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
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PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
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PR 02-OCT-2000; 2000US-0237037.  
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PR 02-OCT-2000; 2000US-0237039.  
PR 13-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
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PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
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PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
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PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
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PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.



PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-488781/53.  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders -  
XX  
XX Disclosure; SEQ ID NO 347; 664pp + Sequence Listing; English.  
XX  
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and  
CC the encoded proteins (AAM43497-AAM43660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 4756 BP; 1041 A; 1298 C; 1342 G; 1075 T; 0 other;

Query Match 69.4%; Score 25; DB 22; Length 4756;  
Best Local Similarity 84.8%; Pred. No. 0.26;  
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 4 ctctagatctcagtcctcacaggcagctgtc 36  
||| | ||||| ||| | ||||| |||||  
DB 3337 CTTGTCATCTCAGTCGCCACACAGGCAGCTGTC 3305

Search completed: December 6, 2001, 10:01:25  
Job time: 4269 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2001, 08:52:34 ; Search time 116.28 Seconds  
(without alignments)  
70.117 Million cell updates/sec

Title: US-09-673-795-4

Perfect score: 36

Sequence: 1 gcccttagatctcagtcctcacaagcgactgtc 36

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

- 1: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/lna/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/lna/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/lna/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/lna/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.4	73.3	39	2	US-08-718-964-4
2	26.4	73.3	39	2	US-09-059-964A-4
3	26.4	73.3	39	2	US-08-842-341-4
4	26.2	72.8	4059	5	PCT-US94-06069-2
5	26.2	72.8	4965	2	US-08-564-313-2
6	26.2	72.8	4965	2	PCT-US94-06069-1
7	26.2	72.8	4965	5	PCT-US94-06069-1
8	26.2	72.8	6553	1	US-08-522-942-1
9	20.8	57.8	440	2	US-08-406-051-1
10	20.8	57.8	440	4	US-08-958-316-1
11	19.2	53.3	1928	4	US-08-675-816-4
12	18.2	50.6	1200	3	US-08-859-167-5
13	18.2	50.6	1200	3	US-09-109-273-5
14	18.2	50.6	1200	4	US-09-276-993-5
15	18.2	50.6	1828	2	US-08-888-497-29
16	18.2	50.6	1828	5	PCT-US94-07926-29
17	18.2	50.6	2272	2	US-08-726-228-1
18	18.2	50.6	2272	3	US-08-870-815-1
19	18.2	50.6	2272	3	US-08-949-004-1
20	18.2	50.6	2581	1	US-08-200-900A-1
21	18.2	50.6	2581	5	PCT-US94-00616-1
22	18.2	50.6	3901	1	US-08-188-582-31
23	18.2	50.6	3901	1	US-08-646-715-31
24	18	50.0	3807	1	US-08-022-835-5
25	18	50.0	3807	1	US-08-388-809-5
26	18	50.0	3807	2	US-08-647-714-5
27	18	50.0	20137	4	US-09-262-773-206

c 28	17.8	49.4	3039	2	US-08-680-326-27	Sequence 27, Appl
c 29	17.8	49.4	15766	4	US-09-338-907-73	Sequence 73, Appl
c 30	17.8	49.4	37950	4	US-09-338-907-183	Sequence 183, App
c 31	17.6	48.9	355	3	US-09-157-177-130	Sequence 130, App
c 32	17.6	48.9	707	1	US-08-592-126-119	Sequence 119, App
c 33	17.6	48.9	1022	4	US-09-257-584-5	Sequence 5, Appl
c 34	17.6	48.9	1023	4	US-09-257-584-4	Sequence 4, Appl
c 35	17.6	48.9	1939	4	US-09-357-251-25	Sequence 25, Appl
c 36	17.6	48.9	4220	4	US-09-183-846A-11	Sequence 11, Appl
c 37	17.4	48.3	1724	3	US-08-993-260-2	Sequence 2, Appl
c 38	17.4	48.3	1769	2	US-08-588-983-19	Sequence 19, Appl
c 39	17.4	48.3	1769	2	US-08-588-976-19	Sequence 19, Appl
c 40	17.4	48.3	2297	2	US-08-588-983-21	Sequence 21, Appl
c 41	17.4	48.3	2297	2	US-08-588-976-21	Sequence 21, Appl
c 42	17.4	48.3	2911	2	US-08-588-983-8	Sequence 8, Appl
c 43	17.4	48.3	2911	2	US-08-588-983-11	Sequence 11, Appl
c 44	17.4	48.3	2911	2	US-08-588-976-8	Sequence 8, Appl
c 45	17.4	48.3	2911	2	US-08-588-976-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-08-718-964-4  
; Sequence 4, Application US/08718964  
; Patent No. 5932694  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre; Mandruzzato, Susanna;  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding A Functional  
; TITLE OF INVENTION: Protein, The Protein So Encoded And Uses Thereof  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felie & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,964  
; FILING DATE: 26-September-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/669,590  
; FILING DATE: 24-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 5932694man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5442.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-718-964-4

Query Match 73.3%; Score 26.4; DB 2; Length 39;  
Best Local Similarity 83.3%; Pred. No. 0.0053;  
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 gcccttagatctcagtcctcacaagcgactgtc 36  
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Db 4 GCCCGAATTCCTCAGTCCCTCACAAGGCAGCTGTC 39

RESULT 2  
US-09-964A-4  
; Sequence 4, Application US/09059964A  
; Patent No. 595228  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre; Mandruzzato, Susanna;  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding A Functional  
; TITLE OF INVENTION: Protein, The Protein So Encoded And Uses Thereof  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski, L.L.P..  
; STREET: 555 Fifth Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/059,964A  
; FILING DATE: 24-JUNE-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/718,964  
; FILING DATE: 26-September-1996  
; APPLICATION NUMBER: 08/669,590  
; FILING DATE: 24-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 595228man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5442.1  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-059-964A-4

Query Match 73.3%; Score 26.4; DB 2; Length 39;  
Best Local Similarity 83.3%; Pred. No. 0.0053;  
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 gccctctagatctcagtcctcctcacaagcagctgtc 36  
Db 4 GCCCGAATTCCTCAGTCCCTCACAAGGCAGCTGTC 39

RESULT 3  
US-08-842-341-4  
; Sequence 4, Application US/08842341  
; Patent No. 5955313  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre; Mandruzzato, Susanna;  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding A Functional  
; TITLE OF INVENTION: Protein, The Protein So Encoded And Uses Thereof  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City

; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/842,341  
; FILING DATE: 24-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/718,964  
; FILING DATE: 26-September-1996  
; APPLICATION NUMBER: 08/669,590  
; FILING DATE: 24-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 5955313man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5442.1  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-842-341-4

Query Match 73.3%; Score 26.4; DB 2; Length 39;  
Best Local Similarity 83.3%; Pred. No. 0.0053;  
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 gccctctagatctcagtcctcctcacaagcagctgtc 36  
Db 4 GCCCGAATTCCTCAGTCCCTCACAAGGCAGCTGTC 39

RESULT 4.  
US-08-564-313-2  
; Sequence 2, Application US/08564313  
; Patent No. 5910488  
; GENERAL INFORMATION:  
; APPLICANT: Nabel, Elizabeth  
; APPLICANT: Nabel, Gary  
; APPLICANT: Lew, Denise  
; APPLICANT: Marquet, Magda  
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/564,313  
; FILING DATE: 01-DEC-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/074,344  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned



; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: VICAL.033CP1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4059 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; IMMEDIATE SOURCE:  
; CLONE: HLA-B7  
; PCT-US94-06069-2

Query Match 72.8%; Score 26.2; DB 2; Length 4059;  
Best Local Similarity 90.3%; Pred. No. 0.015;  
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 ctagatctcagtcctccacaaaggcagctgtc 36  
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DB 1755 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 1785

## RESULT 5

PCT-US94-06069-2  
; Sequence 2, Application PC/TUS9406069  
; GENERAL INFORMATION:  
; APPLICANT: Vical Incorporated  
; APPLICANT: Regents of the University of Michigan  
; APPLICANT: Nabel, Elizabeth  
; APPLICANT: Nabel, Gary  
; APPLICANT: Lew, Denise  
; APPLICANT: Marquet, Magda  
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/06069  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/074,344  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israel, Ned  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: VICAL.033VPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4059 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; STRAIN: HLA-B7  
; PCT-US94-06069-2

Query Match 72.8%; Score 26.2; DB 5; Length 4059;  
Best Local Similarity 90.3%; Pred. No. 0.015;  
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 ctagatctcagtcctccacaaaggcagctgtc 36  
|| |||||  
DB 1755 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 1785

## RESULT 6

US-08-564-313-1/c  
; Sequence 1, Application US/08564313  
; Patent No. 5910488  
; GENERAL INFORMATION:  
; APPLICANT: Nabel, Elizabeth  
; APPLICANT: Nabel, Gary  
; APPLICANT: Lew, Denise  
; APPLICANT: Marquet, Magda  
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/564,313  
; FILING DATE: 01-DEC-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/074,344  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israel, Ned  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: VICAL.033CP1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4965 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; IMMEDIATE SOURCE:  
; CLONE: HLA-B7 and Beta-2  
; US-08-564-313-1



Query Match 72.8%; Score 26.2; DB 2; Length 4965;  
Best Local Similarity 90.3%;  
Matches 28; Conservative 0; Mismatches 3; Indels 0;

QY 6 ctatgctcagtcacctcacaggcagctgtc 36  
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Db 1663 CTGCATCTCAGTCCCTCACAGACAGCTGTC 1633

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RESULT      7
PCT-US94-06069-1/c
: Sequence 1, Application PC/TUS9406069
: GENERAL INFORMATION:
: APPLICANT: Vical Incorporated
: APPLICANT: Regents of the University of Michigan
: APPLICANT: Nabel, Elizabeth
: APPLICANT: Nabel, Gary
: APPLICANT: Lew, Denise
: APPLICANT: Marquet, Magda
: TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobbe, Martens, Olson and Bear
: STREET: 620 Newport Center Drive 16th Floor

```

```

: CITY: Newport Beach
: STATE: CA
: COUNTRY: USA
: ZIP: 92660
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSEQ Version 1.1
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PC7/US94/06069
: FILING DATE:

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CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/074,344  
APPLICATION NUMBER: 07-JUN-1993  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: VICAL.033VPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4965 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
STRAIN: HLA-B7 and Beta-2  
CT-U994-06069-1

Query Match	72.8%;	Score 26.2;	DB 5;	Length 4965;
Best Local Similarity	90.3%;	Pred. No. 0.015;		
Matches	28; Conservative	0; Mismatches	3; Indels	0

6 ctatgatctcagtcacctcaagaagcagctgtc 36  
 || |||||  
 1663 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 1633

RESULT 8

US-08-522-942-1/c  
; Sequence 1, Application US/08522942  
; Patent No. 5753442  
; GENERAL INFORMATION:  
; APPLICANT: Tyan, Dolly B.  
; TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC  
; TITLE OF INVENTION: PREDISPOSITION FOR SERONEGATIVE SPONDYLOARTHROPATHIES AND  
; TITLE OF INVENTION: PRODUCTS THEREFOR

ADDRESS: Pretty, Schroeder, Brueggemann & Clark  
STREET: 4365 Executive Drive, Suite 1500  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/522,942

FILING DATE: 4/15/95  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ramos, Robert T.  
 REGISTRATION NUMBER: 37,915  
 REFERENCE/DOCKET NUMBER: P07 33624  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-546-1995  
 TELEFAX: 619-546-9392  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6553 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: DNA (genomic)  
 US-08-522-942-1

Query Match 72.8%; Score 26.2; DB 1; Length 6553;  
Best Local Similarity 90.3%; Pred. No. 0.016;  
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

6 ctatagatctcagtcctccacaaggcagctgtc 36  
|||  
3579 CTGCATCTCAGTCCCTCACAAGACAGCTGTC 3549

RESULT 9 I  
IS-08-406-057-1/c  
Sequence 1, Application US/08406057  
Patent No. 5856442  
GENERAL INFORMATION:  
APPLICANT: CAROSELLA, EDGARDO D  
APPLICANT: MOREAU, PHILIPPE  
APPLICANT: GLUCKMAN, ELIANE  
APPLICANT: KIRSZENBAUM, MAREK  
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 2202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible



Qy 13 tcagtccctcacaggcagctgtc 36  
 ||| ||||| || |||||  
 Db 29 TCAGACCCCTCACAAAGCTGCTGTC 52



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RESULT 12
US-08-859-167-5
; Sequence 5, Application US/08859167
; Patent No. 6037461
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 33,229
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..988
; US-08-859-167-5

Query Match 50.6%; Score 18.2; DB 3; Length 1200;
Best Local Similarity 74.2%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 tctagatctcagtcctcacaaagcgactgt 35
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 855 TCTTCATCAGAGACTCTCTCAAGCAAGCTGT 885

RESULT 13
US-09-109-273-5
; Sequence 5, Application US/09109273
; Patent No. 6063760
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
```

```
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..988
; US-09-109-273-5

Query Match 50.6%; Score 18.2; DB 3; Length 1200;
Best Local Similarity 74.2%; Pred. No. 34;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 tctagatctcagtcctcacaaagcgactgt 35
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 855 TCTTCATCAGAGACTCTCTCAAGCAAGCTGT 885

RESULT 14
US-09-276-993-5
; Sequence 5, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 233..643
; US-08-888-497-29

Query Match          50.6%; Score 18.2; DB 2; Length 1828;
Best Local Similarity 74.2%; Pred. No. 37;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      4  ctctagatctcagtcacctcacaaaggcagctg 34
        ||||| ||| ||||| ||| ||| |||
Db      823 CTCTACATCAGAGTCCCTCTCTAGGATTCTG 793

Search completed: December 6, 2001, 08:52:36
Job time: 140 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2001, 09:29:42 ; Search time 2220.1 seconds  
(without alignments)  
174.248 Million cell updates/sec

Title: US-09-673-795-4  
Perfect score: 36  
Sequence: 1 gccctctagatctcagtcctcacaaagcgactgtc 36

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*
- 1: em\_estfun:\*\*
  - 2: em\_esthum:\*\*
  - 3: em\_estin:\*\*
  - 4: em\_estom:\*\*
  - 5: em\_estpl:\*\*
  - 6: em\_estba:\*\*
  - 7: em\_estro:\*\*
  - 8: em\_estov:\*\*
  - 9: em\_htc:\*\*
  - 10: gb\_estl:\*\*
  - 11: gb\_est2:\*\*
  - 12: gb\_hic:\*\*
  - 13: gb\_gss:\*\*
  - 14: em\_gss\_fun:\*\*
  - 15: em\_gss\_hum:\*\*
  - 16: em\_gss\_inv:\*\*
  - 17: em\_gss\_pin:\*\*
  - 18: em\_gss\_pro:\*\*
  - 19: em\_gss\_rod:\*\*
  - 20: em\_gss\_vrt:\*\*
  - 21: em\_gss\_other:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.2	78.3	317	10	BE708567
2	28.2	78.3	347	10	BE708216
3	28.2	78.3	399	11	BG978548
4	27.8	77.2	476	11	BF083691
5	27.8	77.2	489	10	AW973450
6	27.8	77.2	559	10	AW361438
7	27.2	75.6	237	10	AW806440
8	27.2	75.6	323	11	BI017003
9	27.2	75.6	479	10	AI801734
10	27.2	75.6	541	10	AI290139
11	27.2	75.6	546	10	AA622717
12	27	75.0	174	10	AW607375

C 13	26.8	74.4	376	10	BE183227
C 14	26.6	73.9	159	10	AW752350
C 15	26.6	73.9	442	11	N93531
C 16	26.6	73.9	461	11	BF875422
C 17	26.6	73.9	515	11	BF770493
C 18	26.6	73.9	515	11	BF771086
C 19	26.6	73.9	546	10	AW380132
C 20	26.6	73.9	682	10	BE312926
C 21	26.6	73.9	768	10	BE292884
C 22	26.6	73.9	1135	10	AL545658
C 23	26.2	72.8	67	10	AA468055
C 24	26.2	72.8	113	11	BI052969
C 25	26.2	72.8	116	11	BI020663
C 26	26.2	72.8	120	10	AW389745
C 27	26.2	72.8	140	10	AW376423
C 28	26.2	72.8	140	11	BE826430
C 29	26.2	72.8	145	10	AW795954
C 30	26.2	72.8	150	11	BI016093
C 31	26.2	72.8	154	10	AW796825
C 32	26.2	72.8	167	10	AW366718
C 33	26.2	72.8	171	10	AW376219
C 34	26.2	72.8	173	11	BG978500
C 35	26.2	72.8	178	11	BE832464
C 36	26.2	72.8	181	11	BG978883
C 37	26.2	72.8	188	10	AW376395
C 38	26.2	72.8	189	10	AW389460
C 39	26.2	72.8	196	10	AW935309
C 40	26.2	72.8	196	10	AW799966
C 41	26.2	72.8	196	11	BE828995
C 42	26.2	72.8	203	10	BE330967
C 43	26.2	72.8	203	10	BE149515
C 44	26.2	72.8	211	10	AW793386
C 45	26.2	72.8	211	11	BF909066

ALIGNMENTS

RESULT	1
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LOCUS	MR0-HT0559-020800-032-d06 HT0559 Homo sapiens cDNA, mRNA sequence.
DEFINITION	MR0-HT0559-020800-032-d06 HT0559 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BE708567
VERSION	BE708567.1 GI:10096832
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 317) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t3-MR0-HT0559-020 800-032-d06t3-2000-08-02&t4=1) Seq primer: puc 18 forward



BASE COUNT  
87 a 97 c 69 g 64 t

RESULT	3	LOCUS	399 bp	EST	12-JUN-2001
DEFINITION	PM1-CN0098	-020101-002-f02	CDNA	Homo sapiens	cdNA, mRNA sequence.
ACCESSION	CG978548				
VERSION	CG978548.1	GI:14381283			
KEYWORDS	EST				
SOURCE	bio				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 399)  
 Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 REFERENCES  
 AUTHORS

TITLE	Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: <a href="mailto:asimpson@ludwig.org.br">asimpson@ludwig.org.br</a> This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

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Project. This entry can be seen in the following URL
' (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=PM1st2-PM1-CN0098-
' 020101-002-f02st3-2001-01-02st4-1)
; Seq primer: puc l8 forward
; High quality sequence start: 16
; High quality sequence stop: 398.
; Location/Qualifiers
;     1. .399
;     /organism="Homo sapiens"
;     /db_xref="taxon:9606"
;     /clone_lib="CN0098"
;     /dev_stage="Adult"
;     /note="Organ: colon_normal; Vector: puc18; Site_1: Sma1;
;     Site_2: Sma1; A mini-library was made by cloning products
;     derived from ORSTES PCR (U.S. Letters Patent application
;     No. 196,716 - Ludwig Institute for Cancer Research)
;     profiles into the pUC 18 vector. Reverse transcription of
```

BASE COUNT	103 a	117 c	100 g	78 t	1 others
ORIGIN					
Query Match					
					78.3% Score 28.2; DB 11; Length 309.

Query Match 78.3%: Score 28 2: DB 11: Length 300.



Best Local Similarity	90.98;	Pred. No. 1;	
Matches 30;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;

  

QY	4	ctctagatctcagtcacctcacaaaggcagctgc	36
Db	99	CTCTGTGCTCTCAGTCCACACAAAGCGAGCTGC	131

RESULT	4				
BF083691/c					
LOCUS		476 bp	mRNA	EST	18-OCT-2000
DEFINITION		BF083691	MR3-C70456-190900-003-c07	C70456	Hom sapiens cDNA, mRNA sequence.
ACCESSION		BF083691			
VERSION		BF083691.1	GI:10877430		
KEYWORDS		EST.			
SOURCE		human.			
ORGANISM		Hom sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS		1 (bases 1 to 476)			
		Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Shpton,A.J.			
TITLE		Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL		Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496	(2000)
MEDLINE		20202663			
COMMENT		Contact: Simpson A.J.G.			

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=stg-MR2-CT0456-190>  
900-003-c07&t3-2000-09-19&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 13  
High quality sequence stop: 475.

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FEATURES
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      Location/Qualifiers
        organism="Homo sapiens"
        db_xref="taxon:9606"
        clone_lib="Cr0456"
        dev_stage="Adult"
        notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
        SmaI; A mini-library was made by cloning products derived
        from ORESTES PCR (U.S. Letters Patent application NO. 196
        ,716 - Ludwig Institute for Cancer Research) profiles
        into the pUC 18 vector. Reverse transcription of tissue
        mRNA and cDNA amplification were performed under low
        stringency conditions."
      119 a 133 c 110 q 114 t
BASE COUNT

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Query Match	77.2%	Score 27.8;	DB 11;	Length 476;
Best Local Similarity	93.5%	Pred. No. 1.5;		
Matches 29; Conservative		0; Mismatches	2; Indels	0; Gaps

**Qy**     6 ctagatctcagtcacctcacaggcagctgtc     36  
            ||| ||||||||| |  
**Dβ**     398 CTACATCTCAGTCCCTCACAGACAGCTGTC     368

RESULT 5  
AW973450

LOCUS	AW973450	489 bp	mRNA	EST	02-JUN-2000
DEFINITION	EST385443 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence.				
ACCESSION	AW973450				
VERSION	AW973450.1 GI:8164521				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 489)				
AUTHORS	Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.				
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 318 Seq primer: Forward.				

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FEATURES
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    Location/Qualifiers
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        /db_xref="taxon:9606"
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        /note="Vector: pBluescriptSKm"
BASE COUNT
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ORIGIN

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Query Match	77.2%	Score	27.8	DB	10	Length	489
Best Local Similarity	93.5%	Pred. No.	1.5				
Matches	29	Conservative	0	Mismatches	2	Indels	0
						Gaps	0

Qy 6 ctatgatctcagttccctcacaaaggcagctgtc 36  
 || |||||  
 Db 387 CTTCGATCTTCAGTCCCTTCAAGACAGCTGTC 417

RESULT	6	
AW361438		
LOCUS	AW361438	559 bp mRNA
DEFINITION	RC3-CT0255-031099-011-e09 CT0255	Homo sapiens EST
ACCESSION	AW361438	04-FEB-2000
VERSION	AW361438.1	GI:5866088
KEYWORDS	EST.	
SOURCE	human.	
CDNA	cdna	
SEQUENCE	sequence	

SOURCE: Homo sapiens  
ORGANISM: Homo sapiens  
REFERENCE: 1 (bases 1 to 559)  
AUTHORS: HCGP <http://www.ludwig.org.br/ORESTES>.  
TITLE: The FAPESP/LICR Human Cancer Genome Project  
JOURNAL: Unpublished (1999)  
COMMENT: Contact: Simpson A.J.G.

Contact: Sampson A.S.S.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genomome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-CT0255>)  
 031039-011-e09&t3=1999-10-03&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 52  
 High quality sequence stop: 541.



Query Match 75.6%; Score 27.2; DB 11; Length 323;  
Best Local Similarity 90.6%; Pred. No. 2.3;  
Matches 29; Conservative 0; Mismatches 3; Indels 0

BASE COUNT	84 a	86 c	79 q	74 t
LOW stringency conditions.				

Query Match 75.6%; Score 27.2; DB 11; Length 323;  
Best Local Similarity 90.6%; Pred. No. 2.3;  
Matches 29; Conservative 0; Mismatches 3; Indels 0



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QY 5 tctagatctcagtcctccacaaaggcagctgtc 36
   ||| | ||||| ||||| ||||| ||||| |||||
Db 130 TCTGTCTCTCAGTCCCAACAGCAGCTGTC 161

RESULT 9
AI801734
LOCUS      479 bp      mRNA      14-DEC-1999
DEFINITION to94f10.x1 NCI-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185963 3'
           similar to gb:MI2678 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27
           B*2705 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AI801734
VERSION    AI801734.1 GI:5367206
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 479)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Greg Lennon, Ph.D.
            CDNA Library Arrayed by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 556 Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 222.

FEATURES             Location/Qualifiers
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                     /clone_lib="NCI-CGAP_Gas4"
                     /tissue_type="poorly differentiated adenocarcinoma with
                     signet ring cell features"
                     /lab_host="DH10B"
                     /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.69 kb. Life Technologies catalog #:
                     11549-011"

BASE COUNT  139 a 109 c 116 g 114 t 1 others
ORIGIN

Query Match      75.6%; Score 27.2; DB 10; Length 479;
Best Local Similarity 90.6%; Pred. No. 2.5;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 tctagatctcagtcctccacaaaggcagctgtc 36
   ||| | ||||| ||||| ||||| ||||| |||||
Db 390 TCTGTCTCTCAGTCCCTCACAAGCAGCTGTC 421

RESULT 10
AI290139
LOCUS      541 bp      mRNA      21-DEC-1998
DEFINITION qw31q10.x1 NCI-CGAP_Ut4 Homo sapiens cDNA clone IMAGE:1992738 3'
           similar to gb:M28204 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8
           B*0801 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AI290139
VERSION    AI290139.1 GI:3931805
KEYWORDS   EST.
SOURCE     human.

```

```

ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 541)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Greg Lennon, Ph.D.
            CDNA Library Arrayed by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1662 Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 249.

FEATURES             Location/Qualifiers
     source           1..541
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1992738"
                     /clone_lib="NCI-CGAP_Ut4"
                     /tissue_type="serous papillary carcinoma, high grade, 2
                     pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.48 kb. Life Technologies catalog #:
                     11542-016"

BASE COUNT  146 a 120 c 120 g 155 t
ORIGIN

Query Match      75.6%; Score 27.2; DB 10; Length 541;
Best Local Similarity 90.6%; Pred. No. 2.5;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 tctagatctcagtcctccacaaaggcagctgtc 36
   ||| | ||||| ||||| ||||| ||||| |||||
Db 410 TCTGTCTCTCAGTCCCTCACAAGCAGCTGTC 441

RESULT 11
AA622717
LOCUS      546 bp      mRNA      21-OCT-1997
DEFINITION np36e01.s1 NCI-CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1118424 3'
           similar to gb:MI2678 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27
           B*2705 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AA622717
VERSION    AA622717.1 GI:2526593
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 546)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
            Ph.D.
            CDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center

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RESULT	15
N93531	
LOCUS	
N93531	442 bp mRNA EST 20-AUG-1996
DEFINITION	2b55f05.s1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone
	IMAGE:307521 3' similar to qb:M28204 HLA CLASS I HISTOCOMPATIBILITY



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:53 ; Search time 170.25 seconds  
(without alignments)  
7.732 Million cell updates/sec

Title: PEPL-MOD8F

Perfect score: 48

Sequence: 1 SLFEGIDFY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	146	5 Q9U667	Q9U667 littorina p
2	48	100.0	153	5 Q9U670	Q9U670 littorina s
3	48	100.0	155	5 Q9U669	Q9U669 littorina s
4	48	100.0	157	5 Q9U665	Q9U665 littorina p
5	48	100.0	158	5 Q9U671	Q9U671 littorina s
6	48	100.0	158	5 Q9U668	Q9U668 littorina p
7	48	100.0	158	5 Q9U666	Q9U666 littorina p
8	48	100.0	220	5 P81159	P81159 aplysia cal
9	48	100.0	278	13 Q90520	Q90520 oncorhynch
10	48	100.0	367	13 Q98899	Q98899 fugu rubrip
11	48	100.0	455	11 Q63718	Q63718 rattus norv
12	48	100.0	467	5 Q44350	Q44350 chondrosia
13	48	100.0	467	5 Q44352	Q44352 petrobiona
14	48	100.0	467	5 Q9NJ92	Q9NJ92 guancha lac
15	48	100.0	468	5 Q44349	Q44349 funiculina
16	48	100.0	469	5 Q44351	Q44351 eunicella c
17	48	100.0	526	13 Q98897	Q98897 fugu rubrip
18	48	100.0	617	10 Q9C7X7	Q9C7X7 arabidopsis
19	48	100.0	628	5 Q93147	Q93147 botryllus s

20	48	100.0	629	5 Q93146	Q93146 botryllus s
21	48	100.0	632	5 O15766	O15766 dictyostell
22	48	100.0	639	13 Q98900	Q98900 fugu rubrip
23	48	100.0	639	13 Q918F9	Q918F9 oryzias lat
24	48	100.0	640	5 Q93601	Q93601 caenorhabdi
25	48	100.0	640	13 Q93240	Q93240 paralichthy
26	48	100.0	641	11 Q63256	Q63256 rattus norv
27	48	100.0	641	11 Q9QWJ5	Q9QWJ5 mus musculu
28	48	100.0	645	5 Q96541	Q96541 setaria dig
29	48	100.0	645	5 Q9NJ77	Q9NJ77 wuchereria
30	48	100.0	645	5 Q9NGK9	Q9NGK9 wuchereria
31	48	100.0	645	10 Q48563	Q48563 brassica na
32	48	100.0	647	3 Q59855	Q59855 schizosacch
33	48	100.0	647	10 Q41027	Q41027 pisum sativ
34	48	100.0	650	5 Q9U777	Q9U777 stylophora
35	48	100.0	650	10 Q9ZS55	Q9ZS55 arabidopsis
36	48	100.0	650	10 Q9LHA8	Q9LHA8 arabidopsis
37	48	100.0	652	10 P93937	P93937 ascophylium
38	48	100.0	653	5 Q94805	Q94805 trichoplusi
39	48	100.0	659	5 Q9XZJ2	Q9XZJ2 crassostrea
40	47	97.9	190	5 Q9U9B4	Q9U9B4 mytilus edu
41	47	97.9	467	5 Q44346	Q44346 asbestoplum
42	47	97.9	467	5 Q44347	Q44347 petrosia fl
43	47	97.9	467	5 Q9GPM5	Q9GPM5 monosiga ov
44	47	97.9	639	13 Q73922	Q73922 oreochromis
45	47	97.9	642	3 Q9UVM0	Q9UVM0 rhizopus st

#### ALIGNMENTS

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RESULT 1
Q9U667 PRELIMINARY; PRT; 146 AA.
ID Q9U667
AC Q9U667;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Littorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191828; AAF12787.1; -.
DR HSSP; PI9120; 1BAL.
DR InterPro; IPR001023; HSP70.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

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Query Match 100.0%; Score 48; DB 5; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.079;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLFEGIDFY 9
Db 79 SLFEGIDFY 87

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ID Q9U670
AC Q9U670;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

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DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 GN HEAT-SHOCK PROTEIN (FRAGMENT).  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191825; AAF12784.1; -  
 DR HSSP; PI9120; IBA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 153  
 SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 100.0%; Score 48; DB 5; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 0.084;  
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QY 1 SLFEGIDFY 9  
 Db 80 SLFEGIDFY 88

RESULT 3  
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 ID Q9U669 PRELIMINARY; PRT; 155 AA.  
 AC Q9U669;  
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 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191826; AAF12785.1; -  
 DR HSSP; PI9120; IBA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 155  
 SQ SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 100.0%; Score 48; DB 5; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 0.085;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
 Db 82 SLFEGIDFY 90

RESULT 4  
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 ID Q9U665 PRELIMINARY; PRT; 157 AA.  
 AC Q9U665;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191830; AAF12789.1; -  
 DR HSSP; PI9120; IBA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F7433B2B285EB2 CRC64;

Query Match 100.0%; Score 48; DB 5; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 0.087;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 Db 84 SLFEGIDFY 92

RESULT 5  
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 ID Q9U671 PRELIMINARY; PRT; 158 AA.  
 AC Q9U671;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191824; AAF12783.1; -  
 DR HSSP; PI9120; IBA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 100.0%; Score 48; DB 5; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 0.087;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 Db 85 SLFEGIDFY 93

RESULT 6  
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 AC Q9U668;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)



DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 CC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191827; AAF12786.1; -.  
 DR HSP; P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 100.0%; Score 48; DB 5; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 0.087;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLFEGIDFY 9  
 Db 85 SLFEGIDFY 93

RESULT 7  
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 ID Q9U666  
 AC Q9U666;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 CC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
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 DR HSP; P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 100.0%; Score 48; DB 5; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 0.087;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 Db 85 SLFEGIDFY 93

RESULT 8  
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 AC P81159;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidea;  
 CC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93077669; PubMed=1360013;  
 RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 the expression of Bip, the major protein chaperon of the ER.";  
 RL J. Cell Biol. 119:1069-1076(1992).  
 CC -I- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15039; CAA78757.1; -.  
 DR HSP; P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 220 220  
 SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 100.0%; Score 48; DB 5; Length 220;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
 Db 138 SLFEGIDFY 146

RESULT 9  
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 ID Q9U520  
 AC Q9U520;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=85036330; PubMed=6092938;  
 RA Kothary R.K., Jones D., Candido E.P.M.;  
 RT "70-Kilodalton heat shock polypeptides from rainbow trout:  
 characterization of cDNA sequences.";  
 RL Mol. Cell. Biol. 4:1785-1791(1984).  
 DR EMBL; K02549; AAA49562.1; -.  
 DR HSP; P08109; 1CKR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 278 278  
 SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 100.0%; Score 48; DB 13; Length 278;



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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 156 SLFEGIDFY 164

RESULT 10
Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
GN HSP70-3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Lim E.H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08578; CAA69892.1; -.
DR HSSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR PRINTS; PF00012; HSP70; 1.
DR PROSITE; PS00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock. 367
FT NON_TER 367
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;

Query Match 100.0%; Score 48; DB 13; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 268 SLFEGIDFY 276

RESULT 11
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AC Q63718;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT SHOCK ROTEN 70 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA D'Ambrosio E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z27118; CAA81642.1; -.
DR HSSP; P08107; 1HJO.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock. 455
FT NON_TER 455
SQ SEQUENCE 455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;

Query Match 100.0%; Score 48; DB 11; Length 455;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 254 SLFEGIDFY 262

RESULT 12
O44350 PRELIMINARY; PRT; 467 AA.
ID O44350
AC O44350;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OC Chondrosia reniformis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Chondrosida; Chondrillidae; Chondrosia.
OX NCBI_TaxID=68574;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelliini C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026517; AAC05362.1; -.
DR HSSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 467
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 100.0%; Score 48; DB 5; Length 467;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
Db 252 SLFEGIDFY 260

RESULT 13
O44352 PRELIMINARY; PRT; 467 AA.
ID O44352
AC O44352;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OC Petrobionia massillana.
OC Eukaryota; Metazoa; Porifera; Calcareia; Calcaronea; Petrobionidae;
OC Petrobionia.
OX NCBI_TaxID=68578;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelliini C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
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DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467  
 SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 100.0%; Score 48; DB 5; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
 |||||  
 Db 252 SLFEGIDFY 260

## RESULT 14

Q9NJ92 Q9NJ92 PRELIMINARY; PRT; 467 AA.  
 AC Q9NJ92;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
 OS Guancha lacunosa.  
 OC Eukaryota; Metazoa; Porifera; Calcarea; Clathrinida;  
 OC Clathrinidae; Guancha.  
 OX NCBI\_TaxID=115120;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borchelli C., Le Parco Y.;  
 RT "Sponges paraphyly and the origin of Metazoa";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF182195; AAF61297.1; -.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 467  
 SQ SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match 100.0%; Score 48; DB 5; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
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 Db 252 SLFEGIDFY 260

## RESULT 15

O44349 O44349 PRELIMINARY; PRT; 468 AA.  
 AC O44349;  
 DT 01-JUN-1998 (TRENBLrel. 06, Created)  
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
 GN HSP70.  
 OS Funiculina quadrangularis.  
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Alcyonaria; Funiculinidae;  
 OC Funiculina.  
 OX NCBI\_TaxID=68568;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borchelli C., Le Parco Y.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026516; AAC05361.1; -.  
 DR HSSP; P08109; 1CKR.  
 DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; UNKNOWN\_1.  
 FT NON\_TER 1  
 FT NON\_TER 468  
 SQ SEQUENCE 468 AA; 51533 MW; EDED2B4699283FBC CRC64;

Query Match 100.0%; Score 48; DB 5; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFY 9  
 |||||  
 Db 253 SLFEGIDFY 261

Search completed: December 6, 2001, 07:56:53  
 Job time: 181 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:57 ; Search time 81.43 Seconds  
(without alignments)  
2.764 Million cell updates/sec

Title: US-09-673-795-2

Perfect score: 51

Sequence: 1 SLFEGIDIYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	90.2	643	4	US-08-797-358B-3
2	44	86.3	646	1	US-08-441-139-14
3	34	66.7	36	1	US-08-487-890A-19
4	34	66.7	36	2	US-08-478-435-19
5	34	66.7	36	2	US-08-337-483-19
6	34	66.7	36	2	US-08-478-373-19
7	34	66.7	36	3	US-08-474-671-19
8	34	66.7	36	3	US-08-483-577A-19
9	34	66.7	36	5	PCT-US95-13975-72
10	34	66.7	301	5	US-08-897-438-19
11	34	66.7	435	3	US-08-911-321-8
12	34	66.7	911	1	US-08-487-890A-107
13	34	66.7	911	2	US-08-478-435-107
14	34	66.7	911	2	US-08-337-483-107
15	34	66.7	911	2	US-08-478-373-107
16	34	66.7	911	3	US-08-474-671-107
17	34	66.7	911	3	US-08-483-577A-107
18	34	66.7	911	4	US-08-897-438-107
19	34	66.7	913	1	US-08-487-890A-5
20	34	66.7	913	2	US-08-478-435-5
21	34	66.7	913	2	US-08-337-483-5
22	34	66.7	913	2	US-08-478-373-5
23	34	66.7	913	3	US-08-474-671-5
24	34	66.7	913	3	US-08-483-577A-5
25	34	66.7	913	4	US-08-897-438-5
26	33	64.7	332	2	US-08-637-763B-6
27	33	64.7	332	2	US-08-637-763B-8
28	33	64.7	332	3	US-09-170-354-6
29	33	64.7	332	3	US-09-170-354-8
30	33	64.7	339	3	US-08-928-692-52
31	33	64.7	789	3	US-08-727-308-1
32	33	64.7	912	1	US-08-487-890A-7
33	33	64.7	912	1	US-08-487-890A-9
34	33	64.7	912	2	US-08-478-435-7
35	33	64.7	912	2	US-08-478-435-9
36	33	64.7	912	2	US-08-337-483-7
37	33	64.7	912	2	US-08-337-483-9
38	33	64.7	912	2	US-08-478-373-7
39	33	64.7	912	2	US-08-478-373-9
40	33	64.7	912	3	US-08-474-671-7
41	33	64.7	912	3	US-08-474-671-9
42	33	64.7	912	3	US-08-483-577A-7
43	33	64.7	912	3	US-08-483-577A-9
44	33	64.7	912	3	US-08-613-009A-15
45	33	64.7	912	4	US-08-897-438-7

Sequence 6, Appli  
Sequence 8, Appli  
Sequence 52, Appli  
Sequence 1, Appli  
Sequence 7, Appli  
Sequence 9, Appli  
Sequence 7, Appli  
Sequence 9, Appli  
Sequence 7, Appli  
Sequence 9, Appli  
Sequence 7, Appli  
Sequence 9, Appli  
Sequence 15, Appli  
Sequence 7, Appli

#### ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-Feb-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 90.2%; Score 46; DB 4; Length 643;  
Best Local Similarity 80.0%; Pred. No. 0.41;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10



Db 288 SLFEGVDFT 297  
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RESULT 2  
US-08-441-139-14  
; Sequence 14, Application US/08441139  
; Patent No. 5773245  
; GENERAL INFORMATION:  
; APPLICANT: Wittrup, Dr. Karl D.  
; APPLICANT: Robinson, Anne S.  
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF  
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441.139  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/089,997  
; FILING DATE: 06-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8646  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 646 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-441-139-14

Query Match 86.3%; Score 44; DB 1; Length 646;  
Best Local Similarity 80.0%; Pred. No. 0.99;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10  
||:|||| |  
Db 286 SLYEGIDFT 295

RESULT 3  
US-08-487-890A-19  
; Sequence 19, Application US/08487890A  
; Patent No. 5708149  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,890A  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,968  
; FILING DATE: 08-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-487-890A-19

Query Match 66.7%; Score 34; DB 1; Length 36;  
Best Local Similarity 75.0%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10  
|||:| |  
Db 28 FEGVAYIT 35

RESULT 4  
US-08-478-435-19  
; Sequence 19, Application US/08478435  
; Patent No. 5922323  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,435  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-478-435-19

Query Match 66.7%; Score 34; DB 2; Length 36;  
Best Local Similarity 75.0%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FEGIDIYT 10  
|||: |||  
Db 28 FEGVAIYT 35

RESULT 5  
US-08-337-483-19  
Sequence 19, Application US/08337483  
Patent No. 5922562  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Murdin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 Unviersity Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-337-483-19

Query Match 66.7%; Score 34; DB 2; Length 36;  
Best Local Similarity 75.0%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FEGIDIYT 10  
|||: |||  
Db 28 FEGVAIYT 35

RESULT 6  
US-08-478-373-19  
Sequence 19, Application US/08478373  
Patent No. 5922841  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Murdin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,373  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:



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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 36 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
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; TOPOLOGY: linear
;
US-08-478-373-19

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Query Match 66.7%; Score 34; DB 2; Length 36;  
Best Local Similarity 75.0%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 1; Indels

QY 3 FEGIDIYT 10  
Db 28 FEGVAIYT 35

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RESULT      7
US-08-474-671-19
; Sequence 19, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:

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Query Match 66.7%; Score 34; DB 3; Length 36;  
Best Local Similarity 75.0%;  
Matches 6; Conservative 1; Mismatches 1; Indels

Qy	3	FEGIDIYT	10
		:	
Db	28	FEGVAIYT	35

```

RESULT      8
US-08-483-577A-19
; Sequence 19, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE/OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 Unviersity Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-577A-19

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Query Match 66.7%; Score 34; DB 3; Length 36;  
Best Local Similarity 75.0%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 1; Indels

QY 3 FEGIDIYT 10  
Db 28 FEGVAIYT 35



```

RESULT 9
US-08-897-438-19
; Sequence 19, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Fele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Kleip, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-897-438-19

Query Match 66.7%; Score 34; DB 4; Length 36;
Best Local Similarity 75.0%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 3 FEGIDIYT 10
Db 28 FEGVAIYT 35

RESULT 10
PCT-US95-13975-72
; Sequence 72, Application PC/TUS9513975

```

```

; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: McDonnell, Michael W.
; TITLE OF INVENTION: Recombinant Feline Herpes virus
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13975
; FILING DATE: 26-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/329,883
; FILING DATE: 26-OCT-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39118-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13975-72

Query Match 66.7%; Score 34; DB 5; Length 301;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10
Db 1 FEGLIYIT 8

RESULT 11
US-08-911-321-8
; Sequence 8, Application US/08911321
; Patent No. 6010703
; GENERAL INFORMATION:
; APPLICANT: Roger K. Maes and Stephen J. Spatz
; TITLE OF INVENTION: Recombinant Foxvirus
; TITLE OF INVENTION: Vaccine Against
; TITLE OF INVENTION: Feline Rhinotracheitis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1

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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/911,321  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/096,183  
;; FILING DATE: July 26, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ian C. McLeod  
;; REGISTRATION NUMBER: 20,931  
;; REFERENCE/DOCKET NUMBER: MSU 4.1-166  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (517) 347-4100  
;; TELEFAX: (517) 347-4103  
;; TELEX: No. 6010703e  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 435  
;; TYPE: Amino Acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE:  
;; DESCRIPTION:  
;; HYPOPHETICAL: No  
;; ANTI-SENSE: No  
;; ORIGINAL SOURCE:  
;; ORGANISM: Feline herpesvirus-1  
;; STRAIN: 1  
;; INDIVIDUAL ISOLATE: C-27  
;; CELL TYPE: N/A  
;; FEATURE:  
;; NAME/KEY:  
;; LOCATION:  
;; IDENTIFICATION METHOD: Deduced Sequence  
;; OTHER INFORMATION: 9G  
US-08-911-321-8

Query Match 66.7%; Score 34; DB 3; Length 435;  
Best Local Similarity 75.0%; Pred. No. 54;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10  
|||: |||  
Db 135 FEGLIYIT 142

RESULT 12  
US-08-487-890A-107  
; Sequence 107, Application US/08487890A  
; Patent No. 5708149  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,435  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,483  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/487,890A  
;; FILING DATE: 07-JUN-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/175,116  
;; FILING DATE: 29-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/148,968  
;; FILING DATE: 08-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stewart, Michael I  
;; REGISTRATION NUMBER: 24,973  
;; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (416) 595-1155  
;; TELEFAX: (416) 595-1163  
;; INFORMATION FOR SEQ ID NO: 107:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 911 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-487-890A-107

Query Match 66.7%; Score 34; DB 1; Length 911;  
Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10  
|||: |||  
Db 228 FEGVAIYT 235

RESULT 13  
US-08-478-435-107  
; Sequence 107, Application US/08478435  
; Patent No. 5922323  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,435  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,483  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116



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; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-435-107

Query Match 66.7%; Score 34; DB 2; Length 911;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10
Db 228 FEGVAIYT 235

RESULT 14
US-08-337-483-107
; Sequence 107, Application US/08337483
; Patent No. 5922562
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION NUMBER: US/08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-337-483-107

Query Match 66.7%; Score 34; DB 2; Length 911;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDIYT 10
Db 228 FEGVAIYT 235

RESULT 15
US-08-478-373-107
; Sequence 107, Application US/08478373
; Patent No. 5922841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/478,373
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-373-107

Query Match 66.7%; Score 34; DB 2; Length 911;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 FEGIDIYT 10  
| | | : | | |  
Db 228 FEGVAIYT 235

Search completed: December 6, 2001, 07:59:57  
Job time: 365 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:27 ; Search time 88.19 seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: US-09-673-795-2

Perfect score: 51

Sequence: 1 SLFEGIDIYVT 10

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	47	92.2	208	2	B44261	dnak-type molecule
2	47	92.2	278	2	I51344	dnak-type molecule
3	47	92.2	467	2	T45477	heat-shock protein
4	47	92.2	467	2	T45479	heat-shock protein
5	47	92.2	468	2	T45476	heat-shock protein
6	47	92.2	469	2	T45478	heat-shock protein
7	47	92.2	632	2	T45471	dnak-type molecule
8	47	92.2	634	2	A25646	dnak-type molecule
9	47	92.2	636	2	A48872	dnak-type molecule
10	47	92.2	638	2	S31766	dnak-type molecule
11	47	92.2	639	2	JC1391	dnak-type molecule
12	47	92.2	639	2	S20139	dnak-type molecule
13	47	92.2	640	1	HHKWA	dnak-type molecule
14	47	92.2	640	2	A29160	dnak-type molecule
15	47	92.2	640	2	S37394	dnak-type molecule
16	47	92.2	640	2	T21394	hypothetical prote
17	47	92.2	640	2	T43724	dnak-type molecule
18	47	92.2	641	2	S53357	dnak-type molecule
19	47	92.2	641	2	S35718	dnak-type molecule
20	47	92.2	641	2	I54542	dnak-type molecule
21	47	92.2	641	2	A45871	dnak-type molecule
22	47	92.2	642	1	HHBYA1	dnak-type molecule
23	47	92.2	642	2	JH0095	dnak-type molecule
24	47	92.2	642	2	B36590	dnak-type molecule
25	47	92.2	644	2	A45635	dnak-type molecule
26	47	92.2	645	2	I51129	dnak-type molecule
27	47	92.2	646	2	T46650	heat shock protein
28	47	92.2	647	1	HHXL70	dnak-type molecule
29	47	92.2	647	2	T41121	heat shock protein

30 46 90.2 209 2 A44261  
31 46 90.2 214 2 A03309  
32 46 90.2 372 2 P00138  
33 46 90.2 379 2 I46588  
34 46 90.2 467 2 T45473  
35 46 90.2 467 2 T45473  
36 46 90.2 641 2 JN0668  
37 46 90.2 641 2 PC7036  
38 46 90.2 643 2 S25585  
39 46 90.2 643 2 S09036  
40 46 90.2 651 2 T45517  
41 46 90.2 651 2 JC7132  
42 44 86.3 209 2 S48024  
43 44 86.3 209 2 S48025  
44 44 86.3 630 2 A34041  
45 44 86.3 636 2 T45468

#### ALIGNMENTS

RESULT 1

B44261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KUH>

A:Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

A:Gene: HSC70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 208;

Best Local Similarity 90.0%; Pred. No. 0.064;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIYVT 10

Db 132 SLFEGIDFVT 141

RESULT 2

I51344

dnak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)

N:Alternate names: 70K heat shock protein

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999

C:Accession: I51344

R:Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o

A:Reference number: I51344; MUID:85036330

A:Accession: I51344

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-278 <KOT>

A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70



C;Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 278;  
Best Local Similarity 90.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10  
|||||

Db 156 SLFEGIDFYT 165

#### RESULT 3

T45477  
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

C;Species: Chondrosia reniformis  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45477

R;Borchliellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z22983

A;Accession: T45477

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-467 <BOR>

A;Cross-references: EMBL:AF026517; PIDN:AAC05362.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 467;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10  
|||||

Db 252 SLFEGIDFYT 261

#### RESULT 4

T45479  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C;Species: Eunicella cavolini

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45479

R;Borchliellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z22983

A;Accession: T45479

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-467 <BOR>

A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 467;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10  
|||||

Db 252 SLFEGIDFYT 261

#### RESULT 5

T45476

heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)

C;Species: Funiculina quadrangularis

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45476

R;Borchliellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z22983

A;Accession: T45476

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-468 <BOR>

A;Cross-references: EMBL:AF026516; PIDN:AAC05361.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 468;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10  
|||||

Db 253 SLFEGIDFYT 262

#### RESULT 6

T45478

heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C;Species: Eunicella cavolini

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45478

R;Borchliellini, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z22983

A;Accession: T45478

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-469 <BOR>

A;Cross-references: EMBL:AF026518; PIDN:AAC05363.1

C;Genetics:

A;Gene: Hsp70

C;Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 469;

Best Local Similarity 90.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIY 10  
|||||

Db 254 SLFEGIDFYT 263

#### RESULT 7

T45471

dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)

N;Alternate names: heat shock cognate protein 70

C;Species: Dictyostelium discoideum

C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000

C;Accession: T45471

R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z22980

A;Accession: T45471

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-632 <BOV>

A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1

A;Experimental source: strain AX3

C;Genetics:

A;Gene: hsc70

A;Note: localized to filopodias and cortex

C;Superfamily: heat shock protein 70



```

Query Match          92.2%; Score 47; DB 2; Length 632;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
   ||||| ||
Db 285 SLFEGIDFYT 294

RESULT 8
A25646
dnaK-type molecular chaperone - chicken
N:Alternate names: heat shock protein 70
C:Species: Gallus gallus (chicken)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C:Accession: A25646
R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
A:Reference number: A25646; MUID:86304452
A:Accession: A25646
A:Molecule type: DNA
A:Residues: 1-634 <MOR>
A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A:Note: The authors translated the codon TCG for residue 583 as Trp
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match          92.2%; Score 47; DB 2; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
   ||||| ||
Db 289 SLFEGIDFYT 298

RESULT 9
A48872
dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agi
C:Species: Dictyostelium discoideum
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C:Accession: A48872
R:Eddy, R.J.; Sauter, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an
A:Reference number: A48872; MUID:94043116
A:Accession: A48872
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-636 <EDD>
A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match          92.2%; Score 47; DB 2; Length 636;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
   ||||| ||
Db 280 SLFEGIDFYT 289

RESULT 10

```

```

S31766
dnaK-type molecular chaperone hsp70 - green monkey
N:Alternate names: heat shock protein 70
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S31766; I36927
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot
A:Reference number: S31766
A:Accession: S31766
A:Molecule type: mRNA
A:Residues: 1-638 <SAI>
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible
A:Reference number: I36927; MUID:95080396
A:Accession: I36927
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-638 <RES>
A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A:Experimental source: kidney; cell line COS-1
C:Genetics:
A:Gene: hsp70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

```

```

Query Match          92.2%; Score 47; DB 2; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
   ||||| ||
Db 284 SLFEGIDFYT 293

```

```

RESULT 11
JC1391
dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N:Alternate names: heat shock protein 70IV; hsp70IV protein
C:Species: Paracentrotus lividus (common urchin)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C:Accession: JC1391
R:Sconzo, G.; Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp
A:Reference number: JC1391; MUID:93077053
A:Accession: JC1391
A:Molecule type: DNA
A:Residues: 1-639 <SCO>
A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
C:Genetics:
A:Gene: hsp70IV
A:Introns: 61/2
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

```

```

Query Match          92.2%; Score 47; DB 2; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
   ||||| ||
Db 286 SLFEGIDFYT 295

```



## RESULT 12

S20139  
 dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: heat shock protein YG102; protein L0971; protein YLL024c  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C:Accession: S20139; S64772; S64775; S69383  
 R:Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A:Reference number: S20139; MUID:89128457  
 A:Accession: S20139  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SLA>  
 A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
 R:Goffeau, A.; Purnelle, B.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64761  
 A:Accession: S64772  
 A:Molecule type: DNA  
 A:Residues: 1-639 <GOF>  
 A:Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL024c  
 A:Experimental source: strain S288C  
 R:Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64775  
 A:Accession: S64775  
 A:Molecule type: DNA  
 A:Residues: 72-639 <DOE>  
 A:Cross-references: EMBL:Z73129; MIPS:YLL024c  
 A:Experimental source: strain S288C  
 R:Purnelle, B.; Goffeau, A.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14  
 mily and a new ABC transporter homologous to the human multidrug resistance protein.  
 A:Reference number: S69380  
 A:Accession: S69383  
 A:Molecule type: DNA  
 A:Residues: 1-639 <PUR>  
 A:Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007  
 C:Genetics:  
 A:Gene: SGD:SSA2  
 A:Cross-references: MIPS:YLL024c; SGD:S0003947  
 A:Map position: 12L  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10  
 ||||| ||

DB 283 SLFEGIDFYT 292

## RESULT 13

HHKW7A  
 dnak-type molecular chaperone hsp70A - Caenorhabditis elegans  
 N:Alternate names: heat shock protein 70 A  
 C:Species: Caenorhabditis elegans  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
 C:Accession: JT0285  
 R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
 Gene 64, 241-255, 1988  
 A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat  
 A:Reference number: JT0285; MUID:88297155  
 A:Accession: JT0285  
 A:Molecule type: DNA; mRNA

A:Residues: 1-640 <SNV>  
 A:Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352  
 A:Note: genomic clones representing six distinct members of the hsp70 gene family wer  
 A:Note: transcripts of hsp70A are abundant in control worms and also increase two- to  
 A:Note: one of the three introns in hsp70A is in a position similar to an intron in D  
 C:Genetics:  
 A:Gene: hsp70A  
 A:Map position: IV  
 A:Introns: 69/1; 331/3; 558/3  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 92.2%; Score 47; DB 1; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10  
 ||||| ||

DB 287 SLFEGIDFYT 296

## RESULT 14

A29160  
 dnak-type molecular chaperone HSPALL - human  
 N:Alternate names: heat shock protein, 70K  
 C:Species: Homo sapiens (man)  
 C>Date: 16-Aug-1988 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
 C:Accession: A29160; I37561; I37562  
 R:Hunt, C.; Morimoto, R.I.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985  
 A:Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the  
 A:Reference number: A29160; MUID:86016721  
 A:Accession: A29160  
 A:Molecule type: DNA  
 A:Residues: 1-640 <HUN>  
 A:Cross-references: GB:M11717; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g386795  
 A:Note: the authors mistranslated residues 463, 491, and 492  
 R:Drabant, B.; Genthe, A.; Benecke, B.J.  
 Nucleic Acids Res. 14, 8933-8948, 1986  
 A:Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepare  
 A:Reference number: I37561; MUID:87066768  
 A:Accession: I37561  
 A:Status: translation not shown; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481  
 A:Accession: I37562  
 A:Status: translation not shown; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 616-640 <RE2>  
 A:Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483  
 C:Genetics:  
 A:Gene: GDB:HSPALL; HSP70-HOM  
 A:Cross-references: GDB:I20058; OMIM:140559  
 A:Map position: 6p21.3-6p21.3  
 A:Introns: #status absent  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10  
 ||||| ||

DB 286 SLFEGIDFYT 295



RESULT 15  
S37394  
dnaK-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostelium discoideum  
C:date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 20-Aug-1999  
C:Accession: S37394  
R:Haas, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schl  
EMBO J. 12, 3763-3771, 1993  
A:Title: The heat shock cognate protein from Dictyostelium affects actin polymerization  
A:Reference number: S37394; MUID:94008983  
A:Accession: S37394  
A:Molecule type: mRNA  
A:Residues: 1-640 <HAU>  
A:Cross-references: EMBL:X75263; NID:g433874; PIDN:CAA53039.1; PID:g433875  
C:Genetics:  
A:Gene: hsc70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10  
| | | | | | | |  
Db 284 SLFEGIDFYT 293

Search completed: December 6, 2001, 07:58:27  
Job time: 275 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:51 ; Search time 50.21 Seconds  
(without alignments)  
7.302 Million cell updates/sec

Title: US-09-673-795-2  
Perfect score: 51  
Sequence: 1 SLFEGIDITYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	92.2	322	1 HS70_ONCVO	P11503 onchocerca
2	47	92.2	503	1 HS70_PENCI	Q92260 penicillium
3	47	92.2	634	1 HS70_CHICK	P08106 gallus gall
4	47	92.2	638	1 HS71_CERAE	Q28222 cercopithec
5	47	92.2	638	1 HS72_YEAST	P10592 saccharomyc
6	47	92.2	639	1 HS74_PARLI	Q06248 paracentrot
7	47	92.2	640	1 HS74_CAEEL	P09446 caenorhabdi
8	47	92.2	640	1 HS7C_DICDI	P36415 dictyosteli
9	47	92.2	641	1 HS71_BOVIN	Q27975 bos taurus
10	47	92.2	641	1 HS71_HUMAN	P08107 homo sapien
11	47	92.2	641	1 HS71_MOUSE	P17879 mus musculu
12	47	92.2	641	1 HS71_PIG	P34930 sus scrofa
13	47	92.2	641	1 HS71_RAT	Q07439 rattus norv
14	47	92.2	641	1 HS71_YEAST	P10591 saccharomyc
15	47	92.2	641	1 HS72_BOVIN	Q27965 bos taurus
16	47	92.2	641	1 HS74_YEAST	P22202 saccharomyc
17	47	92.2	644	1 HS70_BRUMA	P27541 brugia mala
18	47	92.2	644	1 HS70_ONCTS	Q91233 oncorhynch
19	47	92.2	645	1 HS70_PLEWA	Q91291 pleurodelys
20	47	92.2	646	1 HS70_NEUCR	Q01233 neurospora
21	47	92.2	647	1 HS70_XENLA	P02827 xenopus lae
22	47	92.2	649	1 HS70_BLAEM	P48720 blastoclad
23	47	92.2	652	1 HS7D_WANSE	Q90639 manduca sex
24	46	90.2	214	1 HS7A_DROSI	P02826 drosophila
25	46	90.2	372	1 HS72_PARLI	P22623 paracentrot
26	46	90.2	379	1 HS7X_PIG	P34934 sus scrofa
27	46	90.2	638	1 HS70_CERCA	P91902 ceratitidis c
28	46	90.2	641	1 HS7A_DROME	P29843 drosophila
29	46	90.2	643	1 HS76_HUMAN	P17066 homo sapien
30	46	90.2	643	1 HS76_PIG	Q04967 sus scrofa
31	46	90.2	648	1 HS71_PUCGR	Q01877 puccinia gr
32	44	86.3	641	1 HS73_RAT	P55063 rattus norv
33	44	86.3	641	1 HS7H_HUMAN	P34931 homo sapien

34 44 86.3 641 1 HS7T\_MOUSE P16627 mus musculu  
35 44 86.3 642 1 HS72\_PICAN P53623 pichia angu  
36 44 86.3 643 1 HS71\_SCHPO Q10265 schizosacch  
37 44 86.3 644 1 HS71\_PICAN P53421 pichia angu  
38 44 86.3 646 1 HS7C\_CRIGR P19378 cricetulus  
39 44 86.3 646 1 HS7C\_HUMAN P11142 homo sapien  
40 44 86.3 646 1 HS7C\_MOUSE P08109 mus musculu  
41 44 86.3 649 1 HS70\_PARRR P07047 paracoccidi  
42 44 86.3 649 1 HS73\_YEAST P09435 saccharomyc  
43 44 86.3 649 1 HS7C\_BEARE Q90473 brachydanio  
44 44 86.3 650 1 HS7C\_BOVIN P19120 bos taurus  
45 44 86.3 651 1 HS70\_ONCMY P08108 oncorhynch

## ALIGNMENTS

RESULT 1  
HS70\_ONCVO STANDARD; PRT; 322 AA.  
ID HS70\_ONCVO  
AC P11503;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89201313; PubMed=2704388;  
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;  
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in  
microfilaremic individuals from a filariasis-endemic area.";  
RL Mol. Biochem. Parasitol. 33:229-236(1989).  
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A  
MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: J04006; AAA29417.1; -  
DR HSP; P19120; IATR.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70; 1.  
DR PROSITE: PS00297; HSP70\_1; PARTIAL.  
DR PROSITE: PS00329; HSP70\_2; PARTIAL.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock.  
FT NON\_TER 1  
FT NON\_TER 322 322  
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 322;  
Best Local Similarity 90.0%; Pred. No. 0.058;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDITYT 10  
|||||  
DB 43 SLFEGIDITYT 52

RESULT 2  
HS70\_PENCI STANDARD; PRT; 503 AA.  
ID HS70\_PENCI



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AC 092260;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
DN HSP70.
GN Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
RP SEQUENCE FROM N.A.
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
RT "Molecular cloning and expression of a Penicillium citrinum
RT allergen with sequence homology and antigenic cross-reactivity to
RT a hsp70 human heat shock protein.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; U64207; AAB06397.1; -
DR HSSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Allergen.
FT NON_TER
SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;

Query Match          92.2%; Score 47; DB 1; Length 503;
Best Local Similarity 90.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYV 10
DB 154 SLFEGIDFYT 163

RESULT 3
HS70_CHICK
ID HS70_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; J02579; AAA48825.1; -
DR PIR; A25646; A25646.
DR HSSP; P19120; IATR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match          92.2%; Score 47; DB 1; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYV 10
DB 289 SLFEGIDFYT 298

RESULT 4
HS71_CERAE
ID HS71_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RA MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; X70684; CAA50019.1; -

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DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match          92.2%; Score 47; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIVT 10
DB 284 SLFEGIDFYT 293

RESULT 5
HS72_YEAST
ID HS72_YEAST STANDARD; PRT; 638 AA.
AC PI0592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2
GN SSA2 OR YL024C OR L0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=891128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 71-638 FROM N.A.
RA Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RN [4]
RP Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
database.";
RN [6]
RP Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
Saccharomyces cerevisiae.";
RN [6]
RP FEMS Microbiol. Lett. 137:1-8(1996).
RN [5]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC

SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- PTM: PHOSPHORYLATED.
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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-----
DR EMBL; X12927; CAA31394.1; -
DR EMBL; 273129; CAA97472.1; -
DR EMBL; X97560; CAA66167.1; -
DR PIR; S20139; S20139.
DR HSP; P19120; INGI.
DR SWISS-2DPAGE; P10592; YEAST.
DR YEPD; 9800; -.
DR SGD; S0003947; SSA2.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match          92.2%; Score 47; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIVT 10
DB 282 SLFEGIDFYT 291

RESULT 6
HS74_PARLI
ID HS74_PARLI STANDARD; PRT; 639 AA.
AC Q06248;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
GN HSP70IV.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidae; Echinidae;
OC Paracentrotus
OC NCBI_TaxID=7656;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
lividus hsp70 gene family and its expression.";
RN [1]
RP Gene 121:353-358(1992).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-----
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CC -----
DR EMBL; X61379; CAA43653.1; -.
DR PIR; JCI391; JCI391.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;
SQ

Query Match          92.2%; Score 47; DB 1; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYF 10
DB 286 SLFEGIDIYF 295

RESULT 7
HS7A CAEEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
RL Gene 64:241-255(1988).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; M18540; AAA28078.1; -.
DR PIR; JTO285; HHRW7A.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
SQ

Query Match          92.2%; Score 47; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYF 10
DB 286 SLFEGIDIYF 295

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-----
DB 287 SLFEGIDIYF 296

RESULT 8
HS7C DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RT cap32/34."
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RX STRAIN=AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium."
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; X75263; CAA53039.1; -.
DR EMBL; L22736; AAA33219.1; -.
DR PIR; S37394; S37394.
DR HSP; P19120; INGI.
DR SWISS_2DPAGE; P36415; DICTY.
DR Dictydb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone.
KW CONFLICT 1 29
FT CONFLICT 32 32
FT CONFLICT 64 64
FT CONFLICT 180 180
FT CONFLICT 237 237
FT CONFLICT 240 240
FT CONFLICT 341 341
FT CONFLICT 352 352
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;
MSSIGIDIGTYSVGVWQNDREVIAND ->
IHSHINGNATWVSGPVSEVLSFN (IN REF. 2).
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KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 284 SLFEGIDFYT 293

RESULT 9
HS7L_BOVIN STANDARD; PRT; 641 AA.
ID HS7L_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A.; Guerrero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D.; Skow L.C.; Stone R.T.;
RT "An AluI polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: U09861; AAA73914.1; -
CC DR EMBL: U02891; AAA03450.1; -
CC DR HSSP: P19120; INGC.
CC DR InterPro: IPR001023; HSP70.
CC DR Pfam: PF00012; HSP70; 1.
CC DR PRINTS: PR00301; HEATSHOCK70.
CC DR PROSITE: PS00297; HSP70_1; 1.
CC DR PROSITE: PS00329; HSP70_2; 1.
CC DR PROSITE: PS01036; HSP70_3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
|||||
Db 286 SLFEGIDFYT 295

RESULT 10
HS7L_HUMAN STANDARD; PRT; 641 AA.
ID HS7L_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQM0; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Milner C.M.; Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Hunt C.; Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison
with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
RN [3]
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L.; Qin S.; Madan A.; Dickhoff R.; Dors M.; Madan A.; Hicks P.;
RA Loretz C.; Ratcliffe A.; Abbasi N.; Shaffer T.; Hood L.;
RT "Sequence of the human major histocompatibility complex class III
region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RX MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A.; Dunham I.; Trowsdale J.; Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major
heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
RN [5]
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RX MEDLINE=87066768; PubMed=3786141;
RA Drabant B.; Genthe A.; Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts
prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RX MEDLINE=99234376; PubMed=10216320;
RA Osipuk J.; Walsh M.A.; Freeman B.C.; Morimoto R.I.; Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE

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CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATION OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC -----  
 CC EMBL; M59828; AAA63226.1; -  
 CC EMBL; M59830; AAA63227.1; -  
 CC EMBL; AF134726; AAD21816.1; -  
 CC EMBL; AF134726; AAD21815.1; -  
 CC EMBL; M11717; AAA52697.1; -  
 CC EMBL; M24743; AAA59844.1; -  
 CC EMBL; M24744; AAA59845.1; -  
 CC EMBL; X04676; CAA28381.1; -  
 CC EMBL; X04677; CAA28382.1; -  
 CC PIR; A29160; A29160.  
 CC PIR; A45871; A45871.  
 CC PIR; A25773; A25773.  
 CC PDB; 1HJO; 21-OCT-98.  
 CC SWISS-2DPAGE; P08107; HUMAN.  
 CC MIM; 140550; -  
 CC MIM; 603012; -  
 CC InterPro: IPR001023; HSP70.  
 CC Pfam: PF00012; HSP70; 1.  
 CC PRINTS; PR00301; HEATSHOCK70.  
 CC PROSITE; PS00297; HSP70\_1; 1.  
 CC PROSITE; PS00329; HSP70\_2; 1.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;  
 CC 3D-structure. 7 I -> V (IN REF. 2).  
 CC CONFLICT 110 E -> D (IN REF. 3; AAD21816).  
 CC CONFLICT 370 A -> G (IN REF. 2).  
 CC CONFLICT 469 MISSING (IN REF. 2).  
 CC CONFLICT 499 N -> S (IN REF. 3; AAD21815).  
 CC SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;  
 CC  
 CC Query Match 92.2% Score 47; DB 1; Length 641;  
 CC Best Local Similarity 90.0% Pred. No. 0.12;  
 CC Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC Qy 1 SLFEGIDIYT 10  
 CC | | | | | | | |  
 CC Db 286 SLFEGIDFYT 295  
 CC  
 CC RESULT 11  
 CC HS71\_MOUSE STANDARD; PRT; 641 AA.  
 CC AC P17879; O61689;  
 CC 01-AUG-1990 (Rel. 15, Created)  
 CC 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC 30-MAY-2000 (Rel. 39, Last annotation update)  
 CC DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 CC GN HSPAL OR HSP70AL OR HSP70-1 OR HSP70-1.  
 CC OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=90236310; PubMed=2332169;  
 CC RA

RA Hunt C., Calderwood S.;  
 RT "Characterization and sequence of a mouse hsp70 gene and its  
 RT expression in mouse cell lines.";  
 RL Gene 87:199-204(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";  
 RL Gene 146:273-278(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC -----  
 CC EMBL; M35021; AAA37864.1; -  
 CC EMBL; M76613; AAA57233.1; -  
 CC PIR; JH0095; JH0095.  
 CC HSP; P19120; INGC.  
 CC MGD; MGI:99517; Hsp70-1.  
 CC InterPro: IPR001023; HSP70.  
 CC Pfam; PF00012; HSP70; 1.  
 CC PRINTS; PR00301; HEATSHOCK70.  
 CC PROSITE; PS00297; HSP70\_1; 1.  
 CC PROSITE; PS00329; HSP70\_2; 1.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
 CC CONFLICT 342 342 A -> R (IN REF. 1).  
 CC CONFLICT 627 627 P -> PP (IN REF. 1).  
 CC SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;  
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 CC Query Match 92.2% Score 47; DB 1; Length 641;  
 CC Best Local Similarity 90.0% Pred. No. 0.12;  
 CC Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC Qy 1 SLFEGIDIYT 10  
 CC | | | | | | | |  
 CC Db 286 SLFEGIDFYT 295  
 CC  
 CC RESULT 12  
 CC HS71\_PIG STANDARD; PRT; 641 AA.  
 CC AC P34930;  
 CC 01-FEB-1994 (Rel. 28, Created)  
 CC 01-FEB-1994 (Rel. 28, Last sequence update)  
 CC 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).  
 CC GN HSPAL.  
 CC OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CC NCBI\_TaxID=9823;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=92175874; PubMed=1339404;  
 CC Peelman L.J., de Weghe A.R., Coppieters W.R., van Zevenen A.J.,  
 CC RA



RA Bouquet Y.H.;  
 RL Immunogenetics 35:286-289(1992).  
 CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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 CC -----  
 DR EMBL: M69100; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: S35718; S35718.  
 DR HSSP: P19120; INGC.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family.  
 KW SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;  
 SQ  
 Query Match 92.2%; Score 47; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDIYV 10  
 DB 286 SLFEGIDFYV 295  
 RESULT 13  
 HS71\_RAT  
 ID HS71\_RAT STANDARD; PRT; 641 AA.  
 AC Q07439; P42853;  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).  
 GN HSP70-1 AND HSP70-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94096443; PubMed=8271311;  
 RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,  
 RA Massa S.M., Sharp F.R.;  
 RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal  
 RT and injured rat brain";  
 RL J. Neurosci. Res. 36:325-335(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LEW.1W/GUN;  
 RX MEDLINE=95012453; PubMed=7927536;  
 RA Walter L., Rauh F., Guenther E.;  
 RT "Comparative analysis of the three major histocompatibility complex-  
 RT linked heat shock protein 70 (Hsp70) genes of the rat";  
 RL Immunogenetics 40:325-330(1994).

[3]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;  
 RX MEDLINE=94368874; PubMed=8086479;  
 RA Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;  
 RT "Cloning, nucleotide sequence and expression of rat heat inducible  
 RT hsp70 gene.";  
 RL Biochim. Biophys. Acta 1219:64-72(1994).  
 CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -!- INDUCTION: BY HEAT SHOCK.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L16764; AAA17441.1; -  
 DR EMBL: X77208; CAA54423.1; -  
 DR EMBL: X77207; CAA54422.1; -  
 DR EMBL: X74271; CAA52328.1; -  
 DR HSSP: P19120; INGC.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
 FT CONFLICT 71 72 KR -> NG (IN REF. 3).  
 FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).  
 FT CONFLICT 408 408 G -> A (IN REF. 3).  
 SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;  
 Query Match 92.2%; Score 47; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDIYV 10  
 DB 286 SLFEGIDFYV 295  
 RESULT 14  
 HS71\_YEAST  
 ID HS71\_YEAST STANDARD; PRT; 641 AA.  
 AC P10591;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).  
 GN SSA1 OR YAL009C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=89128457; PubMed=2644626;  
 RA Slater M.R., Craig E.A.;  
 RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";



```
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SPO7-CEN1-CDCL15 region.";
RL Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 590-641 FROM N.A.
RX MEDLINE=85087943; PubMed=6096826;
RA Ogden R.C., Lee M.-C., Knapp G.;
RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
RT substrates.";
RL Nucleic Acids Res. 12:9367-9382(1984).
RN [4]
RP REVISIONS TO 207; 417 AND 421.
RA Slater M.R.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [6]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RN [7]
RP FEMS Microbiol. Lett. 137:1-8(1996).
RN [8]
RP ACETYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; X12926; CA31393.1; --
CC EMBL; L22015; AAC04952.1; ALT_SEQ.
CC PIR; S25438; HHBYA1.
CC PIR; S42164; S42164.
CC HSP; P19120; IATR.
CC SWISS-2DRAGE; P10591; YEAST.
CC YEPD; 9788; --
CC SGD; S0000004; SSA1.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC -----
KW Heat shock; ATP-binding; Multigene family; Acetylation.
FT INIT_MET 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;
Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 SLEGGIDIVT 10
DB 282 SLEGGIDFYT 291
RESULT 15
HS72_BOVIN STANDARD; PRT; 641 AA.
ID HS72_BOVIN Q28122;
AC Q27965; Q28122;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 2 (HSP70-2).
GN HSP70-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANGUS;
RA Grosz M.D., Skow L.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94070117; PubMed=8249428;
RA Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,
RA van den Hurk J., Babluk L.A., Zamb T.J.;
RT "Heat-shock promoter-driven synthesis of secreted bovine herpesvirus
RT glycoproteins in transfected cells.";
RL Vaccine 11:1100-1107(1993).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL; J02892; AAA03451.1; --
CC EMBL; M98823; AAA30568.1; --
CC HSP; P19120; INGI.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS01036; HSP70_3; 1.
```



DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family.  
SQ SEQUENCE 641 AA; 70228 MW; 229C19EEBBF610DF CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;  
Best Local Similarity 90.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDYIT 10  
Db |||||||||  
286 SLFEGIDFYT 295

Search completed: December 6, 2001, 08:00:52  
Job time: 420 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:53 ; Search time 170.25 seconds  
(without alignments)  
8.592 Million cell updates/sec

Title: US-09-673-795-2  
Perfect score: 51  
Sequence: 1 SLFEGIDIYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- SPTREMBL\_17:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_invertebrate:\*
  - 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	47	92.2	146	5 Q90667	Q90667 littorina p
2	47	92.2	153	5 Q90670	Q90670 littorina s
3	47	92.2	155	5 Q90669	Q90669 littorina s
4	47	92.2	157	5 Q90665	Q90665 littorina p
5	47	92.2	158	5 Q90671	Q90671 littorina s
6	47	92.2	158	5 Q90668	Q90668 littorina p
7	47	92.2	158	5 Q90666	Q90666 littorina p
8	47	92.2	220	5 P81159	P81159 aplysia cal
9	47	92.2	278	13 Q90520	Q90520 oncorhynch
10	47	92.2	367	13 Q98899	Q98899 fugu rubrip
11	47	92.2	455	11 Q63718	Q63718 rattus norv
12	47	92.2	467	5 O44350	O44350 chondrosia
13	47	92.2	467	5 O44352	O44352 petrobiona
14	47	92.2	467	5 O9NJ92	O9NJ92 quancha lac
15	47	92.2	468	5 O44349	O44349 funiculina
16	47	92.2	469	5 O44351	O44351 eunicella c
17	47	92.2	526	13 Q98897	Q98897 fugu rubrip
18	47	92.2	632	5 O15766	O15766 dictyosteli
19	47	92.2	639	13 Q98900	Q98900 fugu rubrip

20	47	92.2	639	13 Q918F9	Q918f9 oryzias lat
21	47	92.2	640	5 Q93601	Q93601 caenorhabdi
22	47	92.2	640	13 Q93240	Q93240 paralicthcy
23	47	92.2	641	11 Q63256	Q63256 rattus norv
24	47	92.2	641	11 Q90WJ5	Q90WJ5 mus musculu
25	47	92.2	645	5 O96541	O96541 setaria dig
26	47	92.2	645	5 O9NJB7	O9NJB7 wuchereria
27	47	92.2	645	5 O9NGK9	O9NGK9 wuchereria
28	47	92.2	647	3 O59855	O59855 schizosacch
29	47	92.2	650	10 Q9ZS55	Q9ZS55 arabidopsis
30	47	92.2	650	10 Q9LHA8	Q9LHA8 arabidopsis
31	47	92.2	652	10 P93937	P93937 ascomyllum
32	47	92.2	653	5 Q94805	Q94805 trichoplusi
33	47	92.2	659	5 Q9XZJ2	Q9XZJ2 crassostrea
34	46	90.2	190	5 Q9U9B4	Q9U9B4 mytilus edu
35	46	90.2	221	5 P81157	P81157 aplysia cal
36	46	90.2	467	5 O44346	O44346 asbestoplum
37	46	90.2	467	5 O44347	O44347 petrosia fi
38	46	90.2	467	5 Q9GPM5	Q9GPM5 monosiga ov
39	46	90.2	639	13 O73922	O73922 oreochromis
40	46	90.2	642	3 Q9UVM0	Q9UVM0 rhizopus st
41	46	90.2	643	6 Q9NI02	Q9NI02 saguinus oe
42	46	90.2	645	3 O94106	O94106 pneumocysti
43	46	90.2	647	3 O94104	O94104 pneumocysti
44	46	90.2	651	3 Q9UVM1	Q9UVM1 rhizopus st
45	46	90.2	651	10 O22664	O22664 spinacia ol

ALIGNMENTS

RESULT 1					
Q90667	1				
ID	Q90667	PRELIMINARY;	PRT;	146 AA.	
AC	Q90667;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	HEAT-SHOCK PROTEIN (FRAGMENT).				
GN	HSC70.				
OS	Littorina plena.				
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;				
OC	Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.				
OX	NCBI_TaxID=31219;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Hohenlohe P.A.;				
RT	"Heat-shock genes in the heat-stressed genus Littorina.";				
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF191828; AAF12787.1; .				
DR	HSSP; P19120; 1BAL				
DR	InterPro; IPR001023; HSP70.				
DR	PROSITE; PS01036; HSP70_3; 1.				
FT	NON_TER 1				
FT	NON_TER 146				
SQ	SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;				

Query Match 92.2%; Score 47; DB 5; Length 146;  
Best Local Similarity 90.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	SLFEGIDIYT 10			
DB	79	SLFEGIDFYT 88			
RESULT 2					
Q90670	2				
ID	Q90670	PRELIMINARY;	PRT;	153 AA.	
AC	Q90670;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				



DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191825; AAF12784.1; -.  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 153  
SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 92.2%; Score 47; DB 5; Length 153;  
Best Local Similarity 90.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIYT 10  
|||||  
DB 80 SLFEGIDFYT 89

RESULT 3  
Q9U669 PRELIMINARY; PRT; 155 AA.  
ID Q9U669  
AC Q9U669  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191826; AAF12785.1; -.  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 155  
SQ SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 155;  
Best Local Similarity 90.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIYT 10  
|||||  
DB 82 SLFEGIDFYT 91

RESULT 4  
Q9U665 PRELIMINARY; PRT; 157 AA.  
ID Q9U665  
AC Q9U665;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191830; AAF12789.1; -.  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 157  
SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 157;  
Best Local Similarity 90.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIYT 10  
|||||  
DB 84 SLFEGIDFYT 93

RESULT 5  
Q9U671 PRELIMINARY; PRT; 158 AA.  
ID Q9U671  
AC Q9U671;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191824; AAF12783.1; -.  
DR HSSP; P19120; IBA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;  
Best Local Similarity 90.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 SLFEGIDIYT 10  
|||||  
DB 85 SLFEGIDFYT 94

RESULT 6  
Q9U668 PRELIMINARY; PRT; 158 AA.  
ID Q9U668  
AC Q9U668;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)



DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191827; AAF12786.1; -.  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PRO0301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10  
 DB 85 SLFEGIDIFT 94

RESULT 7  
 Q9U666 PRELIMINARY; PRT; 158 AA.  
 ID Q9U666;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191829; AAF12788.1; -.  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PRO0301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10  
 DB 85 SLFEGIDIFT 94

RESULT 8  
 P81159 PRELIMINARY; PRT; 220 AA.  
 ID P81159;  
 AC P81159;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
 OC Aplysiidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-93077669; PubMed-1360013;  
 RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in  
 the expression of BiP, the major protein chaperon of the ER.";  
 RL J. Cell Biol. 119:1069-1076(1992).  
 CC -I- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15039; CAA78757.1; -.  
 DR HSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PRO0301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 220  
 FT NON\_TER 220  
 SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 92.2%; Score 47; DB 5; Length 220;  
 Best Local Similarity 90.0%; Pred. No. 0.32;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIFT 10  
 DB 138 SLFEGIDIFT 147

RESULT 9  
 Q9U520 PRELIMINARY; PRT; 278 AA.  
 ID Q9U520;  
 AC Q9U520;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-85036330; PubMed-6092938;  
 RA Kothary R.K., Jones D., Candido E.P.M.;  
 RT "70-Kilodalton heat shock polypeptides from rainbow trout:  
 characterization of cDNA sequences.";  
 RL Mol. Cell. Biol. 4:1785-1791(1984).  
 DR EMBL; K02549; AAA49562.1; -.  
 DR HSP; P08109; 1CKR.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PRO0301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 278  
 FT NON\_TER 278  
 SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 92.2%; Score 47; DB 13; Length 278;



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Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 156 SLFEGIDFYT 165

RESULT 10
Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
GN HSP70-3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RN SEQUENCE FROM N.A.
RA Lim E.H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08578; CAA69892.1; -.
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock. 367
FT NON_TER 367
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6B3C2CA CRC64;

Query Match 92.2%; Score 47; DB 13; Length 367;
Best Local Similarity 90.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 268 SLFEGIDFYT 277

RESULT 11
Q63718 PRELIMINARY; PRT; 455 AA.
AC Q63718;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT SHOCK ROTEIN 70 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA D'Ambrosio E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z27118; CAA81642.1; -.
DR HSP; P08107; 1HJO.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.
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FT NON_TER 1
FT NON_TER 455
SQ SEQUENCE 455 AA; 50404 MW; 0F45F12CB9A1E2971 CRC64;

Query Match 92.2%; Score 47; DB 11; Length 455;
Best Local Similarity 90.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 254 SLFEGIDFYT 263

RESULT 12
O44350 PRELIMINARY; PRT; 467 AA.
AC O44350;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Chondrosia reniformis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Chondrosida; Chondrillidae; Chondrosia.
OX NCBI_TaxID=68574;
RN [1]
RN SEQUENCE FROM N.A.
RA Borchietlini C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026517; AAC05362.1; -.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 467
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 467;
Best Local Similarity 90.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIYT 10
Db 252 SLFEGIDFYT 261

RESULT 13
O44352 PRELIMINARY; PRT; 467 AA.
AC O44352;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massilliana.
OC Eukaryota; Metazoa; Porifera; Calcareia; Calcaronea; Petrobionidae;
OC Petrobiona.
OX NCBI_TaxID=68578;
RN [1]
RN SEQUENCE FROM N.A.
RA Borchietlini C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
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DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.78;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10  
|||||||  
Db 252 SLFEGIDFYT 261

## RESULT 14

Q9NJ92 PRELIMINARY; PRT; 467 AA.

AC Q9NJ92;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
OS Guancha lacunosa.  
OC Eukaryota; Metazoa; Porifera; Calcarea; Clathrinida;  
OC Clathrinidae; Guancha.  
OX NCBI\_TaxID=115120;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borchelli C., Le Parco Y.;  
RT "Sponges paraphyly and the origin of Metazoa";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF182195; AAF61297.1; -.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51318 MW; F36FC06CBIDEEL131 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.78;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10  
|||||||  
Db 252 SLFEGIDFYT 261

## RESULT 15

O44349 PRELIMINARY; PRT; 468 AA.

AC O44349;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
GN HSP70.  
OS Funiculina quadrangularis.  
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Alcyonaria; Funiculinidae;  
OC Funiculina.  
OX NCBI\_TaxID=68568;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borchelli C., Le Parco Y.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF026516; AAC05361.1; -.  
DR HSSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; UNKNOWN\_1.  
FT NON\_TER 1  
FT NON\_TER 468  
SQ SEQUENCE 468 AA; 51533 MW; EDED2B4699283FBC CRC64;

Query Match 92.2%; Score 47; DB 5; Length 468;  
Best Local Similarity 90.0%; Pred. No. 0.78;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDIVT 10  
|||||||  
Db 253 SLFEGIDFYT 262

Search completed: December 6, 2001, 07:56:53  
Job time: 181 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:55 ; Search time 81.43 Seconds  
(without alignments)  
2.487 Million cell updates/sec

Title: PEPL-MOD8A  
Perfect score: 46  
Sequence: 1 SLFEGIDAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues  
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA: \*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	84.8	643	US-08-797-358B-3	Sequence 3, Appli
2	37	80.4	458	US-09-457-046B-61	Sequence 61, Appl
3	37	80.4	646	US-08-441-139-14	Sequence 14, Appl
4	33	71.7	800	5183745-3	Patent No. 5183745
5	32	69.6	303	US-08-599-171A-32	Sequence 32, Appl
6	32	69.6	303	US-08-646-590B-32	Sequence 32, Appl
7	32	69.6	303	US-09-069-226-32	Sequence 32, Appl
8	32	69.6	303	US-09-412-184-32	Sequence 32, Appl
9	31	67.4	403	US-08-812-412-2	Sequence 2, Appli
10	31	67.4	403	US-09-180-271-5	Sequence 5, Appli
11	31	67.4	495	US-09-079-415-4	Sequence 4, Appli
12	31	67.4	533	US-08-225-488-2	Sequence 2, Appli
13	30	65.2	35	US-08-190-802A-221	Sequence 221, App
14	30	65.2	35	US-08-477-346-221	Sequence 221, App
15	30	65.2	83	US-08-245-511-22	Sequence 22, Appl
16	30	65.2	83	US-08-600-993A-22	Sequence 22, Appl
17	30	65.2	465	US-08-878-989-18	Sequence 18, Appl
18	30	65.2	465	US-08-860-150-7	Sequence 7, Appli
19	30	65.2	465	US-09-338-132-7	Sequence 7, Appli
20	30	65.2	465	US-09-272-796-18	Sequence 18, Appl
21	30	65.2	488	US-08-190-802A-60	Sequence 60, Appl
22	30	65.2	488	US-08-477-346-60	Sequence 60, Appl
23	30	65.2	532	US-08-560-916-8	Sequence 8, Appli
24	30	65.2	532	US-08-676-841-8	Sequence 8, Appli
25	30	65.2	603	US-08-687-865A-2	Sequence 2, Appli
26	30	65.2	603	US-09-043-711-2	Sequence 2, Appli
27	29	63.0	25	US-08-240-012-4	Sequence 4, Appli

28	29	63.0	25	4	US-08-896-162A-4	Sequence 4, Appli
29	29	63.0	53	2	US-08-469-537A-7	Sequence 7, Appli
30	29	63.0	53	2	US-08-469-537A-20	Sequence 20, Appl
31	29	63.0	154	1	US-08-363-010-1	Sequence 1, Appli
32	29	63.0	154	2	US-08-911-434A-4	Sequence 4, Appli
33	29	63.0	192	1	US-08-086-428B-58	Sequence 58, Appl
34	29	63.0	192	2	US-08-468-570-58	Sequence 58, Appl
35	29	63.0	192	2	US-08-290-665A-58	Sequence 58, Appl
36	29	63.0	192	5	PCT-US95-10398-58	Sequence 58, Appl
37	29	63.0	405	4	US-09-537-357-54	Sequence 54, Appl
38	29	63.0	427	4	US-08-481-968A-15	Sequence 15, Appl
39	29	63.0	481	4	US-07-912-122-4	Sequence 4, Appli
40	29	63.0	481	5	PCT-US93-06404-4	Sequence 4, Appli
41	29	63.0	533	1	US-08-294-872-2	Sequence 2, Appli
42	29	63.0	533	5	PCT-US95-09823-2	Sequence 2, Appli
43	29	63.0	566	4	US-09-232-468A-14	Sequence 14, Appl
44	29	63.0	569	4	US-08-686-968C-227	Sequence 227, App
45	29	63.0	616	4	US-09-136-574A-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,358B  
FILING DATE: 11-Feb-1997  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,491  
FILING DATE: 12-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-CE 3165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 643 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-08-797-358B-3  
Query Match 84.8%; Score 39; DB 4; Length 643;  
Best Local Similarity 77.8%; Pred. No. 2.4;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



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Db 288 SLFEGVDFY 296

RESULT 2
US-09-457-046B-61
; Sequence 61, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match 80.4%; Score 37; DB 4; Length 458;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
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Db 165 SLFDGISAY 173

RESULT 3
US-08-441-139-14
; Sequence 14, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441.139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; _LENGTH: 646 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-14

Query Match 80.4%; Score 37; DB 1; Length 646;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
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Db 286 SLFEGIDFY 294

RESULT 4
5183745-3
; Patent No. 5183745
; APPLICANT: DANCHIN, ANTOINE; GLASER, PHILIPPE; KRIN, EVELYN;
; BARZU, OCTAVIEN; LADANT, DANIEL; ULLMAN, AGNES
; TITLE OF INVENTION: ADENYL CYCLASE DERIVATIVES AND THEIR
; BIOLOGICAL USES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,541
; FILING DATE: 25-OCT-1989
; SEQ ID NO: 3
; LENGTH: 800
5183745-3

Query Match 71.7%; Score 33; DB 6; Length 800;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
||:|
Db 721 SIFRGIQAY 729

RESULT 5
US-08-599-171A-32
; Sequence 32, Application US/08599171A
; Patent No. 5814473
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,171A
; FILING DATE: Concurrently
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HERRON, CHARLES J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-38
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-599-171A-32

Query Match 69.6%; Score 32; DB 2; Length 303;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
Db 34 SIFEGIRGY 42

RESULT 6  
US-08-646-590B-32  
Sequence 32, Application US/08646590B  
Patent No. 5962283  
GENERAL INFORMATION:  
APPLICANT: Warren, Patrick V.  
APPLICANT: Swanson, Ronald V.  
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,590B  
FILING DATE: 08-May-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,171  
FILING DATE: 09-FEB-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/01094  
FILING DATE: 21-January-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-646-590B-32

Query Match 69.6%; Score 32; DB 2; Length 303;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
Db 34 SIFEGIRGY 42

RESULT 7  
US-09-069-226-32  
Sequence 32, Application US/09069226  
Patent No. 6013509  
GENERAL INFORMATION:  
APPLICANT: WARREN, Patrick V.  
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,226  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,171  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HERRON, CHARLES J.  
REGISTRATION NUMBER: 28,019  
REFERENCE/DOCKET NUMBER: 331400-38  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-069-226-32

Query Match 69.6%; Score 32; DB 3; Length 303;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
Db 34 SIFEGIRGY 42

RESULT 8  
US-09-412-184-32  
Sequence 32, Application US/09412184  
Patent No. 6268188  
GENERAL INFORMATION:  
APPLICANT: Warren, Patrick V.  
APPLICANT: Swanson, Ronald V.  
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US



ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEO for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/412,184  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,590  
FILING DATE: 08-May-1996  
APPLICATION NUMBER: 08/599,171  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/01094  
FILING DATE: 21-January-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-412-184-32

Query Match 69.6%; Score 32; DB 4; Length 303;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
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Db 34 SIFEGIRGY 42

RESULT 9  
US-08-812-412-2  
Sequence 2, Application US/08812412  
Patent No. 5989869  
GENERAL INFORMATION:  
APPLICANT: FILIPPINI, Silvia  
APPLICANT: LOMOVSKAYA, Natalia  
APPLICANT: FOSTEIN, Leonid  
APPLICANT: COLOMBO, Anna L.  
APPLICANT: HUTCHINSON, C. R.  
TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN AND  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikola, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: PCT/US97/01094  
FILING DATE: 21-January-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,590  
FILING DATE: 08-May-1996  
APPLICATION NUMBER: 08/599,171  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/01094  
FILING DATE: 21-January-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-412-184-32

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica C.  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P1615-7005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-812-412-2

Query Match 67.4%; Score 31; DB 2; Length 403;  
Best Local Similarity 75.0%; Pred. No. 70;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDA 8  
I:|||||  
Db 182 SVFEGIDA 189

RESULT 10  
US-09-180-271-5  
Sequence 5, Application US/09180271  
Patent No. 6210930  
GENERAL INFORMATION:  
APPLICANT: FILIPPINI, Silvia  
APPLICANT: LOMOVSKAYA, Natalia  
APPLICANT: FOSTEIN, Leonid  
APPLICANT: COLOMBO, Anna L.  
APPLICANT: HUTCHINSON, C. Richard  
APPLICANT: OTTEN, Sharee L.  
APPLICANT: BREME, Umberto  
TITLE OF INVENTION: PROCESS FOR PREPARING DOXORUBICIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikola, Marmelstein, Murray & Oram  
STREET: 655 Fifteenth Street N.W. Suite 330  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 14-JAN-1999  
APPLICATION NUMBER: US/09/180,271  
FILING DATE: 14-JAN-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/03938  
FILING DATE: 05-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/901,306  
FILING DATE: 28-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/812,412  
FILING DATE: 06-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitts, Monica C.  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P1615-8010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-5000  
TELEFAX: (202)638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:



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;
; LENGTH: 403 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-180-271-5

Query Match 67.4%; Score 31; DB 4; Length 403;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDA 8
Db 182 SVFERGIDA 189

RESULT 11
US-09-079-415-4
; Sequence 4, Application US/09079415
; Patent No. 6013452
; GENERAL INFORMATION:
; APPLICANT: Christensen, Tove
; APPLICANT: Lehmebeck, Jan
; TITLE OF INVENTION: A Fungus Wherein The areA, pepC and/or
; TITLE OF INVENTION: pepE Genes Have Been Inactivated
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6013452o No. 6013452disk of No. 6013452th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,415
; FILING DATE: 14-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4657.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-415-4

Query Match 67.4%; Score 31; DB 3; Length 495;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EGIDAY 9
Db 173 EGVDA 178

RESULT 12
US-08-225-488-2
; Sequence 2, Application US/08225488
; Patent No. 5846802
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
```

```
;
; APPLICANT: Hinnen, Albert
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: No. 5846802el Fungal Protease
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,488
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,214
; FILING DATE: 13-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-19055/A/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-488-2

Query Match 67.4%; Score 31; DB 2; Length 533;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EGIDAY 9
Db 173 EGVDA 178

RESULT 13
US-08-190-802A-221
; Sequence 221, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
```



```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SOF1 rIII, Fig. 43
; US-08-190-802A-221

Query Match 65.2%; Score 30; DB 1; Length 35;
Best Local Similarity 55.6%; Pred. No. 7.1,
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAY 9
Db 10 SAFQIDSH 18

RESULT 14
US-08-477-346-221
; Sequence 221, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SOF1 rIII, Fig. 43
; US-08-477-346-221

Query Match 65.2%; Score 30; DB 4; Length 35;
Best Local Similarity 55.6%; Pred. No. 7.1,
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAY 9
Db 10 SAFQIDSH 18

RESULT 15
US-08-245-511-22
; Sequence 22, Application US/08245511
; Patent No. 5928900
; GENERAL INFORMATION:
; APPLICANT: Masure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,511
; FILING DATE: 18-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,541
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-069 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-245-511-22

Query Match 65.2%; Score 30; DB 2; Length 83;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FEGIDAY 9
Db 26 FEGVESY 32

Search completed: December 6, 2001, 07:59:56
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:51 ; Search time 50.21 Seconds  
(without alignments)  
6.572 Million cell updates/sec

Title: PEP1-MOD8A  
Perfect score: 46  
Sequence: 1 SLFEGIDAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	87.0	322	1 HS70_ONCVO	P11503 onchocerca
2	40	87.0	372	1 HS72_PARLI	P22623 paracentrot
3	40	87.0	420	1 HS73_MOUSE	Q61696 mus musculu
4	40	87.0	503	1 HS70_PENCI	Q92260 penicillium
5	40	87.0	634	1 HS70_CHICK	P08106 gallus gall
6	40	87.0	638	1 HS71_CERAE	Q28222 cercopithec
7	40	87.0	638	1 HS72_YEAST	P10592 saccharomyc
8	40	87.0	639	1 HS74_PARLI	Q06248 paracentrot
9	40	87.0	640	1 HS7A_CAEEL	P09446 caenorhabdi
10	40	87.0	640	1 HS7C_DICDI	P36415 dictyostell
11	40	87.0	641	1 HS71_BOVIN	Q27975 bos taurus
12	40	87.0	641	1 HS71_HUMAN	P08107 homo sapien
13	40	87.0	641	1 HS71_MOUSE	P17879 mus musculu
14	40	87.0	641	1 HS71_PIG	P34930 sus scrofa
15	40	87.0	641	1 HS71_RAT	P07439 rattus norv
16	40	87.0	641	1 HS71_YEAST	P10591 saccharomyc
17	40	87.0	641	1 HS72_BOVIN	Q27965 bos taurus
18	40	87.0	641	1 HS7A_YEAST	P22202 saccharomyc
19	40	87.0	644	1 HS70_BRUMA	P27541 brugia mala
20	40	87.0	644	1 HS70_ONCTS	Q91233 oncorhynch
21	40	87.0	645	1 HS70_PLEWA	Q01233 pleurodelph
22	40	87.0	646	1 HS70_NEUCR	P02827 xenopus lae
23	40	87.0	647	1 HS70_XENLA	P02827 xenopus lae
24	40	87.0	649	1 HS7D_BLAEM	P48720 blastoclad
25	40	87.0	652	1 HS7D_WANSE	Q9u639 manduca sex
26	39	84.8	214	1 HS7A_DROSI	P02826 drosophila
27	39	84.8	379	1 HS7X_PIG	P34934 sus scrofa
28	39	84.8	641	1 HS7A_DROME	P29843 drosophila
29	39	84.8	643	1 HS76_HUMAN	P17066 homo sapien
30	39	84.8	643	1 HS76_PIG	Q04967 sus scrofa
31	39	84.8	648	1 HS71_PUCGR	Q01877 puccinia gr
32	38	82.6	638	1 HS70_CERCA	P91902 ceratitis c
33	37	80.4	641	1 HS73_RAT	P55063 rattus norv

34	37	80.4	641	1 HS7H_HUMAN	P34931 homo sapien
35	37	80.4	641	1 HS7T_MOUSE	P16627 mus musculu
36	37	80.4	642	1 HS72_PICAN	P53623 pichia angu
37	37	80.4	643	1 HS7L_SCHPO	Q10265 schizosacch
38	37	80.4	644	1 HS71_PICAN	P53421 pichia angu
39	37	80.4	644	1 HS72_LYCES	P27322 lycopersico
40	37	80.4	645	1 HS70_SOYBN	P26413 glycine max
41	37	80.4	645	1 HS7C_CRIGR	P19378 cricetus
42	37	80.4	646	1 HS7C_HUMAN	P11142 homo sapien
43	37	80.4	646	1 HS7C_MOUSE	P08109 mus musculu
44	37	80.4	649	1 HS70_PARRB	P87047 paracoccidi
45	37	80.4	649	1 HS73_ARATH	O65719 arabidopsis

#### ALIGNMENTS

RESULT 1  
HS70\_ONCVO STANDARD; PRT; 322 AA.  
AC P11503;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89201313; PubMed=2704388;  
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;  
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in  
amicrofilaremic individuals from a filariasis-endemic area.";  
RL Mol. Biochem. Parasitol. 33:229-236(1989).  
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A  
MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC

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EMBL; J04006; AAA29417.1; -  
DR HSSP; P19120; LATR.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock.  
FT NON\_TER 1  
FT NON\_TER 322  
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 322;  
Best Local Similarity 88.9%; Pred. No. 0.61;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
DB 43 SLFEGIDFY 51

RESULT 2  
HS72\_PARLI STANDARD; PRT; 372 AA.  
ID HS72\_PARLI



P22623;  
 AT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DE 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).  
 GN HSP70II.  
 OS Paracentrotus lividus (Common sea urchin).  
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 CC Echinoidae; Euechinoidae; Echinacea; Echinoidae; Echinidae;  
 CC Paracentrotus.  
 CC NCBI\_TaxID=7656;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Gonad;  
 RC MEDLINE=91099690; PubMed=2269441;  
 RX la Rosa M., Sconzo G., Giudice G., Rocheri M.C., di Carlo M.;  
 RT "Sequence of a sea urchin hsp70 gene and its 5' flanking region.";  
 RL Gene 96:295-300(1990).  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X16544; CAA34544.1; -  
 DR PIR; PQ0138; PQ0138.  
 DR HSSP; P19120; INGI.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70.1.  
 DR PROSITE; PS00297; HSP70.1; 1. PARTIAL.  
 DR PROSITE; PS00329; HSP70.2; 1. PARTIAL.  
 DR PROSITE; PS01036; HSP70.3; 1.  
 DR ATP-binding; Heat shock; Multigene family.  
 KW NON\_TER 372  
 FT SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;  
 SQ

Query Match 87.0%; Score 40; DB 1; Length 372;  
 Best Local Similarity 88.9%; Pred. No. 0.72;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDAY 9  
 Db 286 SLFEGIDY 294  
 |||||  
 |||||

RESULT 3  
 HS73\_MOUSE  
 ID HS73\_MOUSE STANDARD; PRT; 420 AA.  
 AC O61696; O61697;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).  
 DE HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).  
 GN HSP70-3 OR HSP70A1.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86111900; PubMed=2868009;  
 RA Lowe D.G., Moran L.A.;  
 RT "Molecular cloning and analysis of DNA complementary to three mouse  
 RT Mr = 68,000 heat shock protein mRNAs.";  
 RL J. Biol. Chem. 261:2102-2112(1986).  
 RN [2]  
 RP SEQUENCE OF 155-420 FROM N.A.  
 RX MEDLINE=94357449; PubMed=8076831;

RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";  
 RL Gene 146:273-278(1994).  
 CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -!- INDUCTION: BY HEAT SHOCK.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC -----  
 DR EMBL; M12571; AAA57234.1; -  
 DR EMBL; M12572; AAA57235.1; -  
 DR HSSP; P19120; IATR.  
 DR MGD; MGI:96244; Hsp70-3.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70.1.  
 DR PROSITE; PS00297; HSP70.1; PARTIAL.  
 DR PROSITE; PS00329; HSP70.2; PARTIAL.  
 DR PROSITE; PS01036; HSP70.3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family.  
 KW NON\_TER 1  
 FT VARIANT 188 188 V -> G.  
 SQ SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;  
 DR

Query Match 87.0%; Score 40; DB 1; Length 420;  
 Best Local Similarity 88.9%; Pred. No. 0.82;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDAY 9  
 Db 65 SLFEGIDFY 73  
 |||||  
 |||||

RESULT 4  
 HS70\_PENCI  
 ID HS70\_PENCI STANDARD; PRT; 503 AA.  
 AC Q92260;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
 DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
 GN HSP70.  
 OS Penicillium citrinum.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
 CC NCBI\_TaxID=5077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;  
 RT "Molecular cloning and expression of a Penicillium citrinum  
 RT allergen with sequence homology and antigenic cross-reactivity to  
 RT a hsp70 human heat shock protein.";  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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DR EMBL; U64207; AAB06397.1; -.  
DR HSP; P19120; 3HSC.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR ATP-binding; Chapterone; Heat shock; Allergen.  
KW NON\_TER 1  
FT  
SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 503;  
Best Local Similarity 88.9%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDAY 9  
Db 154 SLFEGIDFY 162  
|||||||

RESULT 5  
HS70\_CHICK  
ID HS70\_CHICK STANDARD; PRT; 634 AA.  
AC P08106;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86304452; PubMed=3017985;  
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
RT "Organization, nucleotide sequence, and transcription of the chicken  
HSP70 gene.";  
RL J. Biol. Chem. 261:12692-12699 (1986).

CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----  
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CC -----

DR EMBL; J02579; AAA48825.1; -.  
DR PIR; A25646; A25646.  
DR HSP; P19120; 1ATP.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR ATP-binding; Chapterone; Heat shock; Multigene family.  
KW  
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 87.0%; Score 40; DB 1; Length 634;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDAY 9

Db 289 SLFEGIDFY 297  
|||||||

RESULT 6  
HS71\_CERAE  
ID HS71\_CERAE STANDARD; PRT; 638 AA.  
AC Q2822;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN 1.  
GN HSPAL.  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=95080396; PubMed=7988690;  
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;  
RT "The hsc70 gene which is slightly induced by heat is the main virus  
inducible member of the hsp70 gene family.";  
RL FEBS Lett. 355:282-286 (1994).

CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
CC STRESS-INDUCED DAMAGE.  
CC -!- INDUCTION: BY HEAT SHOCK.

CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
CC -----  
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CC -----

DR EMBL; X70684; CAA50019.1; -.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chapterone; Heat shock; Multigene family; MHC III.  
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 638;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDAY 9  
Db 284 SLFEGIDFY 292  
|||||||

RESULT 7  
HS72\_YEAST  
ID HS72\_YEAST STANDARD; PRT; 638 AA.  
AC P10592;



DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE HEAT SHOCK PROTEIN SSA2  
GN SSA2 OR YL024C OR L0931.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=S288C;  
RX MEDLINE=89128457; PubMed=2644626;  
RA Slater M.R., Craig E.A.;  
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
RL Nucleic Acids Res. 17:805-806(1989).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=S288C;  
RA Purnelle B., Goffeau A.;  
RT Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE OF 71-638 FROM N.A.  
RA Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;  
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN SEQUENCE OF 91-97 AND 325-341.  
RC STRAIN=S288C;  
RX MEDLINE=95203288; PubMed=7895733;  
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
RA Volpe T., Warner J.R., McLaughlin C.S.;  
RT "Protein identifications for a Saccharomyces cerevisiae protein  
database.";  
RL Electrophoresis 15:1466-1486(1994).  
RN [5]  
RN SEQUENCE OF 186-195.  
RC STRAIN=ATCC 38531 / Y41;  
RX MEDLINE=97089742; PubMed=8935650;  
RA Norbeck J., Blomberg A.;  
RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
Saccharomyces cerevisiae";  
RL FEMS Microbiol. Lett. 137:1-8(1996).  
RN [6]  
RN ACETYLATION, AND PHOSPHORYLATION.  
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
RA Volpe T., Warner J.R., McLaughlin C.S.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE  
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -!- PM: PHOSPHORYLATED.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
-----  
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-----  
CC EMBL: X12927; CAA31394.1; -;  
CC EMBL: Z73129; CAA97472.1; -;  
CC EMBL: X97560; CAA66167.1; -;  
CC PIR: S20139; S20139.  
CC HSSP: P19120; INGIJ.  
CC SWISS-2DPAGE: P10592; YEAST.  
CC YEPD: 9800; -;  
CC SGD: S0003947; SSA2.  
CC InterPro: IPR001023; HSP70.

DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock; ATP-binding; Multigene family; Acetylation;  
KW Phosphorylation.  
KW Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
FT MOD\_RES 1 0 ACETYLATION.  
FT INIT\_MET 0 1  
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;  
  
Query Match 87.0%; Score 40; DB 1; Length 638;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDAY 9  
DB 282 SLFEGIDFY 290  
|||||||  
RESULT 8.  
HS74\_PARLI STANDARD; PRT; 639 AA.  
AC Q06248;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).  
GN HSP70IV.  
OS Paracentrotus lividus (Common sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Echinidae;  
OC Paracentrotus.  
OX NCBI\_TaxID=7656;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=93077053; PubMed=1339375;  
RA Sconzo G., Scardina G., Ferraro M.G.;  
RT "Characterization of a new member of the sea urchin Paracentrotus  
RT lividus hsp70 gene family and its expression.";  
RL Gene 121:353-358(1992).  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC EMBL: X61379; CAA43653.1; -;  
CC PIR: JCI391; JCI391.  
CC HSP: P19120; INGIJ.  
CC InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock; Multigene family.  
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 87.0%; Score 40; DB 1; Length 639;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDAY 9  
DB 286 SLFEGIDFY 294  
|||||||



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RESULT 9
HS7A_CAEEL STANDARD; PRT; 640 AA.
ID P09446;
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
  characterization."
RL Gene 64:241-255(1988).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; M18540; AAA28078.1; -.
DR PIR; JTO285; HHK7A.
DR HSSP; P19120; LNCI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PRO0301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED1540D08C500C2 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
Db 287 SLFEGIDFY 295

RESULT 10
HS7C_DICDI STANDARD; PRT; 640 AA.
ID HS7C_DICDI
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
  polymerization through interaction with the actin-binding protein

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cap32/34.";
EMBO J. 12:3763-3771(1993).
[2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN-AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
  associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
  THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
  STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
  OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
  CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; X75263; CAA53039.1; -.
DR EMBL; L22736; AAA3219.1; -.
DR PIR; S37394; S37394.
DR HSSP; P19120; LNCI.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PRO0301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone.
CC CONFLICT 1 29
  MSSIGIDLTTCVCGVQWQNDVRVEIAND ->
  IHHNGNATWVVEGSPVSEVLSFN (IN REF. 2).
  N -> T (IN REF. 2).
  V -> A (IN REF. 2).
  R -> A (IN REF. 2).
  S -> A (IN REF. 2).
  V -> A (IN REF. 2).
  I -> L (IN REF. 2).
  F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;

Query Match 87.0%; Score 40; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
Db 284 SLFEGIDFY 292

RESULT 11
HS7L_BOVIN STANDARD; PRT; 641 AA.
ID HS7L_BOVIN
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerrilero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:137-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=ANGUS;
MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An AluI polymorphism at the bovine 70 kD heat-shock protein-1
RT (Hsp70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL; U09861; AAA73914.1; -
CC EMBL; U02891; AAA03450.1; -
CC HSP; P19120; INGC.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70. 1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
SQ
Query Match 87.0%; Score 40; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAY 9
| | | | | | | |
Db 286 SLFEGIDFY 294

RESULT 12
HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQM0; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91055806; PubMed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Hunt C., Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison
RT with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
RN [3]
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RX MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major
RT heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
RN [5]
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RX MEDLINE=87066768; PubMed=3786141;
RA Drabent B., Genthe A., Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts
RT prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RX MEDLINE=99234376; PubMed=10216320;
RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; M59828; AAA63226.1; -
CC EMBL; M59830; AAA63227.1; -
CC EMBL; AF134726; AAD21816.1; -
CC EMBL; AF134726; AAD21815.1; -
CC EMBL; M11717; AAA52697.1; -
CC EMBL; M24743; AAA59844.1; -
CC EMBL; M24744; AAA59845.1; -

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DR EMBL; X04676; CAA28381.1; -.
DR EMBL; X04677; CAA28382.1; -.
DR PIR; A29160; A29160.
DR PIR; A45871; A45871.
DR PIR; A25773; A25773.
DR PDB; 1HJO; 21-OCT-98.
DR SWISS-2DPAGE; P08107; HUMAN.
DR MIM; 140550; -.
DR MIM; 603012; -.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
3D-structure. 7
KW CONFLICT 110 110 I -> V (IN REF. 2).
KW CONFLICT 370 370 E -> D (IN REF. 3); AAD21816).
FT CONFLICT 370 370 A -> G (IN REF. 2).
FT CONFLICT 469 469 MISSING (IN REF. 2).
FT CONFLICT 499 499 N -> S (IN REF. 3); AAD21815).
SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
Db 286 SLFEGIDFY 294

RESULT 13
HS71_MOUSE STANDARD; PRT; 641 AA.
AC P17879; Q61689;
DT 01-AUG-1990 (Rel. 15; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169;
RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
RT expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible Hsp70-encoding gene from
RT Mus musculus.";
RL Gene 146:273-278(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M69100; -. NOT_ANNOTATED_CDS.
DR PIR; S35718; S35718.

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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M35021; AAA37864.1; -.
DR EMBL; M76613; AAA57233.1; -.
DR PIR; JH0095; JH0095.
DR HSP; P19120; INGC.
DR MGD; MGI:99517; Hsp70-1.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 342 342 A -> R (IN REF. 1).
FT CONFLICT 627 627 P -> PP (IN REF. 1).
SQ SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 87.0%; Score 40; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
Db 286 SLFEGIDFY 294

RESULT 14
HS71_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28; Created)
DT 01-FEB-1994 (Rel. 28; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPA1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
RA Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M69100; -. NOT_ANNOTATED_CDS.
DR PIR; S35718; S35718.

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DR HSP; P19120; INGC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR EMBL: X77208; CAA54423.1; -.
DR PROSITE: PS00297; HSP70.1; 1.
DR PROSITE: PS00329; HSP70.2; 1.
DR PROSITE: PS01036; HSP70.3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
Db 286 SLFEGIDFY 294

RESULT 15
HS71_RAT
ID HS71_RAT STANDARD; PRT; 641 AA.
AC Q07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
GN HSP70-1 AND HSP70-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94096443; PubMed=8271311;
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
RA Massa S.M., Sharp F.R.;
RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
RT and injured rat brain.";
RL J. Neurosci. Res. 36:325-335(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW 1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94368874; PubMed=8086479;
RA Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
RT "Cloning, nucleotide sequence and expression of rat heat inducible
RT hsp70 gene.";
RL Blochim. Biophys. Acta 1219:64-72(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-----
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DR EMBL: L16764; AAAL7441.1; -.
DR EMBL: X77208; CAA54423.1; -.
DR EMBL: X77207; CAA54422.1; -.
DR EMBL: X74271; CAA52328.1; -.
DR HSP; P19120; INGC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70.1; 1.
DR PROSITE: PS00329; HSP70.2; 1.
DR PROSITE: PS01036; HSP70.3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 71 72 KR -> NG (IN REF. 3).
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).
FT CONFLICT 408 408 G -> A (IN REF. 3).
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 87.0%; Score 40; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9
Db 286 SLFEGIDFY 294

Search completed: December 6, 2001, 08:00:51
Job time: 419 sec
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:56 ; Search time 81.43 Seconds  
(without alignments)  
2.487 Million cell updates/sec

Title: PEPL-MOD8F  
Perfect score: 48  
Sequence: 1 SLFEGIDFY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCrUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	97.9	643	4	US-08-797-358B-3
2	45	93.8	646	1	US-08-441-139-14
3	34	70.8	339	2	US-08-928-692-52
4	33	68.8	2787	4	US-09-245-041-15
5	32	66.7	560	2	US-08-928-692-53
6	32	66.7	679	1	US-08-441-139-5
7	31	64.6	458	4	US-09-457-046B-61
8	31	64.6	465	2	US-08-878-989-18
9	31	64.6	465	3	US-08-860-150-7
10	31	64.6	465	3	US-09-338-132-7
11	31	64.6	465	4	US-09-272-796-18
12	30	62.5	276	1	US-08-467-155A-1
13	30	62.5	276	2	US-08-628-198-1
14	30	62.5	276	4	US-09-201-038-1
15	30	62.5	276	5	PCR-US96-07343-1
16	30	62.5	291	1	US-08-467-155A-11
17	30	62.5	291	2	US-08-628-198-11
18	30	62.5	291	4	US-09-201-038-11
19	30	62.5	291	5	PCR-US96-07343-11
20	30	62.5	509	3	US-08-688-988-40
21	30	62.5	532	2	US-08-560-916-8
22	30	62.5	532	2	US-08-676-841-8
23	30	62.5	560	1	US-08-052-404-23
24	30	62.5	560	1	US-08-479-156-23
25	30	62.5	561	1	US-08-052-404-22
26	30	62.5	561	1	US-08-052-404-24
27	30	62.5	561	1	US-08-479-156-22

28 30 62.5 561 1 US-08-479-156-24 Sequence 24, Appl  
29 30 62.5 654 1 US-08-441-139-11 Sequence 11, Appl  
30 30 62.5 666 1 US-08-441-139-16 Sequence 16, Appl  
31 30 62.5 1233 4 US-09-194-613-5 Sequence 5, Appl  
32 30 62.5 4654 4 US-08-476-515A-84 Sequence 84, Appl  
33 30 62.5 4655 4 US-08-652-877-84 Sequence 86, Appl  
34 30 62.5 4655 4 US-08-652-877-88 Sequence 88, Appl  
35 30 62.5 4655 4 US-08-652-877-90 Sequence 90, Appl  
36 30 62.5 4655 4 US-08-652-877-90 Sequence 7, Appl  
37 29 60.4 53 2 US-08-469-537A-7 Sequence 20, Appl  
38 29 60.4 53 2 US-08-469-537A-20 Sequence 32, Appl  
39 29 60.4 69 4 US-08-563-524A-32 Sequence 10, Appl  
40 29 60.4 274 1 US-08-248-466B-10 Sequence 32, Appl  
41 29 60.4 303 2 US-08-599-171A-32 Sequence 32, Appl  
42 29 60.4 303 2 US-08-646-590B-32 Sequence 32, Appl  
43 29 60.4 303 3 US-09-069-226-32 Sequence 32, Appl  
44 29 60.4 303 4 US-09-412-184-32 Sequence 32, Appl  
45 29 60.4 332 2 US-08-960-756-4 Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-Feb-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 97.9%; Score 47; DB 4; Length 643;  
Best Local Similarity 88.9%; Pred. No. 0.15;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9



Tue Dec 11 08:45:44 2001

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; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
; US-08-928-692-52

Query Match 70.8%; Score 34; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EGIDFY 9
DB 285 EGIDFY 290

RESULT 4
US-09-245-041-15
; Sequence 15, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2787
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-245-041-15

Query Match 68.8%; Score 33; DB 4; Length 2787;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
DB 1590 SLFGVPPF 1598

; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
; US-08-928-692-52

Query Match 70.8%; Score 34; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EGIDFY 9
DB 285 EGIDFY 290

RESULT 4
US-09-245-041-15
; Sequence 15, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2787
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-245-041-15

Query Match 68.8%; Score 33; DB 4; Length 2787;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
DB 1590 SLFGVPPF 1598

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RESULT 5
US-08-928-692-53
; Sequence 53, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727to No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
US-08-928-692-53

Query Match 66.7%; Score 32; DB 2; Length 560;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
DB 304 SLADGIDFH 312

RESULT 6
US-08-441-139-5
; Sequence 5, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-5

Query Match 66.7%; Score 32; DB 1; Length 679;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDF 8
DB 332 SFENGIDF 339

RESULT 7
US-09-457-046B-61
; Sequence 61, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match 64.6%; Score 31; DB 4; Length 458;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9
DB 165 SLFDGISAY 173

RESULT 8
US-08-878-989-18
; Sequence 18, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
```



APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl G.  
APPLICANT: Lal, Preeti  
APPLICANT: Goli, Surya K.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/878,989  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0321 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 465 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 8541070  
US-08-878-989-18

Query Match 64.6%; Score 31; DB 2; Length 465;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDF 8  
Db 380 SFEGVDW 387

RESULT 9  
US-08-860-150-7  
Sequence 7, Application US/08860150B  
Patent No. 5981205  
GENERAL INFORMATION:  
APPLICANT: Hemmings, Brian A.  
APPLICANT: Millward, Thomas A.  
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases  
FILE REFERENCE: 4-20265/A/PCT  
CURRENT APPLICATION NUMBER: US/08/860,150B  
CURRENT FILING DATE: 1997-06-19  
EARLIER APPLICATION NUMBER: PCT/EP95/05052  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: 94810746.1  
EARLIER FILING DATE: 1994-12-22  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7  
LENGTH: 465  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-860-150-7

Query Match 64.6%; Score 31; DB 2; Length 465;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDF 8  
Db 380 SFEGVDW 387

RESULT 10  
US-09-338-132-7  
Sequence 7, Application US/09338132  
Patent No. 6040164  
GENERAL INFORMATION:  
APPLICANT: Hemmings, Brian A.  
APPLICANT: Millward, Thomas A.  
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases  
FILE REFERENCE: 4-20265/A/PCT  
CURRENT APPLICATION NUMBER: US/09/338,132  
CURRENT FILING DATE: 1999-06-22  
EARLIER APPLICATION NUMBER: 08/860,150  
EARLIER FILING DATE: 1997-06-19  
EARLIER APPLICATION NUMBER: PCT/EP95/05052  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: 94810746.1  
EARLIER FILING DATE: 1994-12-22  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 465  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-338-132-7

Query Match 64.6%; Score 31; DB 3; Length 465;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDF 8  
Db 380 SFEGVDW 387

RESULT 11  
US-09-272-796-18  
Sequence 18, Application US/09272796  
Patent No. 6207148  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl G.  
APPLICANT: Lal, Preeti  
APPLICANT: Goli, Surya K.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304



COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/272.796  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/878,989  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0321 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 465 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 8541070  
US-09-272-796-18

Query Match 64.6%; Score 31; DB 4; Length 465;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDF 8  
| | | | |  
Db 380 SFEGVDW 387

RESULT 12  
US-08-467-155A-1  
; Sequence 1, Application US/08467155A  
; Patent No. 5736377  
; GENERAL INFORMATION:  
; APPLICANT: Band, Vimla  
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED  
; TITLE OF INVENTION: MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,155A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00398/100001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906

TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-467-155A-1

Query Match 62.5%; Score 30; DB 1; Length 276;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
| | | | |  
Db 62 SLFNGLSFH 70

RESULT 13  
US-08-628-198-1  
; Sequence 1, Application US/08628198  
; Patent No. 5843694  
; GENERAL INFORMATION:  
; APPLICANT: Band, Vimla  
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED  
; TITLE OF INVENTION: MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/628,198  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/467,155  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00398/100002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-628-198-1

Query Match 62.5%; Score 30; DB 2; Length 276;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFY 9  
| | | | |  
Db 62 SLFNGLSFH 70



RESULT 14  
US-09-201-038-1  
; Sequence 1, Application US/09201038  
; Patent No. 6153387  
; GENERAL INFORMATION:  
; APPLICANT: Band, Vimla  
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED  
; MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201,038  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/628,198  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00398/100002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-201-038-1

Query Match 62.5%; Score 30; DB 4; Length 276;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SLFEGIDFY 9  
Db 62 SLFNGLSFH 70

RESULT 15  
PCT-US96-07343-1  
; Sequence 1, Application PC/TUS9607343  
; GENERAL INFORMATION:  
; APPLICANT: New England Medical Center Hospitals, Inc.  
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED  
; MOLECULES AND METHODS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/07343  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/467,155  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00398/100001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 276 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-07343-1

Query Match 62.5%; Score 30; DB 5; Length 276;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SLFEGIDFY 9  
Db 62 SLFNGLSFH 70

Search completed: December 6, 2001, 07:59:57  
Job time: 365 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:56 ; Search time 81.43 seconds  
(without alignments)  
2.487 Million cell updates/sec

Title: PEPL-MOD8G  
Perfect score: 48  
Sequence: 1 SLFEGIDGY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	38	79.2	303	2	US-08-646-590B-32
3	38	79.2	303	3	US-09-069-226-32
4	38	79.2	303	4	US-09-412-184-32
5	38	79.2	643	4	US-08-797-358B-3
6	36	75.0	646	1	US-08-441-139-14
7	33	68.8	458	2	US-08-483-695-42
8	32	66.7	108	2	US-07-965-285-42
9	32	66.7	108	2	US-08-487-231-42
10	32	66.7	108	4	US-09-201-912-42
11	32	66.7	139	4	US-08-444-818-173
12	32	66.7	269	1	US-08-440-103-16
13	32	66.7	269	1	US-08-440-542-16
14	32	66.7	269	1	US-08-231-368-16
15	32	66.7	269	1	US-08-440-210-16
16	32	66.7	269	4	US-09-046-604-16
17	32	66.7	314	4	US-08-612-973-42
18	32	66.7	314	4	US-08-927-597-42
19	32	66.7	319	4	US-08-612-973-44
20	32	66.7	319	4	US-08-927-597-44
21	32	66.7	338	4	US-08-612-973-38
22	32	66.7	338	4	US-08-927-597-38
23	32	66.7	343	4	US-08-612-973-40
24	32	66.7	343	4	US-08-927-597-40
25	32	66.7	402	1	US-08-460-806-2
26	32	66.7	402	1	US-08-460-806-9
27	32	66.7	402	1	US-08-460-806-9

28 32 66.7 402 1 US-08-325-630-2 Sequence 2, Appli  
29 32 66.7 402 1 US-08-325-630-9 Sequence 9, Appli  
30 32 66.7 428 1 US-08-050-132A-2 Sequence 2, Appli  
31 32 66.7 428 3 US-08-750-222A-2 Sequence 2, Appli  
32 32 66.7 428 3 US-08-815-652B-2 Sequence 2, Appli  
33 32 66.7 428 4 US-08-254-353A-2 Sequence 2, Appli  
34 32 66.7 428 5 PCT-US92-05374A-2 Sequence 2, Appli  
35 32 66.7 428 5 PCT-US95-07084-2 Sequence 2, Appli  
36 32 66.7 463 4 US-08-612-973-46 Sequence 46, Appl  
37 32 66.7 463 4 US-08-927-597-46 Sequence 46, Appl  
38 32 66.7 471 2 US-08-828-488-7 Sequence 7, Appli  
39 32 66.7 480 1 US-08-440-103-18 Sequence 18, Appl  
40 32 66.7 480 1 US-08-440-542-18 Sequence 18, Appl  
41 32 66.7 480 1 US-08-231-368-18 Sequence 18, Appl  
42 32 66.7 480 1 US-08-440-210-18 Sequence 18, Appl  
43 32 66.7 480 4 US-09-046-604-18 Sequence 18, Appl  
44 32 66.7 490 4 US-08-612-973-36 Sequence 36, Appl  
45 32 66.7 490 4 US-08-927-597-36 Sequence 36, Appl

#### ALIGNMENTS

RESULT 1  
US-08-599-171A-32  
; Sequence 32, Application US/08599171A  
; Patent No. 5814473  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Patrick V.  
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/599,171A  
; FILING DATE: Concurrently  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HERRON, CHARLES J.  
; REGISTRATION NUMBER: 28,019  
; REFERENCE/DOCKET NUMBER: 331400-38  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 303 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-599-171A-32

Query Match 79.2%; Score 38; DB 2; Length 303;  
Best Local Similarity 77.8%; Pred. No. 4.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9



```

;
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,226
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,171
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HERRON, CHARLES J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-38
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-09-069-226-32
;
; Query Match 79.2%; Score 38; DB 3; Length 303;
; Best Local Similarity 77.8%; Pred. No. 4.3;
; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 SLFEGIDGY 9
Db 34 SIFEGIRGY 42
;
; RESULT 4
; US-09-412-184-32
; Sequence 32, Application US/09412184
; Patent No. 6268188
; GENERAL INFORMATION:
; APPLICANT: Warren, Patrick V.
; APPLICANT: Swanson, Ronald V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/412,184
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,590
; FILING DATE: 08-MAY-1996
;
; Query Match 79.2%; Score 38; DB 2; Length 303;
; Best Local Similarity 77.8%; Pred. No. 4.3;
; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
;
QY 1 SLFEGIDGY 9
Db 34 SIFEGIRGY 42
;
; RESULT 3
; US-09-069-226-32
; Sequence 32, Application US/09069226
; Patent No. 6013509
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN

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APPLICATION NUMBER: PCT/US97/01094  
FILING DATE: 21-January-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-412-184-32

Query Match 79.2%; Score 38; DB 4; Length 303;  
Best Local Similarity 77.8%; Pred. No. 4.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
I:|||||I  
Db 34 SIFEGIRGY 42

RESULT 5.  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,358B  
FILING DATE: 11-Feb-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,491  
FILING DATE: 12-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-CE 3165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 643 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 79.2%; Score 38; DB 4; Length 643;  
Best Local Similarity 77.8%; Pred. No. 10;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
I:|||||I  
Db 288 SLFEGVDYF 296

RESULT 6  
US-08-441-139-14  
; Sequence 14, Application US/08441139  
; Patent No. 5773245  
; GENERAL INFORMATION:  
; APPLICANT: Wittrup, Dr. Karl D.  
; APPLICANT: Robinson, Anne S.  
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,139  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/089,997  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 8646  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 646 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-441-139-14

Query Match 75.0%; Score 36; DB 1; Length 646;  
Best Local Similarity 77.8%; Pred. No. 26;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
I:|||||I  
Db 286 SLFEGIDFY 294

RESULT 7  
US-09-457-046B-61  
; Sequence 61, Application US/09457046B  
; Patent No. 6287835  
; GENERAL INFORMATION:  
; APPLICANT: Croteau, Rodney et al.  
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway  
; FILE REFERENCE: 53679



Tue Dec 11 08:45:46 2001

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; CURRENT APPLICATION NUMBER: US/09/457.046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-61

Query Match      68.8%; Score 33; DB 4; Length 458;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
Db 165 SLFDGISAY 173

RESULT 8
US-08-483-695-42
; Sequence 42, Application US/08483695
; Patent No. 5866139
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Kremsdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,695
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-695-42

Query Match      66.7%; Score 32; DB 2; Length 108;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGIDGY 9
Db 44 LFAGVGDGH 51

RESULT 10
US-08-487-231-42
; Sequence 42, Application US/08487231
; Patent No. 5919454
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Kremsdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic

```



```
;
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,231
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-487-231-42

Query Match 66.7%; Score 32; DB 2; Length 108;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDGY 9
   ||| |::|
Db 44 LFAGVDGH 51

RESULT 11
US-09-201-912-42
; Sequence 42, Application US/09201912
; Patent No. 6210962
; GENERAL INFORMATION:
; APPLICANT: Brechot, Christian
; APPLICANT: Kremsdorff, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,912
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,285
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-201-912-42

Query Match 66.7%; Score 32; DB 4; Length 108;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDGY 9
   ||| |::|
Db 44 LFAGVDGH 51

RESULT 12
US-08-444-818-173
; Sequence 173, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Japanese isolate (T. Miyamura)
US-08-444-818-173

Query Match 66.7%; Score 32; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDGY 9
Db 78 LFAGVDGH 85

RESULT 13
US-08-440-103-16
; Sequence 16, Application US/08440103
; Patent No. 5670152
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,103
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: US/08-440-103-16
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Query Match 66.7%; Score 32; DB 1; Length 269;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDGY 9
Db 8 LFAGVDGH 15
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RESULT 14
US-08-440-542-16
; Sequence 16, Application US/08440542
; Patent No. 5670153
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,542
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: US-08-440-542-16

Query Match 66.7%; Score 32; DB 1; Length 269;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDGY 9
Db 8 LFAGVDGH 15

RESULT 15
US-08-231-368-16
; Sequence 16, Application US/08231368
; Patent No. 5756312
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,368  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,575  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0205.001  
TELEPHONE: (510) 601-2708  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-231-368-16

Query Match 66.7%; Score 32; DB 1; Length 269;  
Best Local Similarity 62.5%; Pred. No. 58;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEGIDGY 9  
DB 8 LFAGVDGH 15

Search completed: December 6, 2001, 07:59:56  
Job time: 364 sec

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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:26 ; Search time 88.19 Seconds  
(without alignments)  
7.774 Million cell updates/sec

Title: PEPI-MOD8G  
Perfect score: 48  
Sequence: 1 SLFEGIDGY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	83.3	289	2 T17957	hypothetical prote
2	39	81.2	208	2 B4261	dnak-type molecula
3	39	81.2	209	2 A4261	dnak-type molecula
4	39	81.2	278	2 I51344	dnak-type molecula
5	39	81.2	372	2 P00138	dnak-type molecula
6	39	81.2	420	2 A26283	dnak-type molecula
7	39	81.2	467	2 T45477	heat-shock protein
8	39	81.2	467	2 T45479	heat-shock protein
9	39	81.2	468	2 T45476	heat-shock protein
10	39	81.2	469	2 T45478	heat-shock protein
11	39	81.2	617	2 H96605	probable heat shoc
12	39	81.2	632	2 T45471	dnak-type molecula
13	39	81.2	634	2 A25646	dnak-type molecula
14	39	81.2	636	2 A48872	dnak-type molecula
15	39	81.2	638	2 S31766	dnak-type molecula
16	39	81.2	639	2 JC1391	dnak-type molecula
17	39	81.2	639	2 S20139	dnak-type molecula
18	39	81.2	640	1 HHK7A	dnak-type molecula
19	39	81.2	640	2 A29160	dnak-type molecula
20	39	81.2	640	2 S37394	dnak-type molecula
21	39	81.2	640	2 T13394	dnak-type molecula
22	39	81.2	640	2 T43724	hypothetical prote
23	39	81.2	641	2 S53357	dnak-type molecula
24	39	81.2	641	2 S35718	dnak-type molecula
25	39	81.2	641	2 I54542	dnak-type molecula
26	39	81.2	641	2 A45871	dnak-type molecula
27	39	81.2	642	1 HHBYA1	dnak-type molecula
28	39	81.2	642	2 JH0095	dnak-type molecula
29	39	81.2	642	2 B36590	dnak-type molecula

## ALIGNMENTS

## RESULT 1

T17957 hypothetical protein A454L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T17957

R:Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T17957  
A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-289 <GRA>

A:Cross-references: EMBL:U02580; NID:g4028896; PIDN:AAC96822.1

A:Experimental source: specific host Chlorella strain NC64

C:Genetics:

A:Note: A454L

C:Superfamily: Chlorella virus PBCV-1 hypothetical protein A454L

Query Match 83.3%; Score 40; DB 2; Length 289;  
Best Local Similarity 77.8%; Pred. No. 2.2;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9

DB 250 SLFEGLOGY 258  
|||||: ||

## RESULT 2

B4261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B4261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B4261

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KU>

A:Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

A:Gene: HSC70

C:Function:

C:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

30	39	81.2	644	2	A45635	dnak-type molecula
31	39	81.2	645	2	I51129	dnak-type molecula
32	39	81.2	646	2	T46650	heat shock protein
33	39	81.2	647	1	HHXL70	dnak-type molecula
34	39	81.2	647	2	S44168	dnak-type molecula
35	39	81.2	647	2	T41121	heat shock protein
36	39	81.2	650	2	JC7088	heat shock protein
37	38	79.2	214	2	A03309	dnak-type molecula
38	38	79.2	379	2	T46588	dnak-type molecula
39	38	79.2	467	2	T45473	heat-shock protein
40	38	79.2	467	2	T45474	heat-shock protein
41	38	79.2	574	2	S74849	ABC-type transport
42	38	79.2	641	2	JN0668	dnak-type molecula
43	38	79.2	641	2	PC7036	heat shock protein
44	38	79.2	643	2	S25585	dnak-type molecula
45	38	79.2	643	2	S09036	dnak-type molecula



```
Query Match      81.2%; Score 39; DB 2; Length 208;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
   |||||
Db 132 SLFEGIDFY 140

RESULT 3
A44261
dnak-type molecular chaperone HSP70a - California sea hare (fragment)
N:Alternate names: heat shock protein 70
C:Species: Aplysia californica (California sea hare)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999
C:Accession: A44261
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expression of HSP70
A:Reference number: A44261; MUID:93077669
A:Accession: A44261
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-209 <KHU>
A:Note: sequence extracted from NCBI backbone (NCBIP:118951)
C:Genetics:
A:Gene: HSP70a
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      81.2%; Score 39; DB 2; Length 209;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
   |||||
Db 133 SLFEGIDFY 141

RESULT 4
I51344
dnak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
N:Alternate names: 70K heat shock protein
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C:Accession: I51344
R:Kothary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of cDNA clones
A:Reference number: I51344; MUID:85036330
A:Accession: I51344
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-278 <KOT>
A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      81.2%; Score 39; DB 2; Length 278;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
   |||||
Db 156 SLFEGIDFY 164
```

```
RESULT 5
PQ0138
dnak-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)
N:Alternate names: heat shock protein 70
C:Species: Paracentrotus lividus (common urchin)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 20-Aug-1999
C:Accession: PQ0138
R:Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.
Gene 96, 295-300, 1990
A:Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.
A:Reference number: PQ0138; MUID:91099690
A:Accession: PQ0138
A:Molecule type: DNA
A:Residues: 1-372 <ROS>
A:Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001
C:Genetics:
A:Gene: hsp70 II
A:Introns: 68/1; 137/1; 188/3; 281/3
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      81.2%; Score 39; DB 2; Length 372;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
   |||||
Db 286 SLFEGIDFY 294

RESULT 6
A26283
dnak-type molecular chaperone - mouse (fragment)
N:Alternate names: heat shock protein 68
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C:Accession: A26283
R:Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A:Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000
A:Reference number: A26283; MUID:86111900
A:Accession: A26283
A:Molecule type: mRNA
A:Residues: 1-420 <LOW>
A:Cross-references: GB:M12571; NID:g194014; PIDN:AAA57234.1; PID:g387208
A:Note: the authors translated the codon CTG for residue 173 as Val and CGC for resid
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      81.2%; Score 39; DB 2; Length 420;
Best Local Similarity 88.9%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
   |||||
Db 65 SLFEGIDFY 73

RESULT 7
T45477
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C:Species: Chondrosia reniformis
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45477
R:Borchelli, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
```



A:Reference number: Z22983  
A:Accession: T45477  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 81.2%; Score 39; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 252 SLFEGIDFY 260

## RESULT 8

T45476  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)  
C:Species: Eunicella cavolini  
C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45479  
R:Borchellini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 81.2%; Score 39; DB 2; Length 467;  
Best Local Similarity 88.9%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 252 SLFEGIDFY 260

## RESULT 9

T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
C:Species: Funiculina quadrangularis  
C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45476  
R:Borchellini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45476  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-468 <BOR>  
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 81.2%; Score 39; DB 2; Length 468;  
Best Local Similarity 88.9%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||

Db 253 SLFEGIDFY 261

## RESULT 10

T45478  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)  
C:Species: Eunicella cavolini  
C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45478  
R:Borchellini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45478  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-469 <BOR>  
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 81.2%; Score 39; DB 2; Length 469;  
Best Local Similarity 88.9%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 254 SLFEGIDFY 262

## RESULT 11

H96605  
probable heat shock protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: H96605  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwyer,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96605  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-617 <STO>  
A:Cross-references: GB:AE005173; NID:g11024845; PIDN:AAG26930.1; GSPDB:GNO0141  
C:Genetics:  
A:Gene: Fl3N6.9  
A:Map position: 1  
C:Superfamily: heat shock protein 70

Query Match 81.2%; Score 39; DB 2; Length 617;  
Best Local Similarity 88.9%; Pred. No. 8.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 292 SLFEGIDFY 300

## RESULT 12

T45471  
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostellium discoideum  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostellium discoideum



C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T45471

R:Roves, H.; Mintert, U.; Ditttrich, W.; Faix, J.; Gerisch, G.

submitted to the EMBL Data Library, September 1997

A:Reference number: 222980

A:Accession: T45471

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-632 <BOV>

A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1

A:Experimental source: strain AX3

C:Genetics:

A:Gene: hsc70

A>Note: localized to filopodias and cortex

C:Superfamily: heat shock protein 70

Query Match 81.2%; Score 39; DB 2; Length 632;

Best Local Similarity 88.9%; Pred. No. 8.5;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9

|||||||

Db 285 SLFEGIDFY 293

RESULT: 13

A25646

dnaK-type molecular chaperone - chicken

N:Alternate names: heat shock protein 70

C:Species: Gallus gallus (chicken)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999

A:Accession: A25646

R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.

J. Biol. Chem. 261, 12692-12699, 1986

A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.

A:Reference number: A25646; MUID:86304452

A:Accession: A25646

A:Molecule type: DNA

A:Residues: 1-634 <MOR>

A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941

A>Note: the authors translated the codon TCG for residue 583 as Trp

C:Function:

A:Description: Involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 81.2%; Score 39; DB 2; Length 634;

Best Local Similarity 88.9%; Pred. No. 8.6;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9

|||||||

Db 289 SLFEGIDFY 297

RESULT: 14

A48872

dnaK-type molecular chaperone hspB - slime mold (Dictyostellium discoideum) (fragment)

N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein ag

C:Species: Dictyostellium discoideum

C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999

A:Accession: A48872

R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.

J. Biol. Chem. 269, 23267-23274, 1993

A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an

A:Reference number: A48872; MUID:94043116

A:Accession: A48872

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-636 <EDD>

A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180

A>Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 81.2%; Score 39; DB 2; Length 636;

Best Local Similarity 88.9%; Pred. No. 8.6;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9

|||||||

Db 280 SLFEGIDFY 288

RESULT: 15

S31766

dnaK-type molecular chaperone hsp70 - green monkey

N:Alternate names: heat shock protein 70

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999

A:Accession: S31766; I36927

R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.

submitted to the EMBL Data Library, January 1993

A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot

A:Reference number: S31766

A:Accession: S31766

A:Molecule type: mRNA

A:Residues: 1-638 <SAI>

R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.

FES Lett. 355, 282-286, 1994

A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible

A:Reference number: I36927; MUID:95080396

A:Accession: I36927

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-638 <RES>

A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782

A:Experimental source: kidney; cell line COS-1

C:Genetics:

A:Gene: hsp70

C:Function:

A:Description: Involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 81.2%; Score 39; DB 2; Length 638;

Best Local Similarity 88.9%; Pred. No. 8.6;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9

|||||||

Db 284 SLFEGIDFY 292

Search completed: December 6, 2001, 07:58:27

Job time: 275 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: December 6, 2001, 08:00:51 ; Search time 50.21 seconds  
(without alignments)  
6.572 Million cell updates/sec

Title: PEPL-MOD8G  
Perfect score: 48  
Sequence: 1 SLFEGIDGY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	81.2	322	1 HS70_ONCVO	P11503 onchocerca
2	39	81.2	372	1 HS72_PARLI	P22623 paracentrot
3	39	81.2	420	1 HS73_MOUSE	Q61696 mus musculus
4	39	81.2	503	1 HS70_PENCI	Q92260 penicillium
5	39	81.2	634	1 HS70_CHICK	P08106 gallus gall
6	39	81.2	638	1 HS71_CERAE	Q28222 cercopithec
7	39	81.2	638	1 HS72_YEAST	P10592 saccharomyc
8	39	81.2	639	1 HS74_PARLI	Q06248 paracentrot
9	39	81.2	640	1 HS7A_CAEEL	P09446 caenorhabdi
10	39	81.2	640	1 HS7C_DICDI	P36415 dictyosteli
11	39	81.2	641	1 HS71_BOVIN	Q27975 bos taurus
12	39	81.2	641	1 HS71_HUMAN	P08107 homo sapien
13	39	81.2	641	1 HS71_MOUSE	P17879 mus musculus
14	39	81.2	641	1 HS71_PIG	P34930 sus scrofa
15	39	81.2	641	1 HS71_RAT	Q07439 rattus norv
16	39	81.2	641	1 HS71_YEAST	P10591 saccharomyc
17	39	81.2	641	1 HS72_BOVIN	Q27965 bos taurus
18	39	81.2	641	1 HS74_YEAST	P22202 saccharomyc
19	39	81.2	644	1 HS70_BRUMA	P27541 brugia mala
20	39	81.2	644	1 HS70_ONCTS	Q91233 oncorhynch
21	39	81.2	645	1 HS70_PLEWA	Q91291 pleurodeles
22	39	81.2	646	1 HS70_NEUCR	Q01233 neurospora
23	39	81.2	647	1 HS70_XENLA	P02827 xenopus lae
24	39	81.2	649	1 HS70_BLAEM	P08720 blastoclad
25	39	81.2	652	1 HS7D_WANSE	Q96639 manduca sex
26	38	79.2	214	1 HS7A_DROSI	P02826 drosophila
27	38	79.2	379	1 HS7X_PIG	P34934 sus scrofa
28	38	79.2	641	1 HS7A_DROME	P29843 drosophila
29	38	79.2	643	1 HS76_HUMAN	P17066 homo sapien
30	38	79.2	643	1 HS76_PIG	Q04967 sus scrofa
31	38	79.2	648	1 HS71_PUCGR	Q01877 puccinia gr
32	36	75.0	239	1 IPT2_AGRTU	P15653 agrobacteri
33	36	75.0	641	1 HS73_RAT	P55063 rattus norv

34	36	75.0	641	1 HS7H_HUMAN	P34931 homo sapien
35	36	75.0	641	1 HS7T_MOUSE	P16627 mus musculus
36	36	75.0	642	1 HS72_PICAN	P53623 pichia angu
37	36	75.0	643	1 HS71_SCHPO	Q10265 schizosacch
38	36	75.0	644	1 HS71_PICAN	P53421 pichia angu
39	36	75.0	644	1 HS72_LYCES	P27322 lycopersico
40	36	75.0	645	1 HS70_SOYBN	P26413 glycine max
41	36	75.0	646	1 HS7C_CRIGR	P19378 cricetus
42	36	75.0	646	1 HS7C_HUMAN	P11142 homo sapien
43	36	75.0	646	1 HS7C_MOUSE	P08109 mus musculus
44	36	75.0	649	1 HS70_PARRR	P87047 paracoccidi
45	36	75.0	649	1 HS73_ARATH	O65719 arabidopsis

## ALIGNMENTS

```

RESULT 1
HS70_ONCVO STANDARD; PRT; 322 AA.
AC P11503;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201313; PubMed=2704388;
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;
RT Onchocerca volvulus heat shock protein 70 is a major immunogen in
RL Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A
CC MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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-----
CC EMBL; J04006; AAA29417.1; -.
DR HSSP; P19120; 1ATR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1
FT NON_TER 322 322
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

```

Query Match 81.2%; Score 39; DB 1; Length 322;  
Best Local Similarity 88.9%; Pred.No. 2.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 43 SLFEGIDGY 51

RESULT 2  
HS72\_PARLI STANDARD; PRT; 372 AA.  
ID HS72\_PARLI



AC P22623;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DT HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).  
 GN HSP70II.  
 OS Paracentrotus lividus (Common sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinidea; Echinozoa; Echinacea; Echinoida; Echinidae;  
 OC Paracentrotus  
 OC NCBI\_TaxID=7656;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Gonad;  
 RX MEDLINE=91099690; PubMed=2269441;  
 RA la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.;  
 RT "Sequence of a sea urchin hsp70 gene and its 5' flanking region.";  
 RL Gene 96:295-300(1990).  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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 CC  
 CC -----  
 CC EMBL; X16544; CAA34544.1; -;  
 DR PIR; PQ0138; PQ0138.  
 DR HSSP; P19120; INGI.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70.1.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW ATP-binding; Heat shock; Multigene family.  
 FT NON\_TER 372 372  
 FT SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;  
 SQ  
 Query Match 81.2%; Score 39; DB 1; Length 372;  
 Best Local Similarity 88.9%; Pred. No. 2.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGY 9  
 DB 286 SLFEGIDY 294  
 |||||  
 RESULT 3  
 HS73\_MOUSE  
 ID HS73\_MOUSE STANDARD; PRT; 420 AA.  
 AC Q61696; Q61697;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT HEAT SHOCK 70 KDA PROTEIN 3 (HSP70.3) (FRAGMENT).  
 DE HSP70-3 OR HSP70A1.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86111900; PubMed=2868009;  
 RA Lowe D.G., Moran L.A.;  
 RT "Molecular cloning and analysis of DNA complementary to three mouse  
 RT Mr = 68,000 heat shock protein mRNAs.";  
 RL J. Biol. Chem. 261:2102-2112(1986).  
 RN [2]  
 RP SEQUENCE OF 155-420 FROM N.A.  
 RX MEDLINE=94357449; PubMed=8076831;

RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";  
 RL Gene 146:273-278(1994).  
 CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -!- INDUCTION: BY HEAT SHOCK.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC -----  
 CC EMBL; M12571; AAA57234.1; -;  
 DR EMBL; M12572; AAA57235.1; -;  
 DR HSSP; P19120; IAYR.  
 DR MGD; MGI:96244; Hsp70-3.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70.1.  
 DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
 DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family.  
 FT NON\_TER 188 188  
 FT VARIANT 188 188 V -> G.  
 FT SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;  
 SQ  
 Query Match 81.2%; Score 39; DB 1; Length 420;  
 Best Local Similarity 88.9%; Pred. No. 2.9;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGY 9  
 DB 65 SLFEGIDFY 73  
 |||||  
 RESULT 4  
 HS70\_PENCI  
 ID HS70\_PENCI STANDARD; PRT; 503 AA.  
 AC Q92260;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
 GN HSP70.  
 OS Penicillium citrinum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
 OC NCBI\_TaxID=5077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;  
 RT "Molecular cloning and expression of a penicillium citrinum  
 RT allergen with sequence homology and antigenic cross-reactivity to  
 RT a hsp70 human heat shock protein.";  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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DR EMBL; U64207; AAB06397.1; -  
DR HSSP; P19120; 3HSC.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Allergen.  
FT NON\_TER 1  
SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 503;  
Best Local Similarity 88.9%; Pred. No. 3.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 154 SLFEGIDFY 162

RESULT 5  
HS70\_CHICK STANDARD; PRT; 634 AA.  
AC P08106;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86304452; PubMed=3017985;

RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
RT "Organization, nucleotide sequence, and transcription of the chicken  
RT HSP70 gene.";  
RL J. Biol. Chem. 261:12692-12699 (1986).

CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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DR EMBL; J02579; AAA48825.1; -  
DR PIR; A25646; A25646.  
DR HSSP; P19120; 1ATP.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Heat shock; Multigene family.  
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 81.2%; Score 39; DB 1; Length 634;  
Best Local Similarity 88.9%; Pred. No. 4.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9

Db 289 SLFEGIDFY 297  
|||||||

RESULT 6  
HS71\_CERAE STANDARD; PRT; 638 AA.  
AC Q28222;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE HEAT SHOCK 70 KDA PROTEIN 1.  
GN HSPAL.  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
RX MEDLINE=95080396; PubMed=7988690;

RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;  
RT "The hsc70 gene which is slightly induced by heat is the main virus  
RT inducible member of the hsp70 gene family.";  
RL FEBS Lett. 355:282-286 (1994).

CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
CC STRESS-INDUCED DAMAGE.

CC -!- INDUCTION: BY HEAT SHOCK.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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DR EMBL; X70684; CAA50019.1; -  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 638;  
Best Local Similarity 88.9%; Pred. No. 4.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|||||||  
Db 284 SLFEGIDFY 292

RESULT 7  
HS72\_YEAST STANDARD; PRT; 638 AA.  
AC P10592;







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RESULT 9
HS7A_CAEEL
ID HS7A_CAEEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Sutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
characterization.";
RL Gene 64:241-255(1988).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; M18540; AAA28078.1; -.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
DB 287 SLFEGIDFY 295

RESULT 10
HS7C_DICDI
ID HS7C_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
polymerization through interaction with the actin-binding protein

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cap32/34.";
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN=AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
associated with an hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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DR EMBL; X75263; CAA53039.1; -.
DR EMBL; L22736; AAA33219.1; -.
DR PIR; S37394; S37394.
DR HSP; P19120; INGI.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone.
FT CONFLICT 1 29
MSSIGIDLTGYSCVGMQNDRELIAND ->
IHHHNGNATWVSESGPVSEVLSFN (IN REF. 2).
FT CONFLICT 32 32
N -> T (IN REF. 2).
FT CONFLICT 64 64
V -> A (IN REF. 2).
FT CONFLICT 180 180
R -> A (IN REF. 2).
FT CONFLICT 237 237
S -> A (IN REF. 2).
FT CONFLICT 240 240
V -> A (IN REF. 2).
FT CONFLICT 341 341
I -> L (IN REF. 2).
FT CONFLICT 352 352
F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;

Query Match 81.2%; Score 39; DB 1; Length 640;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
DB 284 SLFEGIDFY 292

RESULT 11
HS7L_BOVIN
ID HS7L_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

```



OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=95126904; PubMed=7826329;  
 RA Gutierrez J.A., Guerriero V.;  
 RT "Chemical modifications of a recombinant bovine stress-inducible 70  
 RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";  
 RL Biochem. J. 305:197-203(1995).  
 RN [2]  
 RP SEQUENCE OF 212-641 FROM N.A.  
 RC STRAIN=ANGUS;  
 RX MEDLINE=95030563; PubMed=7943958;  
 RA Grosz M.D., Skow L.C., Stone R.T.;  
 RT "An Alu polymorphism at the bovine 70 kD heat-shock protein-1  
 RT (HSP70-1) locus.";  
 RL Anim. Genet. 25:196-196(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC EMBL; U09861; AAA73914.1; -;  
 CC EMBL; U02891; AAA03450.1; -;  
 CC HSP; P19120; INGC.  
 CC InterPro: IPR001023; HSP70.  
 CC Pfam: PF00012; HSP70; 1.  
 CC PRINTS; PR00301; HEATSHOCK70.  
 CC PROSITE; PS00297; HSP70\_1; 1.  
 CC PROSITE; PS00329; HSP70\_2; 1.  
 CC PROSITE; PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Multigene family.  
 CC SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;  
 SQ  
 Query Match 81.2%; Score 39; DB 1; Length 641;  
 Best Local Similarity 88.9%; Pred. No. 4.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 SLFEGIDGY 9  
 Db 286 SLFEGIDFY 294  
 |||||  
 RESULT 12  
 HS71\_HUMAN STANDARD; PRT; 641 AA.  
 AC P08107; P19790; Q9UQW0; Q9UQW9;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN (HSPA1A OR HSPA1) AND HSPA1B.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91055806; PubMed=1700760;  
 RA Milner C.M., Campbell R.D.;  
 RT "Structure and expression of the three MHC-linked HSP70 genes.";  
 RL Immunogenetics 32:242-251(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86016721; PubMed=3931075;  
 RA Hunt C., Morimoto R.I.;  
 RT "Conserved features of eukaryotic hsp70 genes revealed by comparison  
 RT with the nucleotide sequence of human hsp70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).  
 RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,  
 RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III  
 RT region.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
 RX MEDLINE=89184548; PubMed=2538825;  
 RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;  
 RT "Human major histocompatibility complex contains genes for the major  
 RT heat shock protein HSP70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
 RN [5]  
 RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
 RX MEDLINE=87066768; PubMed=3786141;  
 RA Drabent B., Genthe A., Benicke B.-J.;  
 RT "In vitro transcription of a human hsp 70 heat shock gene by extracts  
 RT prepared from heat-shocked and non-heat-shocked human cells.";  
 RL Nucleic Acids Res. 14:8933-8949(1986).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
 RX MEDLINE=99234376; PubMed=10216320;  
 RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 RT "Structure of a new crystal form of human hsp70 ATPase domain.";  
 RL Acta Crystallogr. D 55:1105-1107(1999).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC EMBL; M59828; AAA63226.1; -;  
 CC EMBL; M59830; AAA63227.1; -;  
 CC EMBL; AF134726; AAD21816.1; -;  
 CC EMBL; AF134726; AAD21815.1; -;  
 CC EMBL; M11717; AAA52697.1; -;  
 CC EMBL; M24743; AAA59844.1; -;  
 CC EMBL; M24744; AAA59845.1; -;  
 DR  
 DR



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DR EMBL; X04676; CAA28381.1; -.
DR EMBL; X04677; CAA28382.1; -.
DR PIR; A29160; A29160.
DR PIR; A45871; A45871.
DR PIR; A25773; A25773.
DR PDB; 1HJO; 21-OCT-98.
DR SWISS-2DPAGE; P08107; HUMAN.
DR MIN; 140550; -.
DR MIN; 603012; -.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
3D-structure. 7 I -> V (IN REF. 2).
FT CONFLICT 110 110 E -> D (IN REF. 3); AAD21816).
FT CONFLICT 370 370 A -> G (IN REF. 2).
FT CONFLICT 469 469 MISSING (IN REF. 2).
FT CONFLICT 499 499 N -> S (IN REF. 3); AAD21815).
SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDGY 9
Db 286 SLFEGIDFY 294

RESULT 13
HS71_MOUSE
ID HS71_MOUSE STANDARD; PRT; 641 AA.
AC P17879; O61689;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169;
RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible Hsp70-encoding gene from
Mus musculus.";
RL Gene 146:273-278(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-----
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DR EMBL; M69100; -. NOT_ANNOTATED_CDS.
DR PIR; S35718; S35718.
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DR EMBL; M35021; AAA37864.1; -.
DR EMBL; M76613; AAA57233.1; -.
DR PIR; JH0095; JH0095.
DR HSSP; P19120; INGC..
DR MGD; MGI:99517; Hsp70-1.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 342 342 A -> R (IN REF. 1).
FT CONFLICT 627 627 P -> PP (IN REF. 1).
SQ SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 81.2%; Score 39; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDGY 9
Db 286 SLFEGIDFY 294

RESULT 14
HS71_PIG
ID HS71_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPA1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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DR EMBL; M69100; -. NOT_ANNOTATED_CDS.
DR PIR; S35718; S35718.
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DR HSP; P19120; INGC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match      81.2%; Score 39; DB 1; Length 641;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9
Db 286 SLFEGIDFY 294

RESULT 15
HS71_RAT
ID HS71_RAT STANDARD; PRT; 641 AA.
AC Q07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
GN HSP70-1 AND HSP70-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94096443; PubMed=8271311;
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
RA Massa S.M., Sharp F.R.;
RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
RT and injured rat brain.";
RL J. Neurosci. Res. 36:325-335(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW 1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94368874; PubMed=8086479;
RA Lisowska K., Krawczyk Z., Wlidlak W., Wolniczka P., Wisniewski J.;
RT "Cloning, nucleotide sequence and expression of rat heat inducible
RT hsp70 gene.";
RL Biochim. Biophys. Acta 1219:64-72(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDiate THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----  
DR EMBL; L16764; AAA17441.1; -;  
DR EMBL; X77208; CAA54423.1; -;  
DR EMBL; X77207; CAA54422.1; -;  
DR EMBL; X74271; CAA52328.1; -;  
DR HSSP; P19120; INGC.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
FT CONFLICT 71 72 KR -> NG (IN REF. 3).  
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).  
FT CONFLICT 408 408 G -> A (IN REF. 3).  
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 641;  
Best Local Similarity 88.9%; Pred. No. 4.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
Db 286 SLFEGIDFY 294

Search completed: December 6, 2001, 08:00:51  
Job time: 419 sec



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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:28 ; Search time 88.19 Seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: PEP2-MOD8A

Perfect score: 51

Sequence: 1 SLFEGIDAVT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	208	2 B44261	dnak-type molecule
2	45	88.2	209	2 A44261	dnak-type molecule
3	45	88.2	278	2 I31344	dnak-type molecule
4	45	88.2	372	2 P00138	dnak-type molecule
5	45	88.2	467	2 T45477	heat-shock protein
6	45	88.2	467	2 T45479	heat-shock protein
7	45	88.2	468	2 T45476	heat-shock protein
8	45	88.2	469	2 T45478	heat-shock protein
9	45	88.2	632	2 T45471	dnak-type molecule
10	45	88.2	634	2 A25646	dnak-type molecule
11	45	88.2	636	2 A48872	dnak-type molecule
12	45	88.2	638	2 S31766	dnak-type molecule
13	45	88.2	639	2 JC1391	dnak-type molecule
14	45	88.2	639	2 S20139	dnak-type molecule
15	45	88.2	640	1 HKKW7A	dnak-type molecule
16	45	88.2	640	2 A29160	dnak-type molecule
17	45	88.2	640	2 S37394	dnak-type molecule
18	45	88.2	640	2 T21394	hypothetical prote
19	45	88.2	640	2 T43724	dnak-type molecule
20	45	88.2	641	2 S33357	dnak-type molecule
21	45	88.2	641	2 S35718	dnak-type molecule
22	45	88.2	641	2 I54542	dnak-type molecule
23	45	88.2	641	2 A45871	dnak-type molecule
24	45	88.2	642	1 HBYA1	dnak-type molecule
25	45	88.2	642	2 JH0095	dnak-type molecule
26	45	88.2	642	2 B36590	dnak-type molecule
27	45	88.2	644	2 A45635	dnak-type molecule
28	45	88.2	645	2 I51129	dnak-type molecule
29	45	88.2	646	2 T46650	heat shock protein

```

30 45 88.2 647 1 HHXL70          dnak-type molecule
31 45 88.2 647 2 T41121          heat shock protein
32 44 86.3 214 2 A03309          dnak-type molecule
33 44 86.3 379 2 I46588          dnak-type molecule
34 44 86.3 467 2 T45473          heat-shock protein
35 44 86.3 467 2 T45474          heat-shock protein
36 44 86.3 641 2 JN0668          dnak-type molecule
37 44 86.3 641 2 PC7036          heat shock protein
38 44 86.3 643 2 S25585          dnak-type molecule
39 44 86.3 643 2 S09036          dnak-type molecule
40 44 86.3 651 2 T45517          heat shock protein
41 44 86.3 651 2 JC7132          heat shock protein
42 82.4 209 2 S48024          dnak-type molecule
43 82.4 209 2 S48025          dnak-type molecule
44 82.4 209 2 C44261          dnak-type molecule
45 82.4 630 2 A34041          dnak-type molecule

```

#### ALIGNMENTS

##### RESULT 1

B44261

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilal, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KUH>

A:Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

A:Gene: HSC70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

```

Query Match Similarity      88.2%; Score 45; DB 2; Length 208;
Best Local Similarity      90.0%; Pred. No. 0.097;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy 1 SLFEGIDAVT 10

Db 132 SLFEGIDFYT 141

##### RESULT 2

A44261

dnak-type molecular chaperone HSP70a - California sea hare (fragment)

N:Alternate names: heat shock protein 70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: A44261

R:Kuhl, D.; Kennedy, T.E.; Barzilal, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: A44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-209 <KUH>

A:Note: sequence extracted from NCBI backbone (NCBIP:118951)

C:Genetics:

A:Gene: HSP70a

C:Function:



A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 209;  
Best Local Similarity 90.0%; Pred. No. 0.097;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||  
Db 133 SLFEGIDYIT 142

## RESULT 3

I51344  
dnaK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)

N:Alternate names: 70K heat shock protein

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999

C:Accession: I51344

R:Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of c

A:Reference number: I51344; MUID:85036330

A:Accession: I51344

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-278 <KOT>

A:Cross-references: GB:K02549; NID:G213803; PIDN:AAA49562.1; PID:G213804

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 278;  
Best Local Similarity 90.0%; Pred. No. 0.13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||  
Db 156 SLFEGIDYIT 165

## RESULT 4

PQ0138  
dnaK-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)

N:Alternate names: heat shock protein 70

C:Species: Paracentrotus lividus (common urchin)

C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 20-Aug-1999

C:Accession: PQ0138

R:Kosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.

Gene 96, 295-300, 1990

A:Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.

A:Reference number: PQ0138; MUID:91099690

A:Accession: PQ0138

A:Molecule type: DNA

A:Residues: 1-372 <ROS>

A:Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001

C:Genetics:

A:Gene: hsp70 II

A:Introns: 68/1; 137/1; 188/3; 281/3

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 372;  
Best Local Similarity 90.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||  
Db 286 SLFEGIDYIT 295

## RESULT 5

T45477  
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)

C:Species: Chondrosia reniformis

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45477

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45477

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match 88.2%; Score 45; DB 2; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||  
Db 252 SLFEGIDYIT 261

## RESULT 6

T45479  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)

C:Species: Eunicella cavolini

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45479

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45479

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-467 <BOR>

A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1

C:Genetics:

A:Gene: Hsp70

C:Superfamily: heat shock protein 70

Query Match 88.2%; Score 45; DB 2; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
|||||  
Db 252 SLFEGIDYIT 261

## RESULT 7

T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)

C:Species: Funiculina quadrangularis

C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45476

R:Borchelli, C.; Le Parco, Y.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z22983

A:Accession: T45476

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA



A:Residues: 1-468 <BOR>  
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
C:Genetics:  
A:Gene: hsp70  
C:Superfamily: heat shock protein 70

Query Match 88.2%; Score 45; DB 2; Length 468;  
Best Local Similarity 90.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10  
||||||| ||  
Db 253 SLFEGIDFYT 262

RESULT 8  
T45478  
heat-shock protein 70 [imported] - Eunicea cavolini (fragment)  
C:Species: Eunicea cavolini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45478  
R:Borchelli, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: 222983  
A:Accession: T45478  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-469 <BOR>  
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C:Genetics:  
A:Gene: hsp70  
C:Superfamily: heat shock protein 70

Query Match 88.2%; Score 45; DB 2; Length 469;  
Best Local Similarity 90.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10  
||||||| ||  
Db 254 SLFEGIDFYT 263

RESULT 9  
T45471  
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostelium discoideum  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T45471  
R:Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: 222980  
A:Accession: T45471  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-632 <BOV>  
A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
A:Experimental source: strain AX3  
C:Genetics:  
A:Gene: hsc70  
A:Note: localized to filopodias and cortex  
C:Superfamily: heat shock protein 70

Query Match 88.2%; Score 45; DB 2; Length 632;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10  
||||||| ||  
Db 285 SLFEGIDFYT 294

RESULT 10  
A25646  
dnaK-type molecular chaperone - chicken  
N:Alternate names: heat shock protein 70  
C:Species: Gallus gallus (chicken)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25646  
R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
J. Biol. Chem. 261, 12692-12699, 1986  
A:Title: Organization, nucleotide sequence, and transcription of the chicken hsp70 gene  
A:Reference number: A25646; MUID:86304452  
A:Accession: A25646  
A:Molecule type: DNA  
A:Residues: 1-634 <MOR>  
A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941  
A:Note: the authors translated the codon TCG for residue 583 as Trp  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 634;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10  
||||||| ||  
Db 289 SLFEGIDFYT 298

RESULT 11  
A48872  
dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)  
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein  
C:Species: Dictyostelium discoideum  
C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
C:Accession: A48872  
R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
J. Biol. Chem. 268, 23267-23274, 1993  
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with  
A:Reference number: A48872; MUID:94043116  
A:Accession: A48872  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-636 <EDD>  
A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180  
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein complex  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 636;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SLFEGIDAYT 10  
||||||| ||  
Db 280 SLFEGIDFYT 289

RESULT 12  
S31766  
dnaK-type molecular chaperone hsp70 - green monkey  
N:Alternate names: heat shock protein 70  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S31766; I36927  
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.



submitted to the EMBL Data Library, January 1993  
 A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
 A:Reference number: S31766  
 A:Accession: S31766  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <SAI>  
 R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FEBS Lett. 355, 282-286, 1994  
 A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me  
 A:Reference number: I36927; MUID:95080396  
 A:Accession: I36927  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <RES>  
 A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
 A:Experimental source: kidney; cell line COS-1  
 C:Genetics:  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein compl  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 0.34;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 ||||| ||

Db 284 SLFEGIDFYT 293

## RESULT 13

JC1391  
 dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
 N:Alternate names: heat shock protein 70IV; hsp70IV protein  
 C:Species: Paracentrotus lividus (common urchin)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C:Accession: JC1391  
 R:Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
 A:Reference number: JC1391; MUID:93077053  
 A:Accession: JC1391  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SCO>  
 A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
 C:Genetics:  
 A:Gene: hsp70IV  
 A:Introns: 61/2  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein compl  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 88.2%; Score 45; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.34;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
 ||||| ||

Db 286 SLFEGIDFYT 295

## RESULT 14

S20139  
 dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: heat shock protein YG102; protein L0971; protein YLL024c  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C:Accession: S20139; S64772; S64775; S69383

R:Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A:Reference number: S20139; MUID:89128457  
 A:Accession: S20139  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SLA>  
 A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
 R:Goffeau, A.; Purnelle, B.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64761  
 A:Accession: S64772  
 A:Molecule type: DNA  
 A:Residues: 1-639 <GOF>  
 A:Cross-references: EMBL:Z73129; NID:gl360201; PIDN:CAA97472.1; PID:gl360202; MIPS:YL  
 A:Experimental source: strain S288C  
 R:Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64775  
 A:Accession: S64775  
 A:Molecule type: DNA  
 A:Residues: 72-639 <DUE>  
 A:Cross-references: EMBL:Z73129; MIPS:YLL024c  
 A:Experimental source: strain S288C  
 R:Purnelle, B.; Goffeau, A.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals  
 mly and a new ABC transporter homologous to the human multidrug resistance protein.

A:Reference number: S69380

A:Accession: S69383

A:Molecule type: DNA

A:Residues: 1-639 <PUR>

A:Cross-references: EMBL:X97560; NID:gl297003; PIDN:CAA66167.1; PID:gl297007

C:Genetics:

A:Gene: SGD:SSA2

A:Cross-references: MIPS:YLL024c; SGD:S0003947

A:Map position: 12L

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 88.2%; Score 45; DB 2; Length 639;

Best Local Similarity 90.0%; Pred. No. 0.34;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10

||||| ||

Db 283 SLFEGIDFYT 292

## RESULT 15

HNK7A  
 dnaK-type molecular chaperone hsp70A - Caenorhabditis elegans

N:Alternate names: heat shock protein 70 A

C:Species: Caenorhabditis elegans

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999

C:Accession: JT0285

R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.

Gene 64, 241-255, 1988

A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri

A:Reference number: JT0285; MUID:88297155

A:Accession: JT0285

A:Molecule type: DNA; mRNA

A:Residues: 1-640 <SNU>

A:Cross-references: GB:M18540; NID:gl56351; PIDN:AAA28078.1; PID:gl56352

A:Note: genomic clones representing six distinct members of the hsp70 gene family wer

A:Note: transcripts of hsp70A are abundant in control worms and also increase two- to

A:Note: one of the three introns in hsp70A is in a position similar to an intron in D

C:Genetics:

A:Gene: hsp70A



A:Map position: IV  
A:Introns: 69/1; 331/3; 558/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein compl  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 88.2%; Score 45; DB 1; Length 640;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
      |||||  
Db 287 SLFEGIDFYT 296

Search completed: December 6, 2001, 07:58:28  
Job time: 276 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:52 ; Search time 50.21 Seconds  
(without alignments)  
7.302 Million cell updates/sec

Title: PEP2-MOD8A

Perfect score: 51

Sequence: 1 SLFEGIDAYT 10

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	322	1 HS70_ONCVO	P11503 onchocerca
2	45	88.2	372	1 HS72_PARLI	P22623 paracentrot
3	45	88.2	503	1 HS70_PENCI	Q32260 penicillium
4	45	88.2	634	1 HS70_CHICK	P08106 gallus gall
5	45	88.2	638	1 HS71_CERAE	Q28222 cercopithec
6	45	88.2	639	1 HS72_YEAST	P10592 saccharomyc
7	45	88.2	639	1 HS74_PARLI	Q06248 paracentrot
8	45	88.2	640	1 HS7A_CAEEL	P09446 caenorhabdi
9	45	88.2	640	1 HS7C_DICDI	P36415 dictyosteli
10	45	88.2	641	1 HS71_BOVIN	Q27975 bos taurus
11	45	88.2	641	1 HS71_HUMAN	P08107 homo sapien
12	45	88.2	641	1 HS71_MOUSE	P17879 mus musculu
13	45	88.2	641	1 HS71_PIG	P34930 sus scrofa
14	45	88.2	641	1 HS71_RAT	Q07439 rattus norv
15	45	88.2	641	1 HS71_YEAST	P10591 saccharomyc
16	45	88.2	641	1 HS72_BOVIN	Q27965 bos taurus
17	45	88.2	641	1 HS74_YEAST	P22202 saccharomyc
18	45	88.2	644	1 HS70_BRUMA	P27541 brugia mala
19	45	88.2	644	1 HS70_ONCTS	Q91233 oncorhynch
20	45	88.2	645	1 HS70_PLEWA	Q91291 pleurodeles
21	45	88.2	645	1 HS70_NEUCR	Q01233 neurospora
22	45	88.2	647	1 HS70_XENLA	P02827 xenopus lae
23	45	88.2	649	1 HS70_BLAEM	P48720 blastoclad
24	45	88.2	652	1 HS7D_MANSE	Q9u639 manduca sex
25	44	86.3	214	1 HS7A_DROSI	P02826 drosophila
26	44	86.3	379	1 HS7X_PIG	P34934 sus scrofa
27	44	86.3	641	1 HS7A_DROME	P29843 drosophila
28	44	86.3	643	1 HS76_HUMAN	P17066 homo sapien
29	44	86.3	643	1 HS76_PIG	Q04967 sus scrofa
30	44	86.3	648	1 HS71_PUCGR	Q01877 puccinia gr
31	43	84.3	638	1 HS70_CERCA	P91902 ceratitis c
32	42	82.4	641	1 HS73_RAT	P55063 rattus norv
33	42	82.4	641	1 HS7H_HUMAN	P34931 homo sapien

34	42	82.4	641	1 HS7T_MOUSE	P16627 mus musculu
35	42	82.4	642	1 HS72_PICAN	P53623 pichia angu
36	42	82.4	643	1 HS71_SCHPO	Q10265 schizosacch
37	42	82.4	644	1 HS71_PICAN	P53421 pichia angu
38	42	82.4	646	1 HS7C_CRIGR	P19378 cricetus
39	42	82.4	646	1 HS7C_HUMAN	P11142 homo sapien
40	42	82.4	646	1 HS7C_MOUSE	P08109 mus musculu
41	42	82.4	649	1 HS70_PARRR	P87047 paracoccidi
42	42	82.4	649	1 HS73_YEAST	P09435 saccharomyc
43	42	82.4	649	1 HS7C_BRARE	Q90473 brachydanio
44	42	82.4	650	1 HS7C_BOVIN	P19120 bos taurus
45	42	82.4	651	1 HS70_ONCMY	P08108 oncorhynch

#### ALIGNMENTS

```

RESULT 1
HS70_ONCVO
ID HS70_ONCVO STANDARD; PRT; 322 AA.
AC P11503;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201313; PubMed=2704388;
RA Rochstein N.M., Higashi G., Yates J., Rajan T.V.;
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in
RT amicrofilaremic individuals from a filariasis-endemic area.";
RL Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A
CC MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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-----
CC EMBL; J04006; AAA29417.1; -.
CC HSSP; P19120; IATR.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; PARTIAL.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Heat shock.
FT NON_TER 1
FT NON_TER 322
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

```

Query Match 88.2%; Score 45; DB 1; Length 322;

Best Local Similarity 90.0%; Pred. No. 0.089; 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLFEGIDAYT 10

Db 43 SLFEGIDYFT 52

RESULT 2

HS72\_PARLI

ID HS72\_PARLI STANDARD; PRT; 372 AA.



```
AC P22623;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
GN HSP70II.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinolidea; Euechinozoa; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gonad;
RX MEDLINE=91099690; PubMed=2269441;
RA la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.;
RT "Sequence of a sea urchin hsp70 gene and its 5' flanking region.";
RL Gene 96:295-300(1990).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; X16544; CAA34544.1; -.
DR PIR; P00138; P00138.
DR HSP; P19120; INGJ.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70.1.
DR PROSITE; PS00297; HSP70.1; 1.
DR PROSITE; PS00329; HSP70.2; PARTIAL.
DR PROSITE; PS01036; HSP70.3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW NON_TER 372 372
FT SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;
SQ SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;

Query Match 88.2%; Score 45; DB 1; Length 372;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10
Db 286 SLFEGIDYIT 295
|||||||

RESULT 3
HS70_PENCI STANDARD; PRT; 503 AA.
AC Q92260;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
GN HSP70.
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
RP SEQUENCE FROM N.A.
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
RT "Molecular cloning and expression of a Penicillium citrinum
RT allergen with sequence homology and antigenic cross-reactivity to
RT a hsp70 human heat shock protein.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; U64207; AAB06397.1; -.
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70.1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70.2; 1.
DR PROSITE; PS01036; HSP70.3; 1.
DR ATP-binding; Chaperone; Heat shock; Allergen.
KW NON_TER 1
FT SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;

Query Match 88.2%; Score 45; DB 1; Length 503;
Best Local Similarity 90.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10
Db 154 SLFEGIDFT 163
|||||||

RESULT 4
HS70_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; J02579; AAA48825.1; -.
DR PIR; A25646; A25646.
DR HSP; P19120; IATR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70.1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70.1; 1.
DR PROSITE; PS00329; HSP70.2; 1.
DR PROSITE; PS01036; HSP70.3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;

Query Match 88.2%; Score 45; DB 1; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.19;
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDAYT 10
    |||||
Db 289 SLFEGIDFTT 298
    |||||
RESULT 5
HS71_CERAE STANDARD; PRT; 638 AA.
AC Q2822;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDiate THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL; X70684; CAA50019.1; -.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 88.2%; Score 45; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDAYT 10
    |||||
Db 284 SLFEGIDFTT 293
    |||||
RESULT 6

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HS72_YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YLL024C OR L0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Purnelle B., Goffeau A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 71-638 FROM N.A.
RA Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC
CC EMBL; X12927; CAA31394.1; -.
CC EMBL; Z73129; CAA97472.1; -.
CC EMBL; X97560; CAA66167.1; -.
CC PIR; S20139; S20139.
CC HSP; P19120; 1NGJ.
CC SWISS-2DPAGE; P10592; YEAST.

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RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RT cap32/34.";
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN-AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauter R.A., Condeelis J.S.;
RT "Agnactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -!- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -!- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; X75263; CAA53039.1; -.
DR EMBL; L22736; AAA33219.1; -.
DR PIR; S37394; S37394.
DR HSSP; P19120; INGC.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone.
FT CONFLICT 1 29
FT CONFLICT 32 32
FT CONFLICT 64 64
FT CONFLICT 180 180
FT CONFLICT 237 237
FT CONFLICT 240 240
FT CONFLICT 341 341
FT CONFLICT 352 352
SQ SEQUENCE 640 AA; 70499 MW; 256BDC2DB96A9F5D CRC64;
MSSIGIDLTGYSCVGVNQDRVELIAND ->
IHHINGNATVWVSEGPVSEVLSFN (IN REF. 2).
N -> T (IN REF. 2).
V -> A (IN REF. 2).
R -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
I -> L (IN REF. 2).
F -> P (IN REF. 2).

Query Match 88.2%; Score 45; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10
DB 284 SLFEGIDFT 293
|||||

RESULT 10
HS71_BOVIN
ID HS71_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.

Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerriero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN-ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An AluI polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDiate THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; U09861; AAA73914.1; -.
DR EMBL; U02891; AAA03450.1; -.
DR HSSP; P19120; INGC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 88.2%; Score 45; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10
DB 286 SLFEGIDFT 295
|||||

RESULT 11
HS71_HUMAN
ID HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQM0; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

```



DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN (HSPAL1 OR HSPAL1) AND HSPALB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=91055806; PubMed=1700760;  
 RA Milner C.M., Campbell R.D.;  
 RT "Structure and expression of the three MHC-linked HSP70 genes.";  
 RL Immunogenetics 32:242-251(1990).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=86016721; PubMed=3931075;  
 RA Hunt C., Morimoto R.I.;  
 RT "Conserved features of eukaryotic hsp70 genes revealed by comparison  
 with the nucleotide sequence of human hsp70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
 RN [3]  
 RN SEQUENCE FROM N.A. (HSPAL1 AND HSPALB).  
 RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,  
 RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III  
 region.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RN SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
 RX MEDLINE=89184548; PubMed=2538825;  
 RA Sargent C.A., Dunham I., Townsdaie J., Campbell R.D.;  
 RT "Human major histocompatibility complex contains genes for the major  
 heat shock protein HSP70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
 RN [5]  
 RN SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
 RX MEDLINE=87066768; PubMed=3786141;  
 RA Drabant B., Genthe A., Benecke B.-J.;  
 RT "In vitro transcription of a human hsp 70 heat shock gene by extracts  
 prepared from heat-shocked and non-heat-shocked human cells.";  
 RL Nucleic Acids Res. 14:8933-8949(1986).  
 RN [6]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
 RX MEDLINE=99234376; PubMed=10216320;  
 RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 RT "Structure of a new crystal form of human hsp70 ATPase domain.";  
 RL Acta Crystallogr. D 55:1105-1107(1999).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
 CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
 CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
 CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
 CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
 CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
 CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
 CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING  
 CC STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC  
 CC EMBL; M59828; AAA63226.1; -;  
 CC EMBL; M59830; AAA63227.1; -;  
 CC EMBL; AF134726; AAD21816.1; -;  
 CC EMBL; AF134726; AAD21815.1; -;

DR EMBL; M11717; AAA52697.1; -;  
 DR EMBL; M24743; AAA59844.1; -;  
 DR EMBL; M24744; AAA59845.1; -;  
 DR EMBL; X04676; CAA28381.1; -;  
 DR EMBL; X04677; CAA28382.1; -;  
 DR PIR; A29160; A29160;  
 DR PIR; A45871; A45871;  
 DR PIR; A25773; A25773;  
 DR PDB; 1HJO; 21-OCT-98.  
 DR SWISS-2DPAGE; P08107; HUMAN.  
 DR MIM; 140550; -;  
 DR MIM; 603012; -;  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;  
 KW 3D-structure.  
 FT CONFLICT 7 7 I -> V (IN REF. 2).  
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).  
 FT CONFLICT 370 370 A -> G (IN REF. 2).  
 FT CONFLICT 469 469 MISSING (IN REF. 2).  
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).  
 FT CONFLICT 641 641 N -> S (IN REF. 3; AAD21815).  
 SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE66 CRC64;  
  
 Query Match 88.2%; Score 45; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.19;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 SLFEGIDAYT 10  
 |||||  
 Db 286 SLFEGIDFYT 295  
  
 RESULT 12  
 HS71\_MOUSE  
 ID HS71\_MOUSE STANDARD; PRT; 641 AA.  
 AC P17879; O61689;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN HSPAL1 OR HSP70A1 OR HSP70-1 OR HCP70.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=90236310; PubMed=2332169;  
 RA Hunt C., Calderwood S.;  
 RT "Characterization and sequence of a mouse hsp70 gene and its  
 RT expression in mouse cell lines.";  
 RL Gene 87:199-204(1990).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Liver;  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Aujame L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from  
 RT Mus musculus.";  
 RL Gene 146:273-278(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES  
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF  
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET  
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION  
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.



```
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL; M35021; AAA37864.1; -
CC EMBL; M76613; AAA57233.1; -
CC PIR; JH0095; JH0095.
CC HSP; P19120; INGC.
CC MGD; MGI:99517; HSP70-1.
CC InterPro; IPR001023; HSP70.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 342 342 A -> R (IN REF. 1).
FT CONFLICT 627 627 P -> PP (IN REF. 1).
SQ SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 88.2%; Score 45; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDAYT 10
DB 286 SLFEGIDFYT 295
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RESULT 13
HS71_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPAL.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
RA Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
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CC EMBL; M69100; -; NOT_ANNOTATED_CDS.
CC PIR; S35718; S35718.
CC HSP; P19120; INGC.
CC InterPro; IPR001023; HSP70.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BE20A03E0A33 CRC64;

Query Match 88.2%; Score 45; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDAYT 10
DB 286 SLFEGIDFYT 295
|||||||

RESULT 14
HS71_RAT STANDARD; PRT; 641 AA.
AC Q07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
GN HSP70-1 AND HSP70-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94096443; PubMed=8271311;
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
RA Massa S.M., Sharp F.R.;
RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
RT and injured rat brain.";
RL J. Neurosci. Res. 36:325-335(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=LEW.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94368874; PubMed=8086479;
RA Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
RT "Cloning, nucleotide sequence and expression of rat heat inducible
RT hsp70 gene.";
RL Biochim. Biophys. Acta 1219:64-72(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----  
DR EMBL; L16764; AAA17441.1; -  
DR EMBL; X77208; CAA54423.1; -  
DR EMBL; X77207; CAA54422.1; -  
DR EMBL; X74271; CAA52328.1; -  
DR HSP; P19120; INGC.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70.1; 1.  
DR PROSITE; PS00329; HSP70.2; 1.  
DR PROSITE; PS01036; HSP70.3; 1.  
DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
KW CONFLICT 71 72 KR -> NG (IN REF. 3).  
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).  
FT CONFLICT 408 408 G -> A (IN REF. 3).  
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;  
  
Query Match 88.2%; Score 45; DB 1; Length 641;  
Best Local Similarity 90.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDAYT 10  
DB 286 SLFEGIDFYT 295  
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RESULT 15  
HS71\_YEAST STANDARD; PRT; 641 AA.  
AC P10591;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).  
GN SSA1 OR YAL005C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C;  
RX MEDLINE-89128457; PubMed-2644626;  
RA Slater M.R., Craig E.A.;  
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";  
RL Nucleic Acids Res. 17:805-806(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C / AB972;  
RX MEDLINE-95028152; PubMed-7941740;  
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,  
RA Delaney S., Ouellette B.F., Barton A.B., Kaback D.B., Bussey H.;  
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of  
RT the 42 kbp SP07-CEN1-CDX15 region.";  
RL Yeast 10:535-541(1994).  
RN [3]  
RP SEQUENCE OF 590-641 FROM N.A.  
RX MEDLINE-85087943; PubMed-6096826;  
RA Ogden R.C., Lee M.-C., Knapp G.;  
RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the  
RT substrates.";  
RL Nucleic Acids Res. 12:9367-9382(1984).  
RN [4]  
RP REVISIONS TO 207; 417 AND 421.  
RA Slater M.R.;

Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
[5]  
RL SEQUENCE OF 91-97 AND 325-341.  
RP STRAIN-S288C;  
RX MEDLINE-95203288; PubMed=7895733;  
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
RA Volpe T., Warner J.R., McLaughlin C.S.;  
RT "Protein identifications for a Saccharomyces cerevisiae protein  
RT database.";  
RL Electrophoresis 15:1466-1486(1994).  
[6]  
RN SEQUENCE OF 186-195.  
RP STRAIN-ATCC 38531 / Y41;  
RX MEDLINE-97089742; PubMed-8935650;  
RA Norbeck J., Blomberg A.;  
RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
RT Saccharomyces cerevisiae.";  
RL FEMS Microbiol. Lett. 137:1-8(1996).  
[7]  
RN ACETYLATION.  
RP Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
RA Volpe T., Warner J.R., McLaughlin C.S.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
CC !- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE  
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
CC !- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC !- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC -----  
DR EMBL; X12926; CAA31393.1; -  
DR EMBL; X22015; AAC04952.1; ALT\_SEQ.  
DR PIR; S25438; HHYAL.  
DR PIR; S42164; S42164.  
DR HSP; P19120; IATR.  
DR SWISS-2DPAGE; P10591; YEAST.  
DR YEPD; 9788; -  
DR SGD; S0000004; SSA1.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70.1; 1.  
DR PROSITE; PS00329; HSP70.2; 1.  
DR PROSITE; PS01036; HSP70.3; 1.  
KW Heat shock; ATP-binding; Multigene family; Acetylation.  
FT INIT\_MET 0 0  
FT MOD\_RES 1 1 ACETYLATION.  
SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;  
  
Query Match 88.2%; Score 45; DB 1; Length 641;  
Best Local Similarity 90.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 SLFEGIDAYT 10  
DB 282 SLFEGIDFYT 291  
|||||||  
Search completed: December 6, 2001, 08:00:52  
Job time: 420 sec



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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:54 ; Search time 170.25 Seconds  
(without alignments)  
8.592 Million cell updates/sec

Title: PEP2-MOD8A

Perfect score: 51

Sequence: 1 SLFEGIDAYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	88.2	146	5 Q9U667	Q9U667 littorina p
2	45	88.2	153	5 Q9U670	Q9U670 littorina s
3	45	88.2	155	5 Q9U669	Q9U669 littorina s
4	45	88.2	157	5 Q9U665	Q9U665 littorina p
5	45	88.2	158	5 Q9U671	Q9U671 littorina s
6	45	88.2	158	5 Q9U668	Q9U668 littorina p
7	45	88.2	158	5 Q9U666	Q9U666 littorina p
8	45	88.2	220	5 P81159	P81159 aplysia cal
9	45	88.2	221	5 P81157	P81157 aplysia cal
10	45	88.2	278	13 Q90520	Q90520 oncorhynch
11	45	88.2	367	13 Q98899	Q98899 fugu rubrip
12	45	88.2	455	11 Q63718	Q63718 rattus norv
13	45	88.2	467	5 Q44350	Q44350 chondrosia
14	45	88.2	467	5 Q44352	Q44352 petrobiona
15	45	88.2	467	5 Q9N792	Q9N792 guancha lac
16	45	88.2	468	5 Q44349	Q44349 funiculina
17	45	88.2	469	5 Q44351	Q44351 eunicella c
18	45	88.2	526	13 Q98897	Q98897 fugu rubrip
19	45	88.2	632	5 O15766	O15766 dictyostell

20	45	88.2	639	13 Q98900	Q98900 fugu rubrip
21	45	88.2	639	13 Q918F9	Q918F9 oryzias lat
22	45	88.2	640	5 Q93601	Q93601 caenorhabdi
23	45	88.2	640	13 Q93240	Q93240 paralichthy
24	45	88.2	641	11 Q63256	Q63256 rattus norv
25	45	88.2	641	11 Q9QWJ5	Q9QWJ5 mus musculu
26	45	88.2	645	5 Q96541	Q96541 setaria dig
27	45	88.2	645	5 Q9NJB7	Q9NJB7 wuchereria
28	45	88.2	645	5 Q9NGK9	Q9NGK9 wuchereria
29	45	88.2	647	3 O59855	O59855 schizosacch
30	45	88.2	650	10 Q9ZS55	Q9ZS55 arabidopsis
31	45	88.2	650	10 Q9LHA8	Q9LHA8 arabidopsis
32	45	88.2	652	10 P93937	P93937 ascohyllum
33	45	88.2	653	5 Q94805	Q94805 trichoplusi
34	45	88.2	659	5 Q9XZJ2	Q9XZJ2 crassostrea
35	45	88.2	663	5 Q24952	Q24952 geodia cydo
36	44	86.3	190	5 Q9U9B4	Q9U9B4 mytilus edu
37	44	86.3	467	5 O44346	O44346 asbestoplum
38	44	86.3	467	5 O44347	O44347 petrosia fi
39	44	86.3	467	5 Q9GPM5	Q9GPM5 monosiga ov
40	44	86.3	639	13 Q73922	Q73922 oreochromis
41	44	86.3	642	3 Q9UVW0	Q9UVW0 rhizopus st
42	44	86.3	643	6 Q9NLU2	Q9NLU2 saginus oe
43	44	86.3	651	3 Q9UVW1	Q9UVW1 rhizopus st
44	44	86.3	651	10 Q22664	Q22664 spinacia ol
45	44	86.3	653	5 Q17310	Q17310 ceratitidis c

#### ALIGNMENTS

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RESULT 1
Q9U667
ID Q9U667 PRELIMINARY; PRT; 146 AA.
AC Q9U667;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Littorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191828; AAF12787.1; -.
DR HSSP; P19120; 1BA1.
DR InterPro; IPR001023; HSP70.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

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Query Match 88.2%; Score 45; DB 5; Length 146;  
Best Local Similarity 90.0%; Pred. No. 0.37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SLFEGIDAYT 10
| | | | | | | |
Db 79 SLFEGIDFYT 88

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RESULT 2
Q9U670 PRELIMINARY; PRT; 153 AA.
ID Q9U670
AC Q9U670;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

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DT	01-JUN-2001 (TreeBLrel. 17, Last annotation update)
DE	HEAT-SHOCK PROTEIN (FRAGMENT).
DE	HSC70.
GN	Littorina scutulana.
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC	Neotaeniolglossa; Littorinoidea; Littorinidae; Littorina.
OX	NCBI_Taxid=31221;
[1]	
RN	SEQUENCE FROM N.A.
RP	Hohenlohe P.A.;
RA	"Heat-shock genes in the heat-stressed genus Littorina."
RT	Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF191825; AAF12784.1; ..
DR	HSSP; P19120; 1BA1
DR	Interpro: IPR001023; HSP70.
DR	PROSITE; PS01036; HSP70_3; 1.
FT	NON_TER 1
FT	NON_TER 153
FT	SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
SO	

Query Match 88.2%; Score 45; DB 5; Length 153;  
Best Local Similarity 90.0%; Pred. No. 0.39;  
Matches 9: Conservative 0; Mismatches 1; Indels

QY	1	SLFEGIDAYT	10
Pb	80	SLFEGIDFYT	89

RESULT	3	
ID	Q9U669	
IQ	PRELIMINARY;	PRT; 155 AA.
AC	Q9U669;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	HEAT-SHOCK PROTEIN (FRAGMENT).	
GN	HSC70.	
OS	Littorina scutulata.	
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;	
NC	Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.	
OX	NCBI_TaxID=31221;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Hohenlohe P. A.;	
RT	"Heat-shock genes in the heat-stressed genus Littorina.";	
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF191826; XAF12785.1; -.	
DR	HSSP; P19120; 1BA1.	
DR	InterPro; IPR001023; HSP70.	
DR	PROSITE; PS01036; HSP70_3; 1.	
FT	NON_TER	1
FT	NON_TER	155
SO	SEQUENCE	155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 88.2%; Score 45; DB 5; Length 155;  
Best Local Similarity 90.0%; Pred. No. 0.4;  
Matches 9; Conservative 0; Mismatches 1; Indels

Qy 1 SLFEGIDAYT 10  
Dbb 82 SLFEGIDFYT 91

RESULT	4
Q9U665	
ID	Q9U665
AC	Q9U665;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBlrel. 17, Last annotation update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
PRELIMINARY:	PRT; 157 AA.

DE	HEAT-SHOCK PROTEIN (FRAGMENT).
EN	HSC70.
GN	Littorina plena.
OS	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC	NeotaenioGLOSS; Littorinidae; Littorinina.
OX	NBI_TaxID=31219;
NC	[1]
RN	SEQUENCE FROM N.A.
RP	Hohenlohe P.A.;
RA	"Heat-shock genes in the heat-stressed genus Littorina.";
RT	Submitted (OCT-1999) to the EMBL/GenBank/DDJB databases.
RL	EMBL; AF191830; AAF12789.1; -.
DR	HSP; P19120; IBA1.
DR	HSP; P19120; IBA1.
DR	InterPro: IPR001023; HSP70.
DR	PRINTS: PR00301; HEATSHOCK70.
DR	PROSITE; PS01036; HSP70_3; 1.
FT	NON_TER 1
FT	NON_TER 157
FT	SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;
SO	

Query Match	88.2%	Score 45;	DB 5;	Length 157;
Best Local Similarity	90.0%	Pred. No. 0.4;		
Matches	9;	Conservative	0;	Mismatches
			1;	Indels
			0;	Gaps
			0;	Gaps

Qy	1	SLFEGIDAYT	10
Db	84	SLFEGIDFYT	93

[illegible]

Query Match 88.2%; Score 45; DB 5; Length 158;  
Best Local Similarity 90.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 1; Indels

Qy	1	SLFEGIDAYT	10
Db	85	SLFEGIDFYT	94
RESULT	6		
Q9U668		PRELIMINARY;	PRT; 158 AA.
ID	Q9U668		
AC	Q9U668;		
DT	01-MAY-2000	(TREMBlrel. 13,	Created)
DT	01-MAY-2000	(TREMBlrel. 13,	Last sequence update)



DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neocaeinoglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191827; AAF12786.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 88.2%; Score 45; DB 5; Length 158;  
Best Local Similarity 90.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 85 SLFEGIDFT 94

RESULT 7  
Q9U666 PRELIMINARY; PRT; 158 AA.  
ID Q9U666  
AC Q9U666;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neocaeinoglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191829; AAF12788.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 88.2%; Score 45; DB 5; Length 158;  
Best Local Similarity 90.0%; Pred. No. 0.41;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 85 SLFEGIDFT 94

RESULT 8  
P81159 PRELIMINARY; PRT; 220 AA.  
ID P81159  
AC P81159;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
GN HSC70.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93077669; PubMed=1360013;  
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
RT "Long-term sensitization training in Aplysia leads to an increase in the expression of Bip, the major protein chaperon of the ER.";  
RL J. Cell Biol. 119:1069-1076(1992)  
CC -!- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL; Z15039; CAA78757.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 220  
SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 88.2%; Score 45; DB 5; Length 220;  
Best Local Similarity 90.0%; Pred. No. 0.6;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 138 SLFEGIDFT 147

RESULT 9  
P81157 PRELIMINARY; PRT; 221 AA.  
ID P81157  
AC P81157;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).  
GN HSP70A.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93077669; PubMed=1360013;  
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
RT "Long-term sensitization training in Aplysia leads to an increase in the expression of Bip, the major protein chaperon of the ER.";  
RL J. Cell Biol. 119:1069-1076(1992).  
CC -!- INDUCTION: BY HEAT SHOCK.  
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL; Z15037; CAA78755.1; -.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 221  
SQ SEQUENCE 221 AA; 24404 MW; 853F794106E83CC9 CRC64;



Query Match 88.2%; Score 45; DB 5; Length 221;  
Best Local Similarity 90.0%; Pred. No. 0.6;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 139 SLFEGIDYTT 148  
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RESULT 10  
Q90520 PRELIMINARY; PRT; 278 AA.  
AC Q90520;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=85036330; PubMed=6092938;  
RA Kothary R.K., Jones D., Candido E.P.M.;  
RT \*70-Kilodalton heat shock polypeptides from rainbow trout:  
RT characterization of cDNA sequences.\*;  
RL Mol. Cell. Biol. 4:1785-1791(1984).  
DR EMBL; K02549; AAA49562.1; -;  
DR HSSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 278  
SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 88.2%; Score 45; DB 13; Length 278;  
Best Local Similarity 90.0%; Pred. No. 0.79;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 156 SLFEGIDYTT 165  
|||||||

RESULT 11  
Q98899 PRELIMINARY; PRT; 367 AA.  
AC Q98899;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
GN HSP70-3.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
[1]  
RN SEQUENCE FROM N.A.  
RA Lim E.H.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y08578; CAA69892.1; -;  
DR HSSP; P19120; 3HSC.  
DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock.  
FT NON\_TER 367  
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRC64;

Query Match 88.2%; Score 45; DB 13; Length 367;  
Best Local Similarity 90.0%; Pred. No. 1.1;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 268 SLFEGIDYTT 277  
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RESULT 12  
Q63718 PRELIMINARY; PRT; 455 AA.  
AC Q63718;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HEAT SHOCK ROTENIN 70 (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
RN SEQUENCE FROM N.A.  
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,  
RA D'Ambrosio E.;  
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z27118; CAA81642.1; -;  
DR HSSP; P08107; 1HJO.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock.  
FT NON\_TER 1  
FT NON\_TER 455  
SQ SEQUENCE 455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;

Query Match 88.2%; Score 45; DB 11; Length 455;  
Best Local Similarity 90.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
DB 254 SLFEGIDYTT 263  
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RESULT 13  
Q44350 PRELIMINARY; PRT; 467 AA.  
ID Q44350;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
GN HSP70.  
OS Chondrosia reniformis.  
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;  
OC Chondrosida; Chondrillidae; Chondrosia.  
OX NCBI\_TaxID=68574;  
[1]  
RN SEQUENCE FROM N.A.  
RP Borchlielini C., Le Parco Y.;



RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF026517; AAC05362.1; -.  
DR HSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 88.2%; Score 45; DB 5; Length 467;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
Db |||||||

RESULT 14

O44352 PRELIMINARY; PRT; 467 AA.  
AC O44352;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
GN HSP70.  
OS Petrobionta massiliiana.  
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarenea; Petrobionidae;  
OC Petrobionta.  
OX NCBI\_TaxID=68578;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borchelliini C., Le Parco Y.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF026520; AAC05364.1; -.  
DR HSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 88.2%; Score 45; DB 5; Length 467;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
Db |||||||

RESULT 15

Q9NJ92 PRELIMINARY; PRT; 467 AA.  
AC Q9NJ92;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
OS Guancha lacunosa.  
OC Eukaryota; Metazoa; Porifera; Calcarea; Clathrinida;  
OC Clathrinidae; Guancha.  
OX NCBI\_TaxID=115120;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Borchelliini C., Le Parco Y.;  
RT "Sponges paraphyly and the origin of Metazoa."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF182195; AAF61297.1; -.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match 88.2%; Score 45; DB 5; Length 467;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAYT 10  
Db |||||||

Search completed: December 6, 2001, 07:56:54  
Job time: 182 sec



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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:59 ; Search time 81.43 seconds  
(without alignments)  
2.764 Million cell updates/sec

Title: PEP2-MOD8F

Perfect score: 53

Sequence: 1 SLFEGIDFYT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA.\*
- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	98.1	643	4	US-08-797-358B-3
2	50	94.3	646	1	US-08-441-139-14
3	39	73.6	339	2	US-08-928-692-52
4	35	66.0	560	1	US-08-052-404-23
5	35	66.0	560	1	US-08-479-156-23
6	35	66.0	561	1	US-08-052-404-22
7	35	66.0	561	1	US-08-052-404-24
8	35	66.0	561	1	US-08-479-156-22
9	35	66.0	561	1	US-08-479-156-24
10	33	62.3	560	2	US-08-928-692-53
11	33	62.3	2787	4	US-09-245-041-15
12	33	62.3	4634	4	US-08-476-515A-84
13	33	62.3	4655	4	US-08-652-877-84
14	33	62.3	4655	4	US-08-652-877-86
15	33	62.3	4655	4	US-08-652-877-88
16	33	62.3	4655	4	US-08-652-877-90
17	32	60.4	418	4	US-08-855-910-11
18	32	60.4	436	2	US-08-899-028A-2
19	32	60.4	436	2	US-09-210-124-2
20	32	60.4	436	4	US-09-210-009-2
21	32	60.4	679	1	US-08-441-139-5
22	31	58.5	309	1	US-08-118-270-56
23	31	58.5	309	5	PCT-US93-08528-56
24	31	58.5	348	2	US-08-390-000A-8
25	31	58.5	458	4	US-09-457-046B-61
26	31	58.5	465	2	US-08-878-989-18
27	31	58.5	465	2	US-08-860-150-7

28	31	58.5	465	3	US-09-338-132-7	Sequence 7, Appli
29	31	58.5	465	4	US-09-272-796-18	Sequence 18, Appl
30	30	56.6	36	1	US-08-487-890A-19	Sequence 19, Appl
31	30	56.6	36	2	US-08-478-435-19	Sequence 19, Appl
32	30	56.6	36	2	US-08-337-483-19	Sequence 19, Appl
33	30	56.6	36	2	US-08-478-373-19	Sequence 19, Appl
34	30	56.6	36	3	US-08-474-671-19	Sequence 19, Appl
35	30	56.6	36	3	US-08-483-577A-19	Sequence 19, Appl
36	30	56.6	36	4	US-08-897-438-19	Sequence 19, Appl
37	30	56.6	43	4	US-09-312-183A-8	Sequence 8, Appli
38	30	56.6	53	2	US-08-469-537A-7	Sequence 7, Appli
39	30	56.6	53	2	US-08-469-537A-20	Sequence 20, Appl
40	30	56.6	276	1	US-08-467-155A-1	Sequence 1, Appli
41	30	56.6	276	2	US-08-628-198-1	Sequence 1, Appli
42	30	56.6	276	4	US-09-201-038-1	Sequence 1, Appli
43	30	56.6	276	5	PCT-US96-07343-1	Sequence 1, Appli
44	30	56.6	291	1	US-08-467-155A-11	Sequence 11, Appl
45	30	56.6	291	2	US-08-628-198-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-FEB-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 98.1%; Score 52; DB 4; Length 643;  
Best Local Similarity 90.0%; Pred. No. 0.032;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDFYT 10



CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.



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; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 560 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
;   IMMEDIATE SOURCE:
;   CLONE: Hum
; US-08-052-404-23

Query Match 66.0%; Score 35; DB 1; Length 560;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFT 10
Db 334 SLARGLDYT 343

RESULT 5
US-08-052-404-23
; Sequence 23, Application US/08479156
; Patent No. 5663066
; GENERAL INFORMATION:
; APPLICANT: Rabin, Nina
; APPLICANT: Nichols, Ralph
; APPLICANT: Plotz, Paul
; APPLICANT: Leff, Richard
; TITLE OF INVENTION: Human Histidyl tRNA Synthetase
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,156
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,404
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 560 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
;   IMMEDIATE SOURCE:
;   CLONE: Hum
; US-08-052-404-23

Query Match 66.0%; Score 35; DB 1; Length 560;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFT 10
Db 334 SLARGLDYT 343

RESULT 6
US-08-052-404-22
; Sequence 22, Application US/08052404
; Patent No. 5484703
; GENERAL INFORMATION:
; APPLICANT: Rabin, Nina
; APPLICANT: Nichols, Ralph
; APPLICANT: Plotz, Paul
; APPLICANT: Leff, Richard
; TITLE OF INVENTION: Human Histidyl tRNA Synthetase
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson, and Bear
; STREET: 620 Newport Center Dr. Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,404
; FILING DATE: 19930422
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 561 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
;   IMMEDIATE SOURCE:
;   CLONE: Yea
; US-08-052-404-22

Query Match 66.0%; Score 35; DB 1; Length 561;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFT 10
Db 335 SLARGLDYT 344

RESULT 7
US-08-052-404-24
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; Sequence 24, Application US/08052404  
; Patent No. 5484703  
; GENERAL INFORMATION:  
; APPLICANT: Rabin, Nina  
; APPLICANT: Nichols, Ralph  
; APPLICANT: Plotz, Paul  
; APPLICANT: Leff, Richard  
; TITLE OF INVENTION: Human Histidyl tRNA Synthetase  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson, and Bear  
; STREET: 620 Newport Center Dr. Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/052,404  
; FILING DATE: 19930422  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fuller, Michael L.  
; REGISTRATION NUMBER: 36,516  
; REFERENCE/DOCKET NUMBER: NIH031.001A  
; TELEPHONE: 619-235-8550  
; TELEFAX: 714-760-9502  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 561 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; IMMEDIATE SOURCE:  
; CLONE: Ham  
; US-08-052-404-24

Query Match 66.08; Score 35; DB 1; Length 561;  
Best Local Similarity 60.08; Pred. No. 50;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
||| :||:|  
Db 335 SLARGLDYIT 344

RESULT 8  
; Sequence 22, Application US/08479156  
; Patent No. 5663066  
; GENERAL INFORMATION:  
; APPLICANT: Rabin, Nina  
; APPLICANT: Nichols, Ralph  
; APPLICANT: Plotz, Paul  
; APPLICANT: Leff, Richard  
; TITLE OF INVENTION: Human Histidyl tRNA Synthetase  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson, and Bear  
; STREET: 620 Newport Center Dr. Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA

; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,156  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/052,404  
; FILING DATE: 22-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fuller, Michael L.  
; REGISTRATION NUMBER: 36,516  
; REFERENCE/DOCKET NUMBER: NIH031.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 714-760-9502  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 561 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; IMMEDIATE SOURCE:  
; CLONE: Yea  
; US-08-479-156-22

Query Match 66.08; Score 35; DB 1; Length 561;  
Best Local Similarity 60.08; Pred. No. 50;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
||| :||:|  
Db 335 SLARGLDYIT 344

RESULT 9  
; Sequence 24, Application US/08479156  
; Patent No. 5663066  
; GENERAL INFORMATION:  
; APPLICANT: Rabin, Nina  
; APPLICANT: Nichols, Ralph  
; APPLICANT: Plotz, Paul  
; APPLICANT: Leff, Richard  
; TITLE OF INVENTION: Human Histidyl tRNA Synthetase  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson, and Bear  
; STREET: 620 Newport Center Dr. Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,156  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/052,404



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; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: Ham
; US-08-479-156-24

Query Match 66.0%; Score 35; DB 1; Length 561;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||:|:|
Db 335 SLARGLDYIT 344

RESULT 10
US-08-928-692-53
; Sequence 53, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727 of No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: Ham
; US-08-479-156-24

Query Match 66.0%; Score 35; DB 1; Length 561;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||:|:|
Db 335 SLARGLDYIT 344

RESULT 10
US-08-928-692-53
; Sequence 53, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727 of No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: Ham
; US-08-479-156-24

Query Match 66.0%; Score 35; DB 1; Length 561;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||:|:|
Db 335 SLARGLDYIT 344

RESULT 10
US-08-928-692-53
; Sequence 53, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727 of No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: Ham
; US-08-479-156-24

Query Match 66.0%; Score 35; DB 1; Length 561;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||:|:|
Db 335 SLARGLDYIT 344

RESULT 10
US-08-928-692-53
; Sequence 53, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727 of No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: Ham
; US-08-479-156-24

Query Match 66.0%; Score 35; DB 1; Length 561;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||:|:|
Db 335 SLARGLDYIT 344

RESULT 10
US-08-928-692-53
; Sequence 53, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727 of No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L.
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH031.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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OPERATING SYSTEM: Windows 95  
SOFTWARE: Word 7.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,515A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/SE94/00483  
FILING DATE: 24-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9301764-8  
FILING DATE: 24-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4654 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-476-515A-84

Query Match 62.3%; Score 33; DB 4; Length 4654;  
Best Local Similarity 70.0%; Pred. No. 1.3e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFVT 10  
||||| I:|  
Db 608 SLFEGQVFFT 617

RESULT 13  
US-08-652-877-84  
Sequence 84, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd., 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.5.1  
SOFTWARE: Word 6.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,877  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: PCT/US95/15203

FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355E-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4655 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-652-877-84

Query Match 62.3%; Score 33; DB 4; Length 4655;  
Best Local Similarity 70.0%; Pred. No. 1.3e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLFEGIDFVT 10  
||||| I:|  
Db 608 SLFEGQVFFT 617

RESULT 14  
US-08-652-877-86  
Sequence 86, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Rask, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd., 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.5.1  
SOFTWARE: Word 6.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,877  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15203  
FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:



; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355E-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4655 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-652-877-86

Query Match 62.3%; Score 33; DB 4; Length 4655;  
Best Local Similarity 70.0%; Pred. No. 1.3e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDFT 10  
||||| I:I  
Db 608 SLFEGQVFT 617

RESULT 15  
US-08-652-877-88  
; Sequence 88, Application US/08652877  
; Patent No. 6187548  
; GENERAL INFORMATION:  
; APPLICANT: Akersstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjaln, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.,  
; STREET: 500 Arcola Rd., 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.5.1  
; SOFTWARE: Word 6.0 (patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,877  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/15203  
; FILING DATE: 22-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,314  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355E-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 4655 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-652-877-88

Query Match 62.3%; Score 33; DB 4; Length 4655;  
Best Local Similarity 70.0%; Pred. No. 1.3e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLFEGIDFT 10  
||||| I:I  
Db 608 SLFEGQVFT 617

Search completed: December 6, 2001, 07:59:59  
Job time: 367 sec



pep2-mod8f.ra1

Tue Dec 11 08:45:55 2001

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:28 ; Search time 88.19 seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: PEP2-MOD8F

Perfect score: 53

Sequence: 1 SLFEGIDFVT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	208	2 B44261	dnaK-type molecule
2	53	100.0	278	2 I51344	dnaK-type molecule
3	53	100.0	467	2 T45477	heat-shock protein
4	53	100.0	467	2 T45479	heat-shock protein
5	53	100.0	468	2 T45476	heat-shock protein
6	53	100.0	469	2 T45478	heat-shock protein
7	53	100.0	632	2 T45471	dnaK-type molecule
8	53	100.0	634	2 A25646	dnaK-type molecule
9	53	100.0	636	2 A48872	dnaK-type molecule
10	53	100.0	638	2 S31766	dnaK-type molecule
11	53	100.0	639	2 J01391	dnaK-type molecule
12	53	100.0	639	2 S20139	dnaK-type molecule
13	53	100.0	640	1 HHKW7A	dnaK-type molecule
14	53	100.0	640	2 A29160	dnaK-type molecule
15	53	100.0	640	2 S37394	dnaK-type molecule
16	53	100.0	640	2 T21394	hypothetical prote
17	53	100.0	640	2 T43724	dnaK-type molecule
18	53	100.0	641	2 S53357	dnaK-type molecule
19	53	100.0	641	2 S35718	dnaK-type molecule
20	53	100.0	641	2 I54542	dnaK-type molecule
21	53	100.0	641	2 A45871	dnaK-type molecule
22	53	100.0	642	1 HHBYA1	dnaK-type molecule
23	53	100.0	642	2 JH0095	dnaK-type molecule
24	53	100.0	642	2 B36590	dnaK-type molecule
25	53	100.0	644	2 A45635	dnaK-type molecule
26	53	100.0	645	2 I51129	dnaK-type molecule
27	53	100.0	646	2 T46650	heat shock protein
28	53	100.0	647	1 HHXL70	dnaK-type molecule
29	53	100.0	647	2 T41121	heat shock protein

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30      52      98.1      214      2      A03309      dnaK-type molecule
31      52      98.1      379      2      I46588      dnaK-type molecule
32      52      98.1      467      2      T45473      heat-shock protein
33      52      98.1      467      2      T45474      heat-shock protein
34      52      98.1      641      2      JN0668      dnaK-type molecule
35      52      98.1      641      2      PC7036      heat shock protein
36      52      98.1      643      2      S25585      dnaK-type molecule
37      52      98.1      643      2      S09036      dnaK-type molecule
38      52      98.1      651      2      T45517      heat shock protein
39      52      98.1      651      2      JC7132      heat shock protein
40      50      94.3      209      2      S48024      dnaK-type molecule
41      50      94.3      209      2      S48025      dnaK-type molecule
42      50      94.3      209      2      A44261      dnaK-type molecule
43      50      94.3      372      2      P00138      dnaK-type molecule
44      50      94.3      630      2      A34041      dnaK-type molecule
45      50      94.3      636      2      T45468      dnaK-type molecule

```

#### ALIGNMENTS

##### RESULT 1

B44261

dnaK-type molecular chaperone HSC70 - California sea hare (fragment)

N:Alternate names: heat shock protein 70 homolog HSC70

C:Species: Aplysia californica (California sea hare)

C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 13-Aug-1999

C:Accession: B44261

R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.

J. Cell Biol. 119, 1069-1076, 1992

A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr

A:Reference number: A44261; MUID:93077669

A:Accession: B44261

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-208 <KUR>

A>Note: sequence extracted from NCBI backbone (NCBIP:118950)

C:Genetics:

A:Gene: HSC70

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

```

Query Match      100.0%; Score 53; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLFEGIDFVT 10

DB 132 SLFEGIDFVT 141

##### RESULT 2

I51344

dnaK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)

N:Alternate names: 70K heat shock protein

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999

C:Accession: I51344

R:Kothary, R.K.; Jones, D.; Candido, E.P.M.

Mol. Cell. Biol. 4, 1785-1791, 1984

A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o

A:Reference number: I51344; MUID:85036330

A:Accession: I51344

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-278 <KOT>

A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PTD:g213804

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70



C;Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 53; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 0.0083;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
Db 156 SLFEGIDFYT 165

## RESULT 3

T45477  
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)  
C;Species: Chondrosia reniformis  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T45477  
R;Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z22983  
A;Accession: T45477  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-467 <BOR>  
A;Cross-references: EMBL:AF026517; PIDN:AAC05362.1  
C;Genetics:  
A;Gene: Hsp70  
C;Superfamily: heat shock protein 70

Query Match 100.0%; Score 53; DB 2; Length 467;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
Db 252 SLFEGIDFYT 261

## RESULT 4

T45479  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)  
C;Species: Eunicella cavolini  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T45479  
R;Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z22983  
A;Accession: T45479  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-467 <BOR>  
A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
C;Genetics:  
A;Gene: Hsp70  
C;Superfamily: heat shock protein 70

Query Match 100.0%; Score 53; DB 2; Length 467;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
Db 252 SLFEGIDFYT 261

## RESULT 5

T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
C;Species: Funiculina quadrangularis  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C;Accession: T45476  
R;Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z22983  
A;Accession: T45476  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-468 <BOR>  
A;Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
C;Genetics:  
A;Gene: Hsp70  
C;Superfamily: heat shock protein 70

Query Match 100.0%; Score 53; DB 2; Length 468;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
Db 253 SLFEGIDFYT 262

## RESULT 6

T45478  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)  
C;Species: Eunicella cavolini  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T45478  
R;Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z22983  
A;Accession: T45478  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-469 <BOR>  
A;Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C;Genetics:  
A;Gene: Hsp70  
C;Superfamily: heat shock protein 70

Query Match 100.0%; Score 53; DB 2; Length 469;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
Db 254 SLFEGIDFYT 263

## RESULT 7

T45471  
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)  
N;Alternate names: heat shock cognate protein 70  
C;Species: Dictyostelium discoideum  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
C;Accession: T45471  
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z22980  
A;Accession: T45471  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-632 <BOV>  
A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
A;Experimental source: strain AX3  
C;Genetics:  
A;Gene: hsc70  
A;Note: localized to filopodias and cortex  
C;Superfamily: heat shock protein 70



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Query Match      100.0%; Score 53; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
    |||||
Db 285 SLFEGIDFYT 294

RESULT 8
A25646
dnak-type molecular chaperone - chicken
N:Alternate names: heat shock protein 70
C:Species: Gallus gallus (chicken)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
A:Accession: A25646
R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
A:Reference number: A25646; MUID:86304452
A:Molecule type: DNA
A:Accession: A25646
A:Residues: 1-634 <MOR>
A:Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A:Note: the authors translated the codon TCG for residue 583 as Trp
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      100.0%; Score 53; DB 2; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
    |||||
Db 289 SLFEGIDFYT 298

RESULT 9
A48872
dnak-type molecular chaperone hspB - slime mold (Dictyostellium discoideum) (fragment)
N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agi
C:Species: Dictyostellium discoideum
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
C:Accession: A48872
R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an
A:Reference number: A48872; MUID:94043116
A:Accession: A48872
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-636 <EDD>
A:Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A:Note: authors translated the codon ACA for residue 10 as Pro, GGT for residue 60 as Va
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      100.0%; Score 53; DB 2; Length 636;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
    |||||
Db 280 SLFEGIDFYT 289

RESULT 10

```

```

S31766
dnak-type molecular chaperone hsp70 - green monkey
N:Alternate names: heat shock protein 70
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S31766; I36927
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot
A:Reference number: S31766
A:Accession: S31766
A:Molecule type: mRNA
A:Residues: 1-638 <SAI>
R:Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible
A:Reference number: I36927; MUID:95080396
A:Accession: I36927
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-638 <RES>
A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A:Experimental source: kidney; cell line COS-1
C:Genetics:
A:Gene: hsp70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match      100.0%; Score 53; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
    |||||
Db 284 SLFEGIDFYT 293

RESULT 11
JC1391
dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
N:Alternate names: heat shock protein 70IV; hsp70IV protein
C:Species: Paracentrotus lividus (common urchin)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C:Accession: JC1391
R:Sconzo, G.; Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp
A:Reference number: JC1391; MUID:93077053
A:Accession: JC1391
A:Molecule type: DNA
A:Residues: 1-639 <SCO>
A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917
C:Genetics:
A:Gene: hsp70IV
A:Introns: 61/2
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match      100.0%; Score 53; DB 2; Length 639;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
    |||||
Db 286 SLFEGIDFYT 295

```



## RESULT 12

S20139  
 dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: heat shock protein YG102; protein L0971; protein YLL024c  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C:Accession: S20139; S64772; S64775; S69383  
 R:Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A:Reference number: S20139  
 A:Accession: S20139  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SLA>  
 A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
 R:Goffeau, A.; Purnelle, B.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64761  
 A:Accession: S64772  
 A:Molecule type: DNA  
 A:Residues: 1-639 <GOF>  
 A:Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL024c  
 R:Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64775  
 A:Accession: S64775  
 A:Molecule type: DNA  
 A:Residues: 72-639 <DUE>  
 A:Cross-references: EMBL:Z73129; MIPS:YLL024c  
 A:Experimental source: strain S288C  
 R:Purnelle, B.; Goffeau, A.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14  
 mly and a new ABC transporter homologous to the human multidrug resistance protein.  
 A:Reference number: S69380  
 A:Accession: S69383  
 A:Molecule type: DNA  
 A:Residues: 1-639 <PUR>  
 A:Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007  
 C:Genetics:  
 A:Gene: SGD:SSA2  
 A:Cross-references: MIPS:YLL024c; SGD:S0003947  
 A:Map position: 12L  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein complex  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 53; DB 2; Length 639;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFYT 10

Db 283 SLFEGIDFYT 292

## RESULT 13

HNK7A  
 dnak-type molecular chaperone hsp70A - Caenorhabditis elegans  
 N:Alternate names: heat shock protein 70 A  
 C:Species: Caenorhabditis elegans  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
 C:Accession: JT0285  
 R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
 Gene 64, 241-255, 1988  
 A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterization  
 A:Reference number: JT0285; MUID:88297155  
 A:Accession: JT0285  
 A:Molecule type: DNA; mRNA

A:Residues: 1-640 <SNUG>

A:Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352

A:Note: genomic clones representing six distinct members of the hsp70 gene family were

A:Note: transcripts of hsp70A are abundant in control worms and also increase two- to

A:Note: one of the three introns in hsp70A is in a position similar to an intron in D

C:Genetics:

A:Gene: hsp70A

A:Map position: IV

A:Introns: 69/1; 331/3; 558/3

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 100.0%; Score 53; DB 1; Length 640;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFYT 10

Db 287 SLFEGIDFYT 296

## RESULT 14

A29160  
 dnak-type molecular chaperone HSPALL - human  
 N:Alternate names: heat shock protein, 70K  
 C:Species: Homo sapiens (man)  
 C>Date: 16-Aug-1988 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
 C:Accession: A29160; I37561; I37562  
 R:Hunt, C.; Morimoto, R.I.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985  
 A:Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the  
 A:Reference number: A29160; MUID:86016721  
 A:Accession: A29160  
 A:Molecule type: DNA  
 A:Residues: 1-640 <HUN>  
 A:Cross-references: GB:M11717; GB:M15432; NID:g184416; PIDN:AAA52697.1; PID:g386785  
 A:Note: the authors mistranslated residues 463, 491, and 492

R:Drabant, B.; Genthe, A.; Benecke, B.J.

Nucleic Acids Res. 14, 8933-8948, 1986

A:Title: In vitro transcription of a human hsp70 heat shock gene by extracts prepared

A:Reference number: I37561; MUID:87066768

A:Accession: I37561

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-22 <RES>

A:Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481

A:Accession: I37562

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 616-640 <RE2>

A:Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483

C:Genetics:

A:Gene: GDB:HSPALL; HSP70-HOM

A:Cross-references: GDB:I20058; OMIM:140559

A:Map position: 6p21.3-6p21.3

A:Introns: #status absent

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 53; DB 2; Length 640;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLFEGIDFYT 10

Db 286 SLFEGIDFYT 295



RESULT 15  
S37394  
dnaK-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostelium discoideum  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 20-Aug-1999  
C:Accession: S37394  
R:Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schl  
EMBO J. 12, 3763-3771, 1993  
A:Title: The heat shock cognate protein from Dictyostelium affects actin polymerization  
A:Reference number: S37394; MUID:94008983  
A:Accession: S37394  
A:Molecule type: mRNA  
A:Residues: 1-640 <HAU>  
A:Cross-references: EMBL:X75263; NID:9433874; PIDN:CAA53039.1; PID:9433875  
C:Genetics:  
A:Gene: hsc70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein compl  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 53; DB 2; Length 640;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 SLFEGIDFYT 10  
Db 284 SLFEGIDFYT 293

Search completed: December 6, 2001, 07:58:28  
Job time: 276 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:53 ; Search time 50.21 seconds  
(without alignments)  
7.302 Million cell updates/sec

Title: PEP2-MOD8F

Perfect score: 53

Sequence: 1 SLFEGIDFYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	53	100.0	322	1	HS70_ONCVO	P11503	onchocerca
2	53	100.0	503	1	HS70_PENCI	Q92260	penicillium
3	53	100.0	634	1	HS70_CHICK	P08106	gallus gall
4	53	100.0	638	1	HS71_CERAE	Q28222	cercopithec
5	53	100.0	638	1	HS72_YEAST	P10592	saccharomyc
6	53	100.0	639	1	HS74_PARLI	Q06248	paracentrot
7	53	100.0	640	1	HS7A_CAEEL	P09446	caenorhabdi
8	53	100.0	640	1	HS7C_DICDI	P36415	dictyosteli
9	53	100.0	641	1	HS7I_BOVIN	Q27975	bos taurus
10	53	100.0	641	1	HS7I_HUMAN	P08107	homo sapien
11	53	100.0	641	1	HS7I_MOUSE	P17879	mus muscucu
12	53	100.0	641	1	HS7I_PIG	P34930	sus scrofa
13	53	100.0	641	1	HS7I_RAT	Q07439	rattus norv
14	53	100.0	641	1	HS7I_YEAST	P10591	saccharomyc
15	53	100.0	641	1	HS72_BOVIN	Q27965	bos taurus
16	53	100.0	641	1	HS74_YEAST	P22202	saccharomyc
17	53	100.0	644	1	HS70_BRUMA	P27541	brugia mala
18	53	100.0	644	1	HS70_ONCTS	Q91233	oncorhynchu
19	53	100.0	645	1	HS70_PLENA	Q91291	pleurodeles
20	53	100.0	646	1	HS70_NEUCR	Q01233	neurospora
21	53	100.0	647	1	HS70_XENLA	P02827	xenopus lae
22	53	100.0	649	1	HS70_BLAEM	P48720	blastoclad
23	53	100.0	652	1	HS7D_MANSE	Q96639	manduca sex
24	52	98.1	214	1	HS7A_DROSI	P02826	drosophila
25	52	98.1	379	1	HS7X_PIG	P34934	sus scrofa
26	52	98.1	641	1	HS7A_DROME	P29843	drosophila
27	52	98.1	643	1	HS76_HUMAN	P17066	homo sapien
28	52	98.1	643	1	HS76_PIG	Q04967	sus scrofa
29	52	98.1	648	1	HS71_PUCGR	Q01877	puccinia gr
30	50	94.3	372	1	HS72_PARLI	P22623	paracentrot
31	50	94.3	641	1	HS73_RAT	P55063	rattus norv
32	50	94.3	641	1	HS7H_HUMAN	P34931	homo sapien
33	50	94.3	641	1	HS7T_MOUSE	P16627	mus muscucu

34	50	94.3	642	1	HS72_PICAN	P53623	pichia anqu
35	50	94.3	643	1	HS71_SCHPO	Q10265	schizosacch
36	50	94.3	644	1	HS71_PICAN	P53421	pichia angu
37	50	94.3	646	1	HS7C_CRIGR	P19378	cricketulus
38	50	94.3	646	1	HS7C_HUMAN	P11142	homo sapien
39	50	94.3	646	1	HS7C_MOUSE	P08109	mus muscucu
40	50	94.3	649	1	HS70_PARRR	P87047	paracoccidi
41	50	94.3	649	1	HS73_YEAST	P09435	saccharomyc
42	50	94.3	649	1	HS7C_BRARE	Q90473	brachydanio
43	50	94.3	650	1	HS7C_BOVIN	P19120	bos taurus
44	50	94.3	651	1	HS70_ONCMY	P08108	oncorhynchu
45	50	94.3	654	1	HS70_HYDMA	Q05944	hydra magni

#### ALIGNMENTS

```

RESULT 1
HS70_ONCVO STANDARD; PRT; 322 AA.
AC P11503.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201313; PubMed=2704388;
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in
amicrofilaremic individuals from a filariasis-endemic area.";
RL Mol. Biochem. Parasitol. 33:229-236(1989).
CC -!- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A
MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-----
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-----
CC EMBL; J04006; AAA29417.1; -.
DR HSSP; P19120; IATR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1
FT NON_TER 322
SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

```

Query Match 100.0%; Score 53; DB 1; Length 322;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
| | | | | | | | | |  
Db 43 SLFEGIDFYT 52

RESULT 2  
HS70\_PENCI STANDARD; PRT; 503 AA.  
ID HS70\_PENCI



```
AC Q92260;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
GN HSP70.
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
SEQUENCE FROM N.A.
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
RT "Molecular cloning and expression of a Penicillium citrinum
RT allergen with sequence homology and antigenic cross-reactivity to
RT a hsp70 human heat shock protein.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; U64207; AAB06397.1; -
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Allergen.
FT NON_TER
FT SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
CC -----
Query Match 100.0%; Score 53; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 SLFEGIDFYT 10
DB 154 SLFEGIDFYT 163
|||||||
CC -----
RESULT 3
ID HS70_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=96304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL; J02579; AAA48825.1; -
DR PIR; A25646; A25646.
DR HSP; P19120; IATR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
CC -----
Query Match 100.0%; Score 53; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 SLFEGIDFYT 10
DB 289 SLFEGIDFYT 298
|||||||
CC -----
RESULT 4.
ID HS71_CERAE STANDARD; PRT; 638 AA.
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL.
OC Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X70684; CAA50019.1; -
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DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PRO0301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||||
DB 284 SLFEGIDFYT 293

RESULT 5
HS72.YEAST STANDARD; PRT; 638 AA.
AC P10592;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YLL024C OR L0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [3]
RP SEQUENCE OF 71-638 FROM N.A.
RA Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC

SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- PTM: PHOSPHORYLATED.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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EMBL: X12927; CAA31394.1; -
EMBL: Z73129; CAA97472.1; -
EMBL: X97560; CAA66167.1; -
PIR: S20139; S20139.
DR HSP: P19120; INGJ.
DR SWISS-2DPAGE; P10592; YEAST.
DR YEPD; 9800; -.
DR SGD; S0003947; SSA2.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PRO0301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation;
KW Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
   |||||
DB 282 SLFEGIDFYT 291

RESULT 6
HS74.PARLI STANDARD; PRT; 639 AA.
AC Q06248;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
GN HSP70IV.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
lividus hsp70 gene family and its expression.";
RL Gene 121:353-358(1992).
RN [2]
RP -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
-----
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CC -----
DR EMBL; X61379; CAA43653.1; -.
DR PIR; JCI391; JCI391.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 100.0%; Score 53; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
|||||
DB 286 SLFEGIDFYT 295

RESULT 7
HS7A_CAEEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
characterization.";
RL Gene 64:241-255(1988).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M18540; AAA28078.1; -.
DR PIR; JTO285; HRKW7A.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
|||||

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Db 287 SLFEGIDFYT 296

RESULT 8
HS7C_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OC NCBI_TaxID=44689;
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN=AX3;
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,
RA Noegel A.A., Schleicher M.;
RT "The heat shock cognate protein from Dictyostelium affects actin
polymerization through interaction with the actin-binding protein
cap32/34.";
RT cap32/34.";
RL EMBO J. 12:3763-3771(1993).
RN 2
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RX STRAIN=AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aginactin, an agonist-regulated F-actin capping activity is
associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -1- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -1- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X75263; CAA53039.1; -.
DR EMBL; L22736; AAA33219.1; -.
DR PIR; S37394; S37394.
DR HSP; P19120; INGI.
DR SWISS-2DPAGE; P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone.
KW CONFLICT 1 29
FT FT 32 32
FT FT N -> T (IN REF. 2).
FT FT V -> A (IN REF. 2).
FT FT R -> A (IN REF. 2).
FT FT S -> A (IN REF. 2).
FT FT V -> A (IN REF. 2).
FT FT I -> L (IN REF. 2).
FT FT F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;
MSSIGIDLGTYSYCVGVNDRVLLIAND ->
IHHHNGNATWVSGVPSEVLSPN (IN REF. 2).

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KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLFEGIDFYT 10
    |||||
Db 284 SLFEGIDFYT 293

RESULT 9
HS71_BOVIN
ID HS71_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerrero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN=ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "Ap Alu1 polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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-----
CC EMBL; U09861; AAA73914.1; -.
CC EMBL; U02891; AAA03450.1; -.
CC HSSP; P19120; INGC.
CC InterPro: IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PK00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLFEGIDFYT 10
    |||||
Db 286 SLFEGIDFYT 295

RESULT 10
HS71_HUMAN
ID HS71_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQM0; Q9UQL9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1) (HSP70-1/HSP70-2).
GN HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91055806; PubMed=1700760;
RA Milner C.M., Campbell R.D.;
RT "Structure and expression of the three MHC-linked HSP70 genes.";
RL Immunogenetics 32:242-251(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016721; PubMed=3931075;
RA Hunt C., Morimoto R.I.;
RT "Conserved features of eukaryotic hsp70 genes revealed by comparison
with the nucleotide sequence of human hsp70.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
RN [3]
RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
region.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
RX MEDLINE=89184548; PubMed=2538825;
RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
RT "Human major histocompatibility complex contains genes for the major
heat shock protein HSP70.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
RN [5]
RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.
RX MEDLINE=87066768; PubMed=3786141;
RA Drabant B., Genthe A., Benecke B.-J.;
RT "In vitro transcription of a human hsp 70 heat shock gene by extracts
prepared from heat-shocked and non-heat-shocked human cells.";
RL Nucleic Acids Res. 14:8933-8949(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
RX MEDLINE=99234376; PubMed=10216320;
RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
RT "Structure of a new crystal form of human hsp70 ATPase domain.";
RL Acta Crystallogr. D 55:1105-1107(1999).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC EMBL; U09861; AAA73914.1; -.
CC EMBL; U02891; AAA03450.1; -.
CC HSSP; P19120; INGC.
CC InterPro: IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PK00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
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CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC
CC -!- INDUCTION: BY HEAT SHOCK.
CC
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M59828; AAA63226.1; -
CC EMBL; M59830; AAA63227.1; -
CC EMBL; AF134726; AAD21816.1; -
CC EMBL; AF134726; AAD21815.1; -
CC EMBL; M11717; AAA52697.1; -
CC EMBL; M24743; AAA59844.1; -
CC EMBL; M24744; AAA59845.1; -
CC EMBL; X04676; CAA28381.1; -
CC EMBL; X04677; CAA28382.1; -
CC PIR; A29160; A29160.
CC PIR; A45871; A45871.
CC PIR; A25773; A25773.
CC FDB; IHQJ; 21-OCT-98.
CC SWISS-2DPAGE; P08107; HUMAN.
CC MIM; 140550; -
CC MIM; 603012; -
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70.1
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70.1; 1.
CC PROSITE; PS00329; HSP70.2; 1.
CC PROSITE; PS01036; HSP70.3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;
CC 3D-structure. 7 7 I -> V (IN REF. 2).
CC CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).
CC CONFLICT 370 370 A -> G (IN REF. 2).
CC CONFLICT 469 469 MISSING (IN REF. 2).
CC CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).
CC SEQUENCE 641 AA; 70052 MW; 78P513118C96DE66 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 286 SLFEGIDFYT 295
|||||

RESULT 11
HS7L_MOUSE STANDARD; PRT; 641 AA.
AC P17879; Q61689;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).
GN HSPAL OR HSP70A1 OR HSP70-1 OR HCP70.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169;
```

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RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
RL expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=94357449; PubMed=8076831;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from
RL Mus musculus.";
RL Gene 146:273-278(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M35021; AAA37864.1; -
CC EMBL; M76613; AAA57233.1; -
CC PIR; JH0095; JH0095.
CC HSP; P19120; LNCG.
CC MGD; MGI:99517; Hsp70-1.
CC InterPro; IPR001023; HSP70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PROSITE; PS00297; HSP70.1; 1.
CC PROSITE; PS00329; HSP70.2; 1.
CC PROSITE; PS01036; HSP70.3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
CC CONFLICT 342 342 A -> R (IN REF. 1).
CC CONFLICT 627 627 P -> PP (IN REF. 1).
CC SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 286 SLFEGIDFYT 295
|||||

RESULT 12
HS7L_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPAL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
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RA Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M69100; -; NOT_ANNOTATED_CDS.
DR PIR; S35718; S35718.
DR HSP; P19120; INGC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db |||||
286 SLFEGIDFYT 295

RESULT 13
HS71_RAT
ID HS71_RAT STANDARD; PRT; 641 AA.
AC Q07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
GN HSP70-1 AND HSP70-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94096443; PubMed=8271311;
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
RA Massa S.M., Sharp F.R.;
FT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
FT and injured rat brain.";
RL J. Neurosci. Res. 36:325-335(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).

```

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RN SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94368874; PubMed=8086479;
RA Lisowska K., Krawczyk Z., Widiak W., Wolniczek P., Wisniewski J.;
RT "Cloning, nucleotide sequence and expression of rat heat inducible
RT hsp70 gene.";
RL Biochim. Biophys. Acta 1219:64-72(1994).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL; L16764; AAA17441.1; -
DR EMBL; X77208; CAA54423.1; -
DR EMBL; X77207; CAA54422.1; -
DR EMBL; X74271; CAA52328.1; -
DR HSP; P19120; INGC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 71 72 KR -> NG (IN REF. 3).
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).
FT CONFLICT 408 408 G -> A (IN REF. 3).
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db |||||
286 SLFEGIDFYT 295

RESULT 14
HS71_YEAST
ID HS71_YEAST STANDARD; PRT; 641 AA.
AC P10591;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
GN SSA1 OR YAL005C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";

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Heat shock; ATP-binding; Multigene family; Acetylation.
INIT_MET 0 0 ACETYLATION.
MOD_RES 1
SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;
Best local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFT 10
| | | | | | | | | |
DB 282 SLFEGIDFT 291

RESULT 15
HS72_BOVIN
IID HS72_BOVIN STANDARD; PRT; 641 AA.
AC Q27965; Q28122;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 2 (HSP70-2).
GN HSP70-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RS SEQUENCE FROM N.A.
RP STRAIN=ANGUS;
RC Groz M.D., Skow L.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RS SEQUENCE OF 1-28 FROM N.A.
RP TISSUE=Liver;
RC Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,
RA van den Hurk J., Babiuk L.A., Zamb T.J.;
RT "Heat-shock promoter-driven synthesis of secreted bovine herpesvirus
glycoproteins in transfected cells.";
RL Vaccine 11:1100-1107(1993).
CC -!- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.
CC -!- INDUCTION: BY HEAT SHOCK.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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EMBL; U02892; AAA03451.1; -
DB EMBL; M98823; AAA30568.1; -
DR HSPSP; P19120; INGI
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.

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DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family.  
SQ SEQUENCE 641 AA; 70228 MW; 229C19EEBBF610DF CRC64;

Query Match 100.0%; Score 53; DB 1; Length 641;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
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|  
|  
|  
Db 286 SLFEGIDFYT 295

Search completed: December 6, 2001, 08:00:53  
Job time: 421 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:54 ; Search time 170.25 seconds  
(without alignments)  
8.592 Million cell updates/sec

Title: PEP2-MOD8F

Perfect score: 53  
Sequence: 1 SLFEGIDFYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Watch 100%

Listing first 45 summaries

Database :

SPTREMBL\_17 :  
1: sp\_archaea :  
2: sp\_bacteria :  
3: sp\_fungi :  
4: sp\_human :  
5: sp\_invertebrate :  
6: sp\_mammal :  
7: sp\_mhc :  
8: sp\_organelle :  
9: sp\_phase :  
10: sp\_plant :  
11: sp\_rodent :  
12: sp\_virus :  
13: sp\_vertebrate :  
14: sp\_unclassified :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	146	5 Q9U667	Q9U667 littorina p
2	53	100.0	153	5 Q9U670	Q9U670 littorina s
3	53	100.0	155	5 Q9U669	Q9U669 littorina s
4	53	100.0	157	5 Q9U665	Q9U665 littorina p
5	53	100.0	158	5 Q9U671	Q9U671 littorina s
6	53	100.0	158	5 Q9U668	Q9U668 littorina p
7	53	100.0	158	5 Q9U666	Q9U666 littorina p
8	53	100.0	220	5 P81159	P81159 aplysia cal
9	53	100.0	278	13 Q90520	Q90520 oncorhynch
10	53	100.0	367	13 Q98899	Q98899 fuigu rubrip
11	53	100.0	455	11 Q63718	Q63718 rattus norv
12	53	100.0	467	5 O44350	O44350 chondrosia
13	53	100.0	467	5 O44352	O44352 petrobiona
14	53	100.0	467	5 Q9NJ92	Q9NJ92 guancha lac
15	53	100.0	468	5 O44349	O44349 funiculina
16	53	100.0	469	5 O44351	O44351 eunicella c
17	53	100.0	526	13 Q98897	Q98897 fuigu rubrip
18	53	100.0	632	5 O15766	O15766 dictyosteli
19	53	100.0	639	13 Q98900	Q98900 fuigu rubrip

20	53	100.0	639	13 Q918F9	Q918f9 oryzias lat
21	53	100.0	640	5 Q93601	Q93601 caenorhabdi
22	53	100.0	640	13 Q93240	Q93240 paralichthy
23	53	100.0	641	11 Q63256	Q63256 rattus norv
24	53	100.0	641	11 Q90WJ5	Q90WJ5 mus musculu
25	53	100.0	645	5 Q96541	Q96541 setaria dig
26	53	100.0	645	5 Q9NJB7	Q9NJB7 wuchereria
27	53	100.0	645	5 Q9NGK9	Q9NGK9 wuchereria
28	53	100.0	647	3 Q59855	Q59855 schizosacch
29	53	100.0	650	10 Q9ZS55	Q9ZS55 arabidopsis
30	53	100.0	650	10 Q9LHA8	Q9LHA8 arabidopsis
31	53	100.0	652	10 P93937	P93937 ascophyllum
32	53	100.0	653	5 Q94805	Q94805 trichoplusi
33	53	100.0	659	5 Q9XZJ2	Q9XZJ2 crassostrea
34	52	98.1	190	5 Q9U9B4	Q9U9B4 mytilus edu
35	52	98.1	467	5 O44346	O44346 asbestoplum
36	52	98.1	467	5 O44347	O44347 petrosia fi
37	52	98.1	467	5 Q9GPM5	Q9GPM5 monosiga ov
38	52	98.1	639	13 Q73922	Q73922 oreochromis
39	52	98.1	642	3 Q9UVM0	Q9UVM0 rhizopus st
40	52	98.1	643	6 Q9NLU2	Q9NLU2 saguinus oe
41	52	98.1	651	3 Q9UVM1	Q9UVM1 rhizopus st
42	52	98.1	651	10 O22664	O22664 spinacia ol
43	52	98.1	653	5 Q17310	Q17310 ceratitis c
44	52	98.1	656	5 O61226	O61226 sycon rapha
45	50	94.3	139	6 Q29578	Q29578 sus scrofa

#### ALIGNMENTS

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RESULT 1
Q9U667 ID Q9U667 PRELIMINARY; PRT; 146 AA.
AC Q9U667;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Littorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191828; AAF12787.1; -.
DR HSSP; P19120; IBA1.
DR InterPro; IPR001023; HSP70.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16607 MW; C3F3556A1AF438BB CRC64;

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Query Match 100.0%; Score 53; DB 5; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLFEGIDFYT 10
    |||||
Db 79 SLFEGIDFYT 88

RESULT 2
Q9U670 ID Q9U670 PRELIMINARY; PRT; 153 AA.
AC Q9U670;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

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DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191825; AAF12784.1; -.  
 DR HSSP; P19120; 1BAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 153  
 SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 100.0%; Score 53; DB 5; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||  
 Db 80 SLFEGIDFYT 89

RESULT 3  
 Q9U669 PRELIMINARY; PRT; 155 AA.  
 AC Q9U669;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191826; AAF12785.1; -.  
 DR HSSP; P19120; 1BAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 155  
 SQ SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 100.0%; Score 53; DB 5; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||  
 Db 82 SLFEGIDFYT 91

RESULT 4  
 Q9U665 PRELIMINARY; PRT; 157 AA.  
 AC Q9U665;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

---

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191830; AAF12789.1; -.  
 DR HSSP; P19120; 1BAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 100.0%; Score 53; DB 5; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||  
 Db 84 SLFEGIDFYT 93

RESULT 5  
 Q9U671 PRELIMINARY; PRT; 158 AA.  
 AC Q9U671;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutulata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191824; AAF12783.1; -.  
 DR HSSP; P19120; 1BAL.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1  
 FT NON\_TER 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 100.0%; Score 53; DB 5; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
 |||||  
 Db 85 SLFEGIDFYT 94

RESULT 6  
 Q9U668 PRELIMINARY; PRT; 158 AA.  
 AC Q9U668;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)



DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191827; AAF12786.1; -  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 100.0%; Score 53; DB 5; Length 158;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDFYT 10  
Db |||||  
85 SLFEGIDFYT 94

RESULT 7  
Q90666 PRELIMINARY; PRT; 158 AA.  
AC Q90666;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191829; AAF12788.1; -  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 158  
SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match 100.0%; Score 53; DB 5; Length 158;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDFYT 10  
Db |||||  
85 SLFEGIDFYT 94

RESULT 8  
P81159 PRELIMINARY; PRT; 220 AA.  
ID P81159  
AC P81159;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HEAT-SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
GN HSC70.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasipidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93077669; PubMed=1360013;  
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
RT "Long-term sensitization training in Aplysia leads to an increase in the expression of Bip, the major protein chaperon of the ER.";  
RL J. Cell Biol. 119:1069-1076(1992)  
CC -!- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
CC -!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
DR EMBL; Z15039; CAA78757.1; -  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 220  
SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 100.0%; Score 53; DB 5; Length 220;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDFYT 10  
Db |||||  
138 SLFEGIDFYT 147

RESULT 9  
Q90520 PRELIMINARY; PRT; 278 AA.  
AC Q90520;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=85036330; PubMed=6092938;  
RA Kothary R.K., Jones D., Candido E.P.M.;  
RT "70-Kilodalton heat shock polypeptides from rainbow trout: characterization of cDNA sequences.";  
RL Mol. Cell. Biol. 4:1785-1791(1984).  
DR EMBL; K02549; AAA49562.1; -  
DR HSSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 278  
SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 100.0%; Score 53; DB 13; Length 278;



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Best Local Similarity 100.0%; Pred. No. 0.028; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 SLFEGIDFYT 10
Db 156 SLFEGIDFYT 165
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RESULT 10
Q98899 ID Q98899 PRELIMINARY; PRT; 367 AA.
AC Q98899;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).
GN HSP70-3.
OS Fugu rubripes (Japanese pufferfish) ("Takifugu rubripes").
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Lim E.H.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08578; CAA69892.1; -.
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock. 367 367
FT NON_TER 367 367
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6B3C2CA CRC64;

Query Match 100.0%; Score 53; DB 13; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 268 SLFEGIDFYT 277
|||||

RESULT 11
Q63718 ID Q63718 PRELIMINARY; PRT; 455 AA.
AC Q63718;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HEAT SHOCK ROTEIN 70 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA D'Ambrosio E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z27118; CAA81642.1; -.
DR HSP; P08107; 1HJO.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock.

Best Local Similarity 100.0%; Score 53; DB 5; Length 467;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 252 SLFEGIDFYT 261
|||||

RESULT 13
Q44352 ID Q44352 PRELIMINARY; PRT; 467 AA.
AC Q44352;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massilliana.
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarenea; Petrobionidae;
OC Petrobiona.
OX NCBI_TaxID=68578;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelli C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
KW Heat shock.

Best Local Similarity 100.0%; Score 53; DB 5; Length 467;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10
Db 252 SLFEGIDFYT 261
|||||

RESULT 13
Q44352 ID Q44352 PRELIMINARY; PRT; 467 AA.
AC Q44352;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massilliana.
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarenea; Petrobionidae;
OC Petrobiona.
OX NCBI_TaxID=68578;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelli C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026520; AAC05364.1; -.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
KW Heat shock.
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DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match 100.0%; Score 53; DB 5; Length 467;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
DB 252 SLFEGIDFYT 261

## RESULT 14

Q9NJ92 PRELIMINARY; PRT; 467 AA.

AC Q9NJ92;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
OS Guancha lacunosa.  
OC Eukaryota; Metazoa; Porifera; Calcarea; Clathrinida;  
OC Clathrinidae; Guancha.  
OX NCBI\_TaxID=115120;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Borchelli C., Le Parco Y.;  
RT "Sponges paraphyly and the origin of Metazoa";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF182195; AAF61297.1; -;  
DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
FT NON\_TER 1  
FT NON\_TER 467  
SQ SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match 100.0%; Score 53; DB 5; Length 467;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
DB 252 SLFEGIDFYT 261

## RESULT 15

O44349 PRELIMINARY; PRT; 468 AA.

AC O44349;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
GN HSP70.  
OS Funiculina quadrangularis.  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Funiculinidae;  
OC Funiculina.  
OX NCBI\_TaxID=68568;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Borchelli C., Le Parco Y.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026516; AAC05361.1; -;  
DR HSSP; P08109; 1CKR.  
DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; UNKNOWN\_1.  
FT NON\_TER 1  
FT NON\_TER 468  
SQ SEQUENCE 468 AA; 51533 MW; EDED2B469283FBC CRC64;

Query Match 100.0%; Score 53; DB 5; Length 468;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDFYT 10  
|||||  
DB 253 SLFEGIDFYT 262

Search completed: December 6, 2001, 07:56:54  
Job time: 182 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:59 ; Search time 81.43 Seconds  
(without alignments)  
2.764 Million cell updates/sec

Title: PEP2-MOD8G

Perfect score: 53

Sequence: 1 SLFEGIDGVT 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA.\*

1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCT05\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	81.1	643	4 US-08-797-358B-3	Sequence 3, Appli
2	41	77.4	646	1 US-08-441-139-14	Sequence 14, Appl
3	38	71.7	303	2 US-08-599-171A-32	Sequence 32, Appl
4	38	71.7	303	2 US-08-646-590B-32	Sequence 32, Appl
5	38	71.7	303	3 US-09-069-226-32	Sequence 32, Appl
6	38	71.7	303	4 US-09-412-184-32	Sequence 32, Appl
7	37	69.8	108	2 US-08-483-695-42	Sequence 42, Appl
8	37	69.8	108	2 US-07-965-285-42	Sequence 42, Appl
9	37	69.8	108	2 US-08-487-231-42	Sequence 42, Appl
10	37	69.8	108	4 US-09-201-912-42	Sequence 42, Appl
11	37	69.8	139	4 US-08-444-818-173	Sequence 173, App
12	37	69.8	269	1 US-08-440-103-16	Sequence 16, Appl
13	37	69.8	269	1 US-08-440-542-16	Sequence 16, Appl
14	37	69.8	269	1 US-08-231-368-16	Sequence 16, Appl
15	37	69.8	269	1 US-08-440-210-16	Sequence 16, Appl
16	37	69.8	269	4 US-09-046-604-16	Sequence 16, Appl
17	37	69.8	314	4 US-08-612-973-42	Sequence 42, Appl
18	37	69.8	314	4 US-08-927-597-42	Sequence 42, Appl
19	37	69.8	319	4 US-08-612-973-44	Sequence 44, Appl
20	37	69.8	319	4 US-08-927-597-44	Sequence 44, Appl
21	37	69.8	338	4 US-08-612-973-38	Sequence 38, Appl
22	37	69.8	338	4 US-08-927-597-38	Sequence 38, Appl
23	37	69.8	343	4 US-08-612-973-40	Sequence 40, Appl
24	37	69.8	343	4 US-08-927-597-40	Sequence 40, Appl
25	37	69.8	402	1 US-08-460-806-2	Sequence 2, Appli
26	37	69.8	402	1 US-08-460-806-9	Sequence 9, Appli
27	37	69.8	402	1 US-08-325-630-2	Sequence 2, Appli

28	37	69.8	402	1 US-08-325-630-9	Sequence 9, Appli
29	37	69.8	428	1 US-08-050-132A-2	Sequence 2, Appli
30	37	69.8	428	3 US-08-750-222A-2	Sequence 2, Appli
31	37	69.8	428	3 US-08-815-652B-2	Sequence 2, Appli
32	37	69.8	428	4 US-08-254-353A-2	Sequence 2, Appli
33	37	69.8	428	5 PCT-US92-05374A-2	Sequence 2, Appli
34	37	69.8	428	5 PCT-US95-07084-2	Sequence 2, Appli
35	37	69.8	463	4 US-08-612-973-46	Sequence 46, Appl
36	37	69.8	463	4 US-08-927-597-46	Sequence 46, Appl
37	37	69.8	480	1 US-08-440-103-18	Sequence 18, Appl
38	37	69.8	480	1 US-08-440-542-18	Sequence 18, Appl
39	37	69.8	480	1 US-08-231-368-18	Sequence 18, Appl
40	37	69.8	480	1 US-08-440-210-18	Sequence 18, Appl
41	37	69.8	480	4 US-09-046-604-18	Sequence 18, Appl
42	37	69.8	490	4 US-08-612-973-36	Sequence 36, Appl
43	37	69.8	490	4 US-08-927-597-36	Sequence 36, Appl
44	37	69.8	692	4 US-08-612-973-48	Sequence 48, Appl
45	37	69.8	692	4 US-08-927-597-48	Sequence 48, Appl

## ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
; Sequence 3, Application US/08797358B  
; Patent No. 6268478  
; GENERAL INFORMATION:  
; APPLICANT: Adams, John  
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,358B  
; FILING DATE: 11-Feb-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/011,491  
; FILING DATE: 12-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-CE 3165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 643 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 81.1%; Score 43; DB 4; Length 643;  
Best Local Similarity 80.0%; Pred. No. 2.2;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGVT 10



```

Db      288 SLFEGVDFT 297
|||||:| |
RESULT 2
US-08-441-139-14
; Sequence 14, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441.139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 646 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-14

Query Match 77.4%; Score 41; DB 1; Length 646;
Best Local Similarity 80.0%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 SLFEGIDGYT 10
||:|||| |
Db 286 SLVEGIDFT 295

RESULT 3
US-08-599-171A-32
; Sequence 32, Application US/08599171A
; Patent No. 5814473
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY

```



NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-646-590B-32

Query Match 71.7%; Score 38; DB 2; Length 303;  
Best Local Similarity 77.8%; Pred. No. 8.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|:||||||  
Db 34 SIFEGIRGY 42

RESULT 5  
US-09-069-226-32  
; Sequence 32, Application US/09069226  
; Patent No. 6013509  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, Patrick V.  
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,226  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,171  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HERRON, CHARLES J.  
REGISTRATION NUMBER: 28,019  
REFERENCE/DOCKET NUMBER: 331400-38  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-069-226-32

Query Match 71.7%; Score 38; DB 3; Length 303;  
Best Local Similarity 77.8%; Pred. No. 8.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|:||||||  
Db 34 SIFEGIRGY 42

RESULT 6  
US-09-412-184-32  
; Sequence 32, Application US/09412184  
; Patent No. 6268188  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Patrick V.  
; APPLICANT: Swanson, Ronald V.  
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/412,184  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,590  
FILING DATE: 08-May-1996  
APPLICATION NUMBER: 08/599,171  
FILING DATE: 09-FEB-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/01094  
FILING DATE: 21-January-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/017001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-412-184-32

Query Match 71.7%; Score 38; DB 4; Length 303;  
Best Local Similarity 77.8%; Pred. No. 8.3;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGY 9  
|:||||||  
Db 34 SIFEGIRGY 42

RESULT 7  
US-08-483-695-42  
; Sequence 42, Application US/08483695  
; Patent No. 5866139  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Krensdorf, Dina  
; APPLICANT: Porchon, Colette



```

; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ATTORNEY/AGENT INFORMATION:
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,695
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,285
; FILING DATE: 18-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-483-695-42

Query Match 69.8%; Score 37; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGDGYT 10
Db 44 LFAGVGDGHT 52

RESULT 8
US-07-965-285-42
; Sequence 42, Application US/07965285
; Patent No. 5879904
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Krensdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ATTORNEY/AGENT INFORMATION:
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,231
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-965-285-42

Query Match 69.8%; Score 37; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGDGYT 10
Db 44 LFAGVGDGHT 52

RESULT 9
US-08-487-231-42
; Sequence 42, Application US/08487231
; Patent No. 5919454
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Krensdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ATTORNEY/AGENT INFORMATION:
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,231
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.

```



; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-487-231-42

Query Match 69.8%; Score 37; DB 2; Length 108;  
Best Local Similarity 66.7%; Pred. No. 4;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGDGYT 10  
|||:|:|:  
Db 44 LFAGVDGHT 52

RESULT 10  
US-09-201-912-42  
; Sequence 42, Application US/09201912  
; Patent No. 6210962  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/09/201,912  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,285  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-201-912-42

Query Match 69.8%; Score 37; DB 4; Length 108;  
Best Local Similarity 66.7%; Pred. No. 4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 LFEIGDGYT 10  
|||:|:|:  
Db 44 LFAGVDGHT 52

RESULT 11  
US-08-444-818-173  
; Sequence 173, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 173:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Japanese isolate (T. Miyamura)  
US-08-444-818-173

Query Match 69.8%; Score 37; DB 4; Length 139;  
Best Local Similarity 66.7%; Pred. No. 5.3;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGDGYT 10  
|||:|:|:  
Db 78 LFAGVDGHT 86

RESULT 12  
US-08-440-103-16  
; Sequence 16, Application US/08440103  
; Patent No. 5670152  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Amy J.  
; APPLICANT: Houghton, Michael  
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
US-08-440-103-16



```

; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,103
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-103-16

Query Match 69.8%; Score 37; DB 1; Length 269;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGIDGYT 10
Db 8 LFAGVGDGHT 16

RESULT 13
US-08-440-542-16
; Sequence 16, Application US/08440542
; Patent No. 5670153
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,542
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368

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; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-542-16

Query Match 69.8%; Score 37; DB 1; Length 269;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGIDGYT 10
Db 8 LFAGVGDGHT 16

RESULT 14
US-08-231-368-16
; Sequence 16, Application US/08231368
; Patent No. 5756312
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-368-16

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16



Query Match 69.8%; Score 37; DB 1; Length 269;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGIDGYT 10  
|||:|:|  
Db 8 LFAGVGDGHT 16

RESULT 15  
US-08-440-210-16  
; Sequence 16, Application US/08440210  
; Patent No. 5766845  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, Amy J.  
; APPLICANT: Houghton, Michael  
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,210  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/231,368  
; FILING DATE:  
; APPLICATION NUMBER: US 07/759,575  
; FILING DATE: 13-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McClung, Barbara G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0205.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 269 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-440-210-16

Query Match 69.8%; Score 37; DB 1; Length 269;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LFEIGIDGYT 10  
|||:|:|  
Db 8 LFAGVGDGHT 16

Search completed: December 6, 2001, 07:59:59  
Job time: 367 sec

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GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:28 ; Search time 88.19 Seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: PEP2-MOD8G  
Perfect score: 53  
Sequence: 1 SLFEGIDGTYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: PIR68:\*  
2: pirl:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	83.0	208	2	B44261	dnak-type molecula
2	44	83.0	209	2	A44261	dnak-type molecula
3	44	83.0	278	2	I51344	dnak-type molecula
4	44	83.0	372	2	P00138	dnak-type molecula
5	44	83.0	467	2	T45477	heat-shock protein
6	44	83.0	467	2	T45479	heat-shock protein
7	44	83.0	468	2	T45476	heat-shock protein
8	44	83.0	469	2	T45478	heat-shock protein
9	44	83.0	632	2	T45471	dnak-type molecula
10	44	83.0	634	2	A25646	dnak-type molecula
11	44	83.0	636	2	A48872	dnak-type molecula
12	44	83.0	638	2	S31766	dnak-type molecula
13	44	83.0	639	2	UC1391	dnak-type molecula
14	44	83.0	639	2	S20139	dnak-type molecula
15	44	83.0	640	1	HHKW74	dnak-type molecula
16	44	83.0	640	2	A29160	dnak-type molecula
17	44	83.0	640	2	S37394	dnak-type molecula
18	44	83.0	640	2	T21394	hypothetical prote
19	44	83.0	640	2	T43724	dnak-type molecula
20	44	83.0	641	2	S53577	dnak-type molecula
21	44	83.0	641	2	S53578	dnak-type molecula
22	44	83.0	641	2	I54542	dnak-type molecula
23	44	83.0	641	2	A45871	dnak-type molecula
24	44	83.0	642	1	HHBYA1	dnak-type molecula
25	44	83.0	642	2	JH0095	dnak-type molecula
26	44	83.0	642	2	B36590	dnak-type molecula
27	44	83.0	644	2	A45635	dnak-type molecula
28	44	83.0	645	2	I51129	dnak-type molecula
29	44	83.0	646	2	T46650	heat shock protein

30	44	83.0	647	1	HHXL70	dnak-type molecula
31	44	83.0	647	2	T41121	heat shock protein
32	43	81.1	214	2	A03309	dnak-type molecula
33	43	81.1	379	2	I46588	dnak-type molecula
34	43	81.1	467	2	T45473	heat-shock protein
35	43	81.1	467	2	T45474	heat-shock protein
36	43	81.1	641	2	JN0658	dnak-type molecula
37	43	81.1	641	2	PC7036	heat shock protein
38	43	81.1	643	2	S23585	dnak-type molecula
39	43	81.1	643	2	S09036	dnak-type molecula
40	43	81.1	651	2	T45517	heat shock protein
41	43	81.1	651	2	JC7132	heat shock protein
42	41	77.4	209	2	S48024	dnak-type molecula
43	41	77.4	209	2	S48025	dnak-type molecula
44	41	77.4	209	2	C44261	dnak-type molecula
45	41	77.4	630	2	A34041	dnak-type molecula

## ALIGNMENTS

```

RESULT 1
B44261
dnak-type molecular chaperone HSC70 - California sea hare (fragment)
N:Alternate names: heat shock protein 70 homolog HSC70
C:Species: Aplysia californica (California sea hare)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999
C:Accession: B44261
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr
A:Reference number: A44261; MUID:93077669
A:Accession: B44261
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-208 <KUH>
A>Note: sequence extracted from NCBI backbone (NCBIP:118950)
C:Genetics:
A:Gene: HSC70
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 208;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGTYT 10
DB 132 SLFEGIDGTYT 141

RESULT 2
A44261
dnak-type molecular chaperone HSP70a - California sea hare (fragment)
N:Alternate names: heat shock protein 70
C:Species: Aplysia californica (California sea hare)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999
C:Accession: A44261
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr
A:Reference number: A44261; MUID:93077669
A:Accession: A44261
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-209 <KUH>
A>Note: sequence extracted from NCBI backbone (NCBIP:118951)
C:Genetics:
A:Gene: HSP70a
C:Function:

```



A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 209;  
 Best Local Similarity 90.0%; Pred. No. 0.43;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 SLFEGIDGYT 10  
 |||||||  
 Db 133 SLFEGIDYTT 142

RESULT 3  
 I51344  
 dnak-type molecular chaperone (clone PTHS70.7) - rainbow trout (fragment)  
 N:Alternate names: 70K heat shock protein  
 C:Species: Oncorhynchus mykiss (rainbow trout)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999  
 C:Accession: I51344  
 R:Kothary, R.K.; Jones, D.; Candido, E.P.M.  
 Mol. Cell. Biol. 4, 1785-1791, 1984  
 A:Title: 70-Kilodalton heat shock polypeptides from rainbow trout: Characterization of c  
 A:Reference number: I51344; MUID:85036330  
 A:Accession: I51344  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-278 <KOT>  
 A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804  
 C:Function:  
 A:Description: Involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 278;  
 Best Local Similarity 90.0%; Pred. No. 0.59;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 SLFEGIDGYT 10  
 |||||||  
 Db 156 SLFEGIDFYT 165

RESULT 4  
 P00138  
 dnak-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)  
 N:Alternate names: heat shock protein 70  
 C:Species: Paracentrotus lividus (common urchin)  
 C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 20-Aug-1999  
 C:Accession: P00138  
 R:Rosa, M.L.; Sconzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.  
 Gene 96, 295-300, 1990  
 A:Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.  
 A:Reference number: P00138; MUID:91099690  
 A:Accession: P00138  
 A:Molecule type: DNA  
 A:Residues: 1-372 <ROS>  
 A:Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001  
 C:Genetics:  
 A:Gene: hsp70 II  
 A:Introns: 68/1; 137/1; 188/3; 281/3  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 372;  
 Best Local Similarity 90.0%; Pred. No. 0.82;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SLFEGIDGYT 10  
 |||||||  
 Db 286 SLFEGIDYTT 295

RESULT 5  
 T45477  
 heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)  
 C:Species: Chondrosia reniformis  
 C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T45477  
 R:Borchelliini, C.; Le Parco, Y.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z22983  
 A:Accession: T45477  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-467 <BOR>  
 A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1  
 C:Genetics:  
 A:Gene: Hsp70  
 C:Superfamily: heat shock protein 70

Query Match 83.0%; Score 44; DB 2; Length 467;  
 Best Local Similarity 90.0%; Pred. No. 1.1;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 SLFEGIDGYT 10  
 |||||||  
 Db 252 SLFEGIDFYT 261

RESULT 6  
 T45479  
 heat-shock protein 70 [imported] - Euniceella cavolini (fragment)  
 C:Species: Euniceella cavolini  
 C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T45479  
 R:Borchelliini, C.; Le Parco, Y.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z22983  
 A:Accession: T45479  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-467 <BOR>  
 A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
 C:Genetics:  
 A:Gene: Hsp70  
 C:Superfamily: heat shock protein 70

Query Match 83.0%; Score 44; DB 2; Length 467;  
 Best Local Similarity 90.0%; Pred. No. 1.1;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 SLFEGIDGYT 10  
 |||||||  
 Db 252 SLFEGIDFYT 261

RESULT 7  
 T45476  
 heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
 C:Species: Funiculina quadrangularis  
 C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T45476  
 R:Borchelliini, C.; Le Parco, Y.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z22983  
 A:Accession: T45476  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA



A:Residues: 1-468 <BOR>  
A:Cross-references: EMBL:AF026516; PIDN:AMC05361.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 83.0%; Score 44; DB 2; Length 468;  
Best Local Similarity 90.0%; Pred. No. 1.1;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDGYT 10  
||| ||| ||  
DB 253 SLFEGIDFYT 262

RESULT 8  
T45478  
heat-shock protein 70 [imported] - Euniceella cavollini (fragment)  
C:Species: Euniceella cavollini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45478  
R:Bochheliini, C.; Le Parco, Y.  
Submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45478  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-469 <BOR>  
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 83.0%; Score 44; DB 2; Length 469;  
Best Local Similarity 90.0%; Pred. No. 1.1;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
||| ||| ||  
DB 254 SLFEGIDFYT 263

RESULT 9  
T45471  
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostellium discoideum)  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostellium discoideum  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T45471  
R:Boyes, H.; Minter, U.; Dittich, W.; Paix, J.; Gerisch, G.  
Submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22980  
A:Accession: T45471  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-632 <BOV>  
A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
A:Experimental source: strain AX3  
C:Genetics:  
A:Gene: hsc70  
A:Note: localized to filopodias and cortex  
C:Superfamily: heat shock protein 70

Query Match 83.0%; Score 44; DB 2; Length 632;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDGYT 10  
||| ||| ||  
DB 265 SLFEGIDFYT 294

RESULT 10  
A25646  
dnaK-type molecular chaperone - chicken  
N:Alternate names: heat shock protein 70  
C:Species: Gallus gallus (chicken)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25646  
R:Motomoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
J. Biol. Chem. 261, 12692-12699, 1986  
A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene  
A:Reference number: A25646; MUID:86304452  
A:Accession: A25646  
A:Molecule type: DNA  
A:Residues: 1-634 <MOR>  
A:Cross-references: GB:J02579; MID:9211940; PIDN:AAA48825.1; PID:9211941  
A:Note: the authors translated the codon TCG for residue 583 as Trp  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 634;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
||| ||| ||  
DB 289 SLFEGIDFYT 298

RESULT 11  
A48872  
dnaK-type molecular chaperone hspB - slime mold (Dictyostellium discoideum) (fragment)  
N:Alternate names: 70k heat shock cognate protein aglnactin; F-actin capping protein  
C:Species: Dictyostellium discoideum  
C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
C:Accession: A48872  
J:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
J. Biol. Chem. 268, 23267-23274, 1993  
A:Title: Aglnactin, an agonist-regulated F-actin capping activity is associated with  
A:Reference number: A48872; MUID:94043116  
A:Accession: A48872  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-636 <EDD>  
A:Cross-references: GB:L22736; MID:g433179; PIDN:AAA33219.1; PID:g433180  
A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 636;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
||| ||| ||  
DB 280 SLFEGIDFYT 289

RESULT 12  
S31766  
dnaK-type molecular chaperone hsp70 - green monkey  
N:Alternate names: heat shock protein 70  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S31766; MUID:136927  
R:Salnis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.



submitted to the EMBL Data Library, January 1993  
 A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
 A:Reference number: S31766  
 A:Accession: S31766  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <SAI>  
 R:Salts, I.: Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FEBS Lett. 355, 282-286, 1994  
 A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me  
 A:Reference number: 136927, MUID:95080396  
 A:Accession: 136927  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <RES>  
 A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
 A:Experimental source: kidney; cell line COS-1  
 C:Genetics:  
 A:Gene: hsp70  
 C:Function:  
 A:Description: Involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||||  
 Db 284 SLFEGIDPYT 293

RESULT 13  
 JCI391  
 dnak-type molecular chaperone 701V - sea urchin (Paracentrotus lividus)  
 N:Alternate names: heat shock protein 701V; hsp701V protein  
 C:Species: Paracentrotus lividus (common urchin)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C:Accession: JCI391  
 R:Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
 A:Reference number: JCI391; MUID:93077053  
 A:Accession: JCI391  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SCO>  
 A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
 C:Genetics:  
 A:Gene: hsp701V  
 A:Introns: 61/2  
 C:Function:  
 A:Description: Involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 83.0%; Score 44; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||||  
 Db 286 SLFEGIDPYT 295

RESULT 14  
 S20139  
 dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: heat shock protein YG102; protein I0971; protein YLL024C  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C:Accession: S20139; S64772; S64775; S69383

R:Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A:Reference number: S20139; MUID:89128457  
 A:Accession: S20139

A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SLA>  
 A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546  
 R:Goffeau, A.; Purnelle, B.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64761  
 A:Accession: S64772

A:Molecule type: DNA  
 A:Residues: 1-639 <GOF>  
 A:Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YL  
 A:Experimental source: strain S288C  
 R:Puesterhoef, A.; Floeth, M.; Heuss-Netzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64775  
 A:Accession: S64775

A:Molecule type: DNA  
 A:Residues: 72-639 <DUE>  
 A:Cross-references: EMBL:Z73129; MIPS:YLL024C  
 A:Experimental source: strain S288C  
 R:Purnelle, B.; Goffeau, A.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals  
 mly and a new ABC transporter homologous to the human multidrug resistance protein.  
 A:Reference number: S69380  
 A:Accession: S69383

A:Molecule type: DNA  
 A:Residues: 1-639 <PUR>  
 A:Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007  
 C:Genetics:  
 A:Gene: SGD:SSA2  
 A:Cross-references: MIPS:YLL024C; SGD:S0003947  
 A:Map position: 12L  
 C:Function:  
 A:Description: Involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 83.0%; Score 44; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||||  
 Db 283 SLFEGIDPYT 292

RESULT 15  
 HHK7A  
 dnak-type molecular chaperone hsp70A - Caenorhabditis elegans  
 N:Alternate names: heat shock protein 70 A  
 C:Species: Caenorhabditis elegans  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
 C:Accession: JTO285  
 R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
 Gene 64, 241-255, 1988  
 A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri  
 A:Reference number: JTO285; MUID:88297155  
 A:Accession: JTO285  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-640 <SNU>  
 A:Cross-references: GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352  
 A:Note: genomic clones representing six distinct members of the hsp70 gene family wer  
 A:Note: transcripts of hsp70A are abundant in control worms and also increase two- to  
 C:Note: one of the three introns in hsp70A is in a position similar to an intron in D  
 C:Genetics:  
 A:Gene: hsp70A



A:Map position: IV  
A:Introns: 69/1; 331/3; 558/3  
C:Function:  
A:Description: Involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 83.0%; Score 44; DB 1; Length 640;  
Best Local Similarity 90.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLEPGIDGYT 10  
|||||  
Db 287 SLEPGIDFTT 296

Search completed: December 6, 2001, 07:58:28  
Job time: 276 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:52 ; Search time 50.21 Seconds  
(without alignments)  
7.302 Million cell updates/sec

Title: PEP2-MOD8G  
Perfect score: 53  
Sequence: 1 SLFEGIDGYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	83.0	322	1 HS70_ONCVO	P11503 onchocerca
2	44	83.0	372	1 HS72_PARLI	P22623 paracentrot
3	44	83.0	503	1 HS70_PENCI	O92260 penicillium
4	44	83.0	634	1 HS70_CHICK	P08106 gallus galli
5	44	83.0	638	1 HS71_CERAE	O28222 cercopithec
6	44	83.0	638	1 HS72_YEAST	P10592 saccharomyc
7	44	83.0	639	1 HS74_PARLI	O06248 paracentrot
8	44	83.0	640	1 HS7A_CAEEL	P09446 caenorhabdi
9	44	83.0	640	1 HS7C_DICDI	P36415 dictyosteli
10	44	83.0	641	1 HS71_BOVIN	O27975 bos taurus
11	44	83.0	641	1 HS71_HUMAN	P08107 homo sapien
12	44	83.0	641	1 HS71_MOUSE	P17879 mus musculu
13	44	83.0	641	1 HS71_PIG	P34930 sus scrofa
14	44	83.0	641	1 HS71_RAT	O07439 rattus norv
15	44	83.0	641	1 HS71_YEAST	P10591 saccharomyc
16	44	83.0	641	1 HS72_BOVIN	O27965 bos taurus
17	44	83.0	641	1 HS74_YEAST	P22202 saccharomyc
18	44	83.0	644	1 HS70_BRUMA	P27541 brugia mala
19	44	83.0	644	1 HS70_ONCYS	O91233 oncorhynch
20	44	83.0	645	1 HS70_PLEWA	O91291 pleurodeles
21	44	83.0	645	1 HS70_NEUCR	O01233 neurospora
22	44	83.0	647	1 HS70_XENLA	P02827 xenopus lae
23	44	83.0	649	1 HS70_BLAEM	P46720 blastoclad
24	44	83.0	652	1 HS7D_MANSE	O94639 manduca sex
25	43	81.1	214	1 HS7A_DROSI	P02826 drosophila
26	43	81.1	379	1 HS7X_PIG	P34934 sus scrofa
27	43	81.1	643	1 HS7A_DROME	P29843 drosophila
28	43	81.1	643	1 HS76_HUMAN	P17066 homo sapien
29	43	81.1	643	1 HS76_PIG	O04967 sus scrofa
30	43	81.1	648	1 HS71_PUCGR	O01877 puccinia gr
31	41	77.4	641	1 HS73_RAT	P55063 rattus norv
32	41	77.4	641	1 HS7H_HUMAN	P34931 homo sapien
33	41	77.4	641	1 HS7T_MOUSE	P16627 mus musculu

34	41	77.4	642	1 HS72_PICAN	P53623 pichia angu
35	41	77.4	643	1 HS71_SCHRO	O10265 schizosacch
36	41	77.4	644	1 HS71_PICAN	P53421 pichia angu
37	41	77.4	646	1 HS7C_CRIGR	P19378 cricetus
38	41	77.4	646	1 HS7C_HUMAN	P11142 homo sapien
39	41	77.4	646	1 HS7C_MOUSE	P08109 mus musculu
40	41	77.4	649	1 HS70_PARRR	P87047 paracoccidi
41	41	77.4	649	1 HS73_YEAST	P09435 saccharomyc
42	41	77.4	649	1 HS7C_BRARE	O90473 brachydanio
43	41	77.4	650	1 HS7C_BOVIN	P19120 bos taurus
44	41	77.4	651	1 HS70_ONCMY	P08108 oncorhynch
45	41	77.4	654	1 HS70_HYDMA	O05944 hydra magni

## ALIGNMENTS

RESULT 1	
ID HS70_ONCVO	STANDARD: PRT: 322 AA.
AC P11503:	
DT 01-OCT-1989 (Rel. 12, Created)	
DT 01-FEB-1996 (Rel. 33, Last sequence update)	
DT 01-FEB-1996 (Rel. 33, Last annotation update)	
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).	
OS Onchocerca volvulus.	
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;	
OC Onchocercidae; Onchocerca.	
OX NCBI_TaxID=6282;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=89201313; PubMed=2704388;	
RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;	
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in	
RT amicrofilaricemic individuals from a filariasis-endemic area.";	
RL Mol. Biochem. Parasitol. 33:229-236(1989).	
CC -I- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A	
CC MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.	
CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.	
CC	
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CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC -----	
DR EMBL: J04006; AAA29417.1; -	
DR HSP70; P19120; IATR.	
DR InterPro: IPR001023; HSP70.	
DR Pfam: PF00012; HSP70; 1.	
DR PROSITE: PS00297; HSP70.1; PARTIAL.	
DR PROSITE: PS00329; HSP70.2; PARTIAL.	
DR PROSITE: PS01036; HSP70.3; 1.	
KW ATP-binding; Heat shock.	
FT NON_TER 1	
FT NON_TER 322	
FT SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;	
Query Match	83.0%; Score 44; DB 1; Length 322;
Best Local Similarity	90.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 1 SLFEGIDGYT 10	
DB 43 SLFEGIDGYT 52	
RESULT 2	
ID HS72_PARLI	STANDARD: PRT: 372 AA.



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AC P22623;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
GN HSP70II.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinodermata; Echinacea; Echinoidae; Echinidae;
OC Paracentrotus
OC NCBL_TaxID=7656;
OX NCBL_TaxID=7656;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Conad;
RX MEDLINE=91099690; PubMed=2269441;
RA la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.;
RT "sequence of a sea urchin hsp70 gene and its 5' flanking region.";
RL Gene 96:295-300(1990).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL: X16544; CNA34544.1; -.
DR PIR: P00138; P00138.
DR HSSP: P19120; INGU.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PROSITE: PS00297; HSP70_1; 1
DR PROSITE: PS00329; HSP70_2; PARTIAL.
DR PROSITE: PS01036; HSP70_3; 1.
DR ATP-Binding; Heat shock; Multigene family.
KW NON_TER 372 372
FT SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;
SQ
Query Match 83.0%; Score 44; DB 1; Length 372;
Best Local Similarity 90.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLEPGIDGYT 10
Db 286 SLEPGIDYTT 295
RESULT 3
HS70_PENCI STANDARD; PRT; 503 AA.
ID HS70_PENCI
AC Q92260;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
GN HSP70.
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBL_TaxID=5077;
RN [1]
RP SEQUENCE FROM N.A.
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
RT "Molecular cloning and expression of a Penicillium citrinum
RT allergen with sequence homology and antigenic cross-reactivity to
RT a hsp70 human heat shock protein.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL: U64207; AAB06397.1; -.
DR HSSP: P19120; 3HSC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR ATP-Binding; Chaperone; Heat shock; Allergen.
KW NON_TER 1 1
FT SEQUENCE 503 AA; 55125 MW; B7433C11FAA1320 CRC64;
SQ
Query Match 83.0%; Score 44; DB 1; Length 503;
Best Local Similarity 90.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLEPGIDGYT 10
Db 154 SLEPGIDGYT 163
RESULT 4
HS70_CHICK STANDARD; PRT; 634 AA.
ID HS70_CHICK
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBL_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02579; AAA48825.1; -.
DR PIR: A25646; A25646.
DR HSSP: P19120; IATR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR ATP-Binding; Heat shock; Multigene family.
KW SEQUENCE 634 AA; 69750 MW; 4270F7F08D565AEB CRC64;
SQ
Query Match 83.0%; Score 44; DB 1; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.91;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SLEFEGIDGYT 10  
Db 289 SLEFEGIDGYT 298

## RESULT 5

HS71\_CERAE STANDARD; PRT: 638 AA.  
ID HS71\_CERAE Q28222;  
AC 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DE HEAT SHOCK 70 KDA PROTEIN 1.  
GN HSPAL.  
OS Cercopithecus aethiops (Green monkey) (Griwet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=95080396; PubMed=7988690;  
RA Sains I.; Angelidis C.; Pagoulatos G.; Lazaridis I.;  
RT "The hsc70 gene which is slightly induced by heat is the main virus  
inducible member of the hsp70 gene family.";  
RL FEBS Lett. 335:282-286(1994).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE  
PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING  
OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN  
ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC  
RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR  
PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION  
PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE  
PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE  
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE  
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES  
DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING  
STRESS-INDUCED DAMAGE.  
CC -1- INDUCTION: BY HEAT SHOCK.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC EMBL; X70684; CAA50019.1; -.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
SQ SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CMC64;

Query Match 83.0%; Score 44; DB 1; Length 638;  
Best Local Similarity 90.0%; Pred. No. 0.92;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SLEFEGIDGYT 10  
Db 284 SLEFEGIDGYT 293

## RESULT 6

HS72\_YEAST STANDARD; PRT: 638 AA.  
ID HS72\_YEAST P10592;  
AC 01-JUL-1989 (Rel. 11, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DE HEAT SHOCK PROTEIN SSA2.  
GN SSA2 OR YL024C OR I0931.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
CC Saccharomycetales; Saccharomycetaceae; Saccharomycus.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C;  
RX MEDLINE=89128457; PubMed=2644626;  
RA Slater M.R.; Craig E.A.;  
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae";  
RL Nucleic Acids Res. 17:805-806(1989).

[2] SEQUENCE FROM N.A.  
RC STRAIN=S288C;  
RA Purnelle B.; Goffeau A.;  
RT Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 71-638 FROM N.A.  
RA Duesterhoeft A.; Ploeth M.; Heuss-Neitzel D.; Hilbert H.; Moestl D.;  
RT Submitted (May-1996) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 91-97 AND 325-341.  
RC STRAIN=S288C;  
RX MEDLINE=95203288; PubMed=7895733;  
RA Garrels J.I.; Fitcher B.; Kobayashi R.; Latter G.I.; Schwender B.;  
RT "Protein identifications for a Saccharomyces cerevisiae protein  
database";  
RL Electrophoresis 15:1466-1486(1994).

[5] SEQUENCE OF 186-195.  
RC STRAIN=ATCC 38531 / Y41;  
RX MEDLINE=97089742; PubMed=8935650;  
RA Norbeck J.; Blomberg A.;  
RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
Saccharomyces cerevisiae";  
RL FEMS Microbiol. Lett. 137:1-8(1996).

[6] ACETYLATION, AND PHOSPHORYLATION.  
RA Garrels J.I.; Fitcher B.; Kobayashi R.; Latter G.I.; Schwender B.;  
RT Voipe T.; Warner J.R.; McLaughlin C.S.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
CC -1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE  
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- PTM: PHOSPHORYLATED.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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CC EMBL; X12927; CAA31394.1; -.  
DR EMBL; Z73129; CAA97472.1; -.  
DR EMBL; X97560; CAA66167.1; -.  
DR PIR; S20139; S20139.  
DR HSSP; P19120; INCI.  
DR SWISS-2DPAGE; P10592; YEAST.



DR YEED; 9800; -  
 DR SGD; S0003947; SNA2.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR Heat shock; ATP-binding; Multigene family; Acetylation;  
 KW Phosphorylation.  
 FT INIT\_MET 0  
 FT MOD\_RES 1  
 FT MOD\_RES 1  
 SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match 83.0%; Score 44; DB 1; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
 Db 282 SLFEGIDFYT 291

RESULT 7  
 HS74\_PARLI STANDARD; PRT; 639 AA.  
 AC Q06248;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).  
 GN HSP70IV.  
 OS Paracentrotus lividus (Common sea urchin).  
 OS Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Euechinozoa; Echinoidae; Echinoida; Echinidae;  
 OC Paracentrotus.  
 NC NCBL\_TaxID=7656;  
 RX SCONZO G., SCARDINE G., FERRARO M.G.;  
 RX MEDLINE=93077053; PubMed=1339375;  
 RT "Characterization of a new member of the sea urchin Paracentrotus  
 RT lividus hsp70 gene family and its expression.";  
 RL Gene 121:353-358(1992).  
 CC -! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X61379; CAA3653.1; -  
 DR PIR: JCI391; JCI391.  
 DR HSP: P19120; INGI.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Heat shock; Multigene family.  
 KW SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 83.0%; Score 44; DB 1; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10

Db 286 SLFEGIDFYT 295

RESULT 8  
 HS7A\_CAEL STANDARD; PRT; 640 AA.  
 AC P09446;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN A.  
 GN HSP-1 OR HSP70A.  
 OS Caenorhabditis elegans.  
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 NC NCBL\_TaxID=6239;  
 RX MEDLINE=88297155; PubMed=2841196;  
 RX Snutch T.P., Heschl M.F.P., Baillie D.L.;  
 RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic  
 RT characterization.";  
 RL Gene 64:241-255(1988).  
 CC -! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M18540; AAA28078.1; -  
 DR PIR: JTO285; HHKWT7A.  
 DR HSP: P19120; INGI.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Heat shock; Multigene family.  
 KW SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 83.0%; Score 44; DB 1; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
 Db 287 SLFEGIDFYT 296

RESULT 9  
 HS7C\_DICDI STANDARD; PRT; 640 AA.  
 AC P36415;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1997 (Rel. 35, Last annotation update)  
 DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).  
 GN HSPB OR HSC70.  
 OS Dictyostelium discoideum (Slime mold).  
 OS Eukaryota; Mycetozoa; Dictyostelidia; Dictyostellium.  
 NC NCBL\_TaxID=44689;  
 RX MEDLINE=94008983; PubMed=8404847;  
 RX Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,



Query Match	83.0%	Score 44;	DB 1;	Length 640;
Best Local Similarity	90.0%	Pred. No. 0.92;		
Matches 9;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 1 SLFEGIDGTY 10				
Db 284 SLFEGIDFYT 293				
<p>RESULT 10</p> <p>HS71_BOVIN STANDARD; PRT; 641 AA.</p> <p>AC Q27975; Q27964;</p> <p>DT 01-NOV-1997 (Rel. 35, Created)</p> <p>DT 01-NOV-1997 (Rel. 35, Last sequence update)</p> <p>DT 15-JUL-1989 (Rel. 38, Last annotation update)</p> <p>DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).</p> <p>EN HSP70-1.</p>				

OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OX	NCB1_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skeletal muscle;
RX	MEDLINE=95126904; PubMed=7826329;
RA	Gutierrez J.A., Guerriero V.;
RT	"Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues.";
RL	Biochem. J. 305:197-203(1995).
RN	[2]
RP	SEQUENCE OF 212-641 FROM N.A.
RC	STRAIN=ANGUS;
RX	MEDLINE=95030563; PubMed=7943958;
RA	Grosz M.D., Skow L.C., Stone R.T.;
RT	"An Alu polymorphism at the bovine 70 kD heat-shock protein-1 (HSP70-1) locus.";
RL	Anim. Genet. 25:196-196(1994).
CC	-I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC	-I- INDUCTION: BY HEAT SHOCK.
CC	-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC	-----
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CC	-----
DR	EMBL: U09861; AAA73914.1; -.
DR	EMBL: U02891; AAA03450.1; -.
DR	HSSP: P19120; INGC.
DR	InterPro: IPR001023; HSP70.
DR	Pfam: PF00012; HSP70.1.
DR	PRINTS: PR00301; HEATSHOCK70.
DR	PROSITE: PS00297; HSP70_1; 1.
DR	PROSITE: PS00329; HSP70_2; 1.
DR	PROSITE: PS01036; HSP70_3; 1.
KW	ATP-binding; Chaperone; Heat shock; Multigene family.
SQ	SEQUENCE 641 AA; 70250 MW; 6DS4826398780F9 CRC64;
OY	1 SLFEGIDGYT 10
DB	11 286 SLFESIDRYT 295
Query Match	83.0%; Score 44; DB 1; Length 641;
Best Local Similarity	90.0%; Pred. No. 0.92;
Matches 9; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
RESULT 11	
HS71_HUMAN	STANDARD: PRT: 641 AA.
ID	HS71_HUMAN
AC	Posblot; P19790; Q9UNOM; Q9UNLG;
DT	01-AUG-1988 (Rel. 08, Created)
DT	01-FEB-1994 (Rel. 28, Last annotation update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)



DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 OS (HSP70.1 OR HSP70.1) AND HSP70.1.  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91055806; PubMed=1700760;  
 RA Miller C.M., Campbell R.D.;  
 RT "Structure and expression of the three MHC-linked HSP70 genes.";  
 RL Immunogenetics 32:242-251(1990).  
 [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86016721; PubMed=3931075;  
 RA Hunt C., Morimoto R.I.;  
 RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
 [3]  
 RP SEQUENCE FROM N.A. (HSP70.1 AND HSP70.1B).  
 RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III region.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
 RX MEDLINE=89184548; PubMed=2538825;  
 RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;  
 RT "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
 [5]  
 RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
 RX MEDLINE=87066768; PubMed=3786141;  
 RA Driabent B., Genthe A., Bencke B.-J.;  
 RT "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";  
 RL Nucleic Acids Res. 14:8933-8949(1986).  
 [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
 RX MEDLINE=99234376; PubMed=10216320;  
 RA Osipuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 RT "Structure of a new crystal form of human hsp70 ATPase domain.";  
 RL Acta Crystallogr. D 55:1105-1107(1999).  
 [1]  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NEW HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLLOCATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M59828; AAA63226.1; -;  
 CC EMBL; M59830; AAA63227.1; -;  
 CC EMBL; AF134726; AAD21816.1; -;  
 CC EMBL; AF134726; AAD21815.1; -;

DR EMBL; M11717; AAA52697.1; -;  
 DR EMBL; M24743; AAA59844.1; -;  
 DR EMBL; M24744; AAA59845.1; -;  
 DR EMBL; X04676; CAA28381.1; -;  
 DR EMBL; X04677; CAA28382.1; -;  
 DR PIR; A29160; A29160.  
 DR PIR; A45871; A45871.  
 DR PIR; A25773; A25773.  
 DR PDB; 1H70; 21-OCT-98.  
 DR SWISS-2DPAGE; P08107; HUMAN.  
 DR MIM; 140550; -;  
 DR MIM; 603012; -;  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70.1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III; 3D-structure.  
 KW 3D-structure.  
 FT CONFLICT 7 7 I -> V (IN REF. 2).  
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).  
 FT CONFLICT 370 370 A -> G (IN REF. 2).  
 FT CONFLICT 469 469 MISSING (IN REF. 2).  
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).  
 FT CONFLICT  
 SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96D86 CRC64;

Query Match 83.0%; Score 44; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLFEGIDGYT 10  
 ID 1111111111  
 Db 286 SLFEGIDGYT 295  
 RESULT 12  
 HS71 MOUSE  
 ID HS71 MOUSE STANDARD; PRT; 641 AA.  
 AC P17879; 061689;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN HSP70.1 OR HSP70.1 OR HSP70.1.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90236310; PubMed=2332169;  
 RA Hunt C., Calderwood S.;  
 RT "Characterization and sequence of a mouse hsp70 gene and its expression in mouse cell lines.";  
 RL Gene 87:199-204(1990).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-LIVER;  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Aujeime L., Shchang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from Mus musculus.";  
 RL Gene 146:273-278(1994).  
 [1]  
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NEW HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLLOCATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.



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CC -----
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M35021; AAA37864.1; -
DR EMBL: M76613; AAA57233.1; -
DR PIR: JH0095; JH0095.
DR HSSP: P19120; INGC.
DR MGD: MGI:99517; HSP70-1.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KM ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 342 342 A -> R (IN REF. 1).
FT CONFLICT 627 627 P -> PP (IN REF. 1).
SQ SEQUENCE 641 AA; 69994 MW; 41475360F6749F2F CRC64;

Query Match 83.0%; Score 44; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDGYT 10
Db 286 SLEFGIDFYT 295

RESULT 13
HS7L_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPA1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92173874; PubMed=1339404;
RA Peelan L.J., de Weyhe A.R., Coppieters W.R., van Zeveren A.J.,
RA Bouquet Y.H.;
RT "Complete nucleotide sequence of a porcine HSP70 gene.";
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: M69100; -; NOT_ANNOTATED_CDS.
DR PIR: S35718; S35718.
DR HSSP: P19120; INGC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KM ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match 83.0%; Score 44; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDGYT 10
Db 286 SLEFGIDFYT 295

RESULT 14
HS7L_RAT STANDARD; PRT; 641 AA.
AC Q07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
GN HSP70-1 AND HSP70-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94096443; PubMed=8271311;
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
RA Massa S.M., Sharp F.R.;
RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
RT and injured rat brain.";
RL J. Neurosci. Res. 36:325-335(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LEM.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Raub F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94368874; PubMed=8086479;
RA Lisowska K., Krawczyk Z., Wlidlak W., Wolniczka P., Wisniewski J.;
RT "Cloning, nucleotide sequence and expression of rat heat inducible
RT hsp70 gene.";
RL Biochim. Biophys. Acta 1219:64-72(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: L16764; AAA17441.1; -  
 DR EMBL: X77208; CAA54423.1; -  
 DR EMBL: X77207; CAA54422.1; -  
 DR EMBL: X74271; CAA52328.1; -  
 DR HSSP: P19120; IMG.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
 FT CONFLICT 71 72 KR -> NG (IN REF. 3).  
 FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).  
 FT CONFLICT 408 408 G -> A (IN REF. 3).  
 SO SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 83.0%; Score 44; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDGYT 10  
 ||||||| 11  
 Db 286 SLEFGIDGYT 295

RESULT 15  
 HS71 YEAST STANDARD; PRT; 641 AA.  
 ID HS71 YEAST  
 AC P10591;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).  
 DE SSA1 OR YAL005C.  
 GN Saccharomyces cerevisiae (Baker's yeast).  
 OS Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CC NCBI\_TaxID=4932;  
 OK [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-S288C;  
 RC MEDLINE=89128457; PubMed=2644626;  
 RX Slater M.R., Craig E.A.;  
 RA "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae";  
 RT Nucleic Acids Res. 17:805-806(1989).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-S288C / AB972;  
 RC MEDLINE=95028152; PubMed=7941740;  
 RX Clark M.W., Kang T., Storms R.K., Zhong W., Fortin N., Zeng B.,  
 RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;  
 RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of  
 RT the 42 kbp SP07-CEN1-CD15 region.";  
 RL Yeast 10:535-541(1994).  
 RN [3]  
 RN SEQUENCE OF 590-641 FROM N.A.  
 RP MEDLINE=85087943; PubMed=6096826;  
 RA Ogden R.C., Lee M.C., Knapp G.;  
 RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the  
 RT substrates";  
 RL Nucleic Acids Res. 12:9367-9382(1984).  
 RN [4]  
 RN REVISIONS TO 207; 417 AND 421.  
 RA Slater M.R.;

RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN SEQUENCE OF 91-97 AND 325-341.  
 RP STRAIN-S288C;  
 RC MEDLINE=95203288; PubMed=7895733;  
 RX Gargels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RT "Protein identifications for a Saccharomyces cerevisiae protein  
 RT database";  
 RL Electrophoresis 15:1466-1486(1994).  
 RN [6]  
 RN SEQUENCE OF 186-195.  
 RC STRAIN=ATCC 38531 / YAL1;  
 RX MEDLINE=97089742; PubMed=8935650;  
 RA Norbeck J., Blomberg A.;  
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
 RT Saccharomyces cerevisiae";  
 RL FEMS Microbiol. Lett. 137:1-8(1996).  
 RN [7]  
 RN ACTIVATION.  
 RA Gargels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
 CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
 CC ENDOPASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
 CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE  
 CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: X12926; CAA31393.1; -  
 DR EMBL: L22015; AAC04952.1; ALT\_SEQ.  
 DR PIR: S25438; HHRVAL.  
 DR PIR: S42164; S42164.  
 DR HSSP: P19120; 1ATR.  
 DR SWISS-2DPAGE: P10591; YEAST.  
 DR YEPD: 9788; -  
 DR SGD: S000004; SSA1.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW Heat shock; ATP-binding; Multigene family; Acetylation.  
 FT INIT\_MET 0  
 FT MOD\_RES 1  
 SO SEQUENCE 641 AA; 69526 MW; FA9389BA9B1D7DA CRC64;

Query Match 83.0%; Score 44; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDGYT 10  
 ||||||| 11  
 Db 282 SLEFGIDGYT 291

Search completed: December 6, 2001, 08:00:53  
 Job time: 421 sec







DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutolata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191825; AAF12784.1; -  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 153  
 FT NON\_TER 153 153  
 SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match 83.0%; Score 44; DB 5; Length 153;  
 Best Local Similarity 90.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||  
 Db 80 SLFEGIDGYT 89

RESULT 3  
 Q9U669 PRELIMINARY; PRT; 155 AA.  
 AC Q9U669;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutolata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191826; AAF12785.1; -  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 155  
 FT NON\_TER 155 155  
 SQ SEQUENCE 155 AA; 17676 MW; C191FE5B1F346C2 CRC64;

Query Match 83.0%; Score 44; DB 5; Length 155;  
 Best Local Similarity 90.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||  
 Db 82 SLFEGIDGYT 91

RESULT 4  
 Q9U665 PRELIMINARY; PRT; 157 AA.  
 AC Q9U665;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191830; AAF12789.1; -  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 157  
 FT NON\_TER 157 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 83.0%; Score 44; DB 5; Length 157;  
 Best Local Similarity 90.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||  
 Db 84 SLFEGIDGYT 93

RESULT 5  
 Q9U671 PRELIMINARY; PRT; 158 AA.  
 AC Q9U671;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutolata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31221;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF191824; AAF12783.1; -  
 DR HSSP; P19120; 1BA1.  
 DR InterPro; IPR001023; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 158  
 FT NON\_TER 158 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41E5356A2ACAD2F CRC64;

Query Match 83.0%; Score 44; DB 5; Length 158;  
 Best Local Similarity 90.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDGYT 10  
 |||||  
 Db 85 SLFEGIDGYT 94

RESULT 6  
 Q9U668 PRELIMINARY; PRT; 158 AA.  
 AC Q9U668;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)



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DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Littorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotaenioioglossa; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF191827; AAF12786.1; -.
DR HSSP: P19120; 1BA1.
DR InterPro: IPR001023; HSP70.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match
Best Local Similarity 83.0%; Score 44; DB 5; Length 158;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDGYT 10
DB 85 SLEEGIDFTY 94

RESULT 7
ID Q9U666 PRELIMINARY; PRT; 158 AA.
AC Q9U666;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Littorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotaenioioglossa; Littorinoidea; Littorinidae; Littorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Littorina.";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF191829; AAF12788.1; -.
DR HSSP: P19120; 1BA1.
DR InterPro: IPR001023; HSP70.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;

Query Match
Best Local Similarity 83.0%; Score 44; DB 5; Length 158;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDGYT 10
DB 85 SLEEGIDFTY 94

RESULT 8
ID P81159 PRELIMINARY; PRT; 220 AA.
AC P81159;
DT 01-JUN-1998 (TREMBLrel. 06, Created)

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DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DE HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
GN HSC70.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93077669; PubMed=1360013;
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;
RT "Long-term sensitization training in Aplysia leads to an increase in
the expression of BIP, the major protein chaperon of the ER.";
RL J. Cell Biol. 119:1069-1076(1992).
CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: Z15039; CAA78757.1; -.
DR HSSP: P19120; 1BA1.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR Heat shock; Multigene family.
FT NON_TER 1
FT NON_TER 220
SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match
Best Local Similarity 83.0%; Score 44; DB 5; Length 220;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDGYT 10
DB 138 SLEEGIDFTY 147

RESULT 9
ID P81157 PRELIMINARY; PRT; 221 AA.
AC P81157;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).
GN HSP70A.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93077669; PubMed=1360013;
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;
RT "Long-term sensitization training in Aplysia leads to an increase in
the expression of BIP, the major protein chaperon of the ER.";
RL J. Cell Biol. 119:1069-1076(1992).
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: Z15037; CAA78755.1; -.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR Heat shock; Multigene family.
FT NON_TER 1
FT NON_TER 221
SQ SEQUENCE 221 AA; 24404 MW; 853F794106E83C9 CRC64;

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Query Match 83.0%; Score 44; DB 5; Length 221;  
Best Local Similarity 90.0%; Pred. No. 2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDGYT 10  
DB 139 SLEFGIDGYT 148

## RESULT 10

Q90520 PRELIMINARY; PRT; 278 AA.  
ID 090520;  
AC 090520;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;

RN [1]  
RX SEQUENCE FROM N.A.  
RX MEDLINE=85036330; PubMed=6092938;  
RA Kothary R.K., Jones D., Candido E.P.M.;  
RT "70-kilodalton heat shock polypeptides from rainbow trout:  
RT characterization of cDNA sequences.";  
RL Mol. Cell. Biol. 4:1785-1791(1984).  
DR EMBL: K02549; AAA49562.1; -.  
DR HSSP: P08109; ICKR.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70.1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 278 278  
SQ SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match 83.0%; Score 44; DB 13; Length 278;  
Best Local Similarity 90.0%; Pred. No. 2.6;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDGYT 10  
DB 156 SLEFGIDGYT 165

## RESULT 11

Q98899 PRELIMINARY; PRT; 367 AA.

AC 098899;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
OS HSP70-3.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;

RN [1]  
RX SEQUENCE FROM N.A.  
RA Iam E.H.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y08578; CAA6892.1; -.  
DR HSSP: P19120; 3HSC.  
DR InterPro: IPR001023; HSP70.

DR Pfam: PF00012; HSP70; 1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock.  
FT NON\_TER 367 367  
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF653C2CA CRC64;

Query Match 83.0%; Score 44; DB 13; Length 367;  
Best Local Similarity 90.0%; Pred. No. 3.6;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDGYT 10  
DB 268 SLEFGIDGYT 277

## RESULT 12

Q63718 PRELIMINARY; PRT; 455 AA.  
ID 063718;  
AC 063718;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathu; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN [1]  
RX SEQUENCE FROM N.A.  
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,  
RA D'Amprosio E.;  
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z27118; CAA81642.1; -.  
DR HSSP: P08107; IHUO.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70.1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock.  
FT NON\_TER 1  
FT NON\_TER 455 455  
SQ SEQUENCE 455 AA; 50404 MW; 0F45P12CBA1E2971 CRC64;

Query Match 83.0%; Score 44; DB 11; Length 455;  
Best Local Similarity 90.0%; Pred. No. 4.7;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDGYT 10  
DB 254 SLEFGIDGYT 263

## RESULT 13

Q44350 PRELIMINARY; PRT; 467 AA.  
ID 044350;  
AC 044350;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
OS HSP70.  
OS Chondrosia reniformis.  
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;  
OC Chondrosida; Chondrillidae; Chondrosia.  
OX NCBI\_TaxID=68574;

RN [1]  
RX SEQUENCE FROM N.A.  
RA Borchellini C., Le Parco Y.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y08578; CAA6892.1; -.  
DR HSSP: P19120; 3HSC.  
DR InterPro: IPR001023; HSP70.



RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF026517; AAC05362.1; -.  
 DR HSSP: P08109; 1CKR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 467 467  
 SO SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match 83.0%; Score 44; DB 5; Length 467;  
 Best Local Similarity 90.0%; Pred. No. 4.8;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
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 DB 252 SLFEGIDFYT 261

RESULT 14  
 ID 044352 PRELIMINARY; PRT; 467 AA.  
 AC 044352;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
 GN HSP70.  
 OS Petrobionta massiliana.  
 OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarea; Petrobionidae;  
 OC Petrobionta.  
 OX NCBI\_TaxID=68578;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borchelliini C., Le Parco Y.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF026520; AAC05364.1; -.  
 DR HSSP: P08109; 1CKR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 467 467  
 SO SEQUENCE 467 AA; 51458 MW; 23EB28FPD1873DA6 CRC64;

Query Match 83.0%; Score 44; DB 5; Length 467;  
 Best Local Similarity 90.0%; Pred. No. 4.8;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
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 DB 252 SLFEGIDFYT 261

RESULT 15  
 ID 09NJ92 PRELIMINARY; PRT; 467 AA.  
 AC 09NJ92;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
 OS Guancha lacunosa.  
 OC Eukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida;  
 OC Clathrinidae; Guancha.  
 OX NCBI\_TaxID=115120;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Borchelliini C., Le Parco Y.;  
 RT "Sponges paraphyly and the origin of Metazoa."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF182195; AAF61297.1; -.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 467 467  
 SO SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match 83.0%; Score 44; DB 5; Length 467;  
 Best Local Similarity 90.0%; Pred. No. 4.8;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDGYT 10  
 |||||  
 DB 252 SLFEGIDFYT 261

Search completed: December 6, 2001, 07:56:54  
 Job time: 182 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:57 : Search time 81.43 Seconds  
(without alignments)  
2.764 Million cell updates/sec

Title: PEP2-MOD81  
Perfect score: 51  
Sequence: 1 SLFEGIDLVT 10

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued Patents, AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	46	90.2	643	4	US-08-797-358B-3
2	44	86.3	646	1	US-08-441-139-14
3	33	64.7	339	2	US-08-928-692-52
4	33	64.7	415	4	US-09-198-956-6
5	32	62.7	36	1	US-08-487-890A-19
6	32	62.7	36	2	US-08-478-435-19
7	32	62.7	36	2	US-08-337-483-19
8	32	62.7	36	2	US-08-474-671-19
9	32	62.7	36	3	US-08-483-577A-19
10	32	62.7	36	4	US-08-897-438-19
11	32	62.7	81	4	US-08-817-811-55
12	32	62.7	161	3	US-09-205-264-2
13	32	62.7	309	5	PCR-US95-13975-72
14	32	62.7	301	4	US-09-347-803-14
15	32	62.7	422	4	US-09-625-188-12
16	32	62.7	435	3	US-08-911-321-8
17	32	62.7	435	3	US-08-716-873-5
18	32	62.7	436	4	US-09-368-431-5
19	32	62.7	439	4	US-08-716-873-2
20	32	62.7	439	4	US-08-716-873-4
21	32	62.7	439	4	US-09-368-431-2
22	32	62.7	439	4	US-09-368-431-4
23	32	62.7	458	4	US-09-457-046B-61
24	32	62.7	691	3	US-08-946-475-2
25	32	62.7	691	4	US-09-340-479-2
26	32	62.7	711	3	US-08-946-475-9
27	32	62.7	711	3	US-08-946-475-9

28	32	62.7	711	4	US-09-340-479-9	Sequence 9, Appl
29	32	62.7	911	1	US-08-487-890A-107	Sequence 107, App
30	32	62.7	911	2	US-08-478-435-107	Sequence 107, App
31	32	62.7	911	2	US-08-337-483-107	Sequence 107, App
32	32	62.7	911	2	US-08-478-373-107	Sequence 107, App
33	32	62.7	911	3	US-08-474-671-107	Sequence 107, App
34	32	62.7	911	4	US-08-483-577A-107	Sequence 107, App
35	32	62.7	911	4	US-08-897-438-107	Sequence 107, App
36	32	62.7	913	1	US-08-487-890A-5	Sequence 5, Appl
37	32	62.7	913	2	US-08-478-435-5	Sequence 5, Appl
38	32	62.7	913	2	US-08-337-483-5	Sequence 5, Appl
39	32	62.7	913	3	US-08-478-373-5	Sequence 5, Appl
40	32	62.7	913	3	US-08-474-671-5	Sequence 5, Appl
41	32	62.7	913	3	US-08-483-577A-5	Sequence 5, Appl
42	32	62.7	913	4	US-08-897-438-5	Sequence 5, Appl
43	31	60.8	120	4	US-08-679-006-34	Sequence 34, Appl
44	31	60.8	332	2	US-08-637-763B-6	Sequence 6, Appl
45	31	60.8	332	2	US-08-637-763B-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-08-797-358B-3  
Sequence 3, Application US/08797358B  
Patent No. 6268478  
GENERAL INFORMATION:  
APPLICANT: Adams, John  
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,358B  
FILING DATE: 11-Feb-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,491  
FILING DATE: 12-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-CE 3165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 643 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-797-358B-3

Query Match 90.2%; Score 46; DB 4; Length 643;  
Best Local Similarity 80.0%; Pred. No. 0.29;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDLVT 10



Db 288 SLFEGVDFT 297

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US-08-441-139-14
; Sequence 14, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrop, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 646 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-441-139-14

Query Match 86.3%; Score 44; DB 1; Length 646;
Best Local Similarity 80.0%; Pred. No. 0.71;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10
||:|||||
Db 286 SLFEGIDFT 295

RESULT 3
US-08-928-692-52
; Sequence 52, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
```

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STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-9655
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
; US-08-928-692-52
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Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EGIDLYT 10
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Db 285 EGIDFT 291
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RESULT 4
US-09-198-956-6
; Sequence 6, Application US/09198956
; Patent No. 6165769
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schuelein, Martin
; APPLICANT: Lange, Niels Erik K.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Schnorr, Kirk
; TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
; TITLE OF INVENTION: Licheniformis
; FILE REFERENCE: 5377.200-US
; CURRENT APPLICATION NUMBER: US/09/198,956
; CURRENT FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1344/97
; EARLIER FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: 60/067,240
; EARLIER FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
; US-09-198-956-6
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Query Match 64.7%; Score 33; DB 4; Length 415;
Best Local Similarity 71.4%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FEGIDLY 9
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Db 111:111  
118 FEGVLY 124

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RESULT 5
US-08-487-890A-19
; Sequence 19, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Hartness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-487-890A-19

Query Match 62.7%; Score 32; DB 1; Length 36;
Best Local Similarity 62.5%; Pred. No. 6.6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 3 FEGIDLYT 10  
111:111  
28 FEGVLYT 35

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RESULT 6
US-08-478-435-19
; Sequence 19, Application US/08478435
; Patent No. 5922323
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Hartness, Robin
```

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APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-435-19

Query Match 62.7%; Score 32; DB 2; Length 36;
Best Local Similarity 62.5%; Pred. No. 6.6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 3 FEGIDLYT 10  
111:111  
28 FEGVLYT 35

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RESULT 7
US-08-337-483-19
; Sequence 19, Application US/08337483
; Patent No. 5922562
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Hartness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
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NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jdb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19: \*  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-337-483-19

Query Match 62.7%; Score 32; DB 2; Length 36;  
Best Local Similarity 62.5%; Pred. No. 6.6;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 FEGIDLYT 10  
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DB 28 FEGVAITYT 35

RESULT 8  
US-08-478-373-19  
Sequence 19, Application US/08478373  
Patent No. 5922841  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Murdin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,373  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-478-373-19

Query Match 62.7%; Score 32; DB 2; Length 36;  
Best Local Similarity 62.5%; Pred. No. 6.6;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 FEGIDLYT 10  
| | | : | |  
DB 28 FEGVAITYT 35

RESULT 9  
US-08-474-671-19  
Sequence 19, Application US/08474671  
Patent No. 6008326  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Murdin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,671  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-465 MIS.vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-474-671-19

Query Match          62.7%  Score 32: DB 3: Length 36:
Best Local Similarity 62.5%  Pred. No. 6,6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 FEGIDLYT 10
   111: 11
Db 28 FEGVAIYT 35

RESULT 10
US-08-483-577A-19
; Sequence 19, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-483-577A-19

Query Match          62.7%  Score 32: DB 3: Length 36:
Best Local Similarity 62.5%  Pred. No. 6,6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 FEGIDLYT 10
   111: 11
Db 28 FEGVAIYT 35

RESULT 11
US-08-897-438-19
; Sequence 19, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids

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TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-897-438-19

Query Match 62.7%; Score 32; DB 4; Length 36;  
Best Local Similarity 62.5%; Pred. No. 6.6;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 SFEGLDLYT 10  
111:111  
DB 28 FEGVALYT 35

RESULT 12  
US-08-817-811-55  
Sequence 55, Application US/08817811  
Patent No. 6174528  
GENERAL INFORMATION:

APPLICANT: Cooper, Juan A.  
APPLICANT: Relf, Wendy A.  
APPLICANT: Good, Michael F.  
APPLICANT: Saul, Allan J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
TITLE OF INVENTION: COMPRISING SAME  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817/811  
FILING DATE: 14-APR-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:

LENGTH: 81 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: linear

US-08-817-811-55

Query Match 62.7%; Score 32; DB 4; Length 81;  
Best Local Similarity 50.0%; Pred. No. 16;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 SFEGLDLYT 10  
1:11:111  
DB 20 SLEGLNLYS 29

RESULT 13  
US-09-205-264-2

Sequence 2, Application US/09205264

Patent No. 6114145  
GENERAL INFORMATION:

APPLICANT: Olsen, et al.  
TITLE OF INVENTION: Synferon

FILE REFERENCE: PE404  
CURRENT APPLICATION NUMBER: US/09/205,264

CURRENT FILING DATE: 1998-12-02  
EARLIER APPLICATION NUMBER: 60/067,746  
EARLIER FILING DATE: 1997-12-05

NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2  
LENGTH: 161

TYPE: PRT  
ORGANISM: Homo sapiens

US-09-205-264-2

Query Match 62.7%; Score 32; DB 3; Length 161;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SFEGLDLY 9  
1:1:111  
DB 120 SYFGISLY 128

RESULT 14  
PCT-US95-13975-72

Sequence 72, Application PC/TUS9513975  
GENERAL INFORMATION:

APPLICANT: Cochran, Mark D.  
APPLICANT: McDowell, Michael W.

TITLE OF INVENTION: Recombinant Feline Herpes virus  
NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White

STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York

COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13975  
FILING DATE: 26-OCT-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/329,883  
FILING DATE: 26-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 39118-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0400

TELEFAX: (212)391-0525  
INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:

LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
PCT-US95-13975-72

Query Match 62.7%; Score 32; DB 5; Length 301;



Best Local Similarity 62.5%; Pred. No. 71;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDLYT 10  
111:11  
Db 1 FEGIDLYT 8

RESULT 15  
US-09-347-803-14  
; Sequence 14, Application US/09347803  
; Patent No. 6274379  
; GENERAL INFORMATION:  
; APPLICANT: Farnodu, Layo O.  
; APPLICANT: Hitz, Bill  
; APPLICANT: Kinney, Tony  
; APPLICANT: Orozco, Buddy  
; TITLE OF INVENTION: Plant sorbitol Biosynthetic Enzymes  
; FILE REFERENCE: BB-1176  
; CURRENT APPLICATION NUMBER: US/09/347,803  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: 60/092,952  
; EARLIER FILING DATE: July 15, 1998  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 14  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-347-803-14

Query Match 62.7%; Score 32; DB 4; Length 309;  
Best Local Similarity 66.7%; Pred. No. 73;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLY 9  
::111111  
Db 300 AVFWGIDLY 308

Search completed: December 6, 2001, 07:59:58  
Job time: 366 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:27 ; Search time 88.19 Seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: PEP2-MOD8L  
Perfect score: 51  
Sequence: 1 SLEFGIDLYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : PIR68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	92.2	208	2 B44261	dnak-type molecula
2	47	92.2	278	2 I51344	dnak-type molecula
3	47	92.2	467	2 T45477	heat-shock protein
4	47	92.2	467	2 T45476	heat-shock protein
5	47	92.2	468	2 T45476	heat-shock protein
6	47	92.2	469	2 T45478	heat-shock protein
7	47	92.2	632	2 T45471	dnak-type molecula
8	47	92.2	634	2 A25646	dnak-type molecula
9	47	92.2	636	2 A48872	dnak-type molecula
10	47	92.2	638	2 S31766	dnak-type molecula
11	47	92.2	639	2 JCI391	dnak-type molecula
12	47	92.2	639	2 S20139	dnak-type molecula
13	47	92.2	640	1 HHRK7A	dnak-type molecula
14	47	92.2	640	2 A29160	dnak-type molecula
15	47	92.2	640	2 S37394	dnak-type molecula
16	47	92.2	640	2 T21394	hypothetical prote
17	47	92.2	640	2 T43724	dnak-type molecula
18	47	92.2	641	2 S53357	dnak-type molecula
19	47	92.2	641	2 S35718	dnak-type molecula
20	47	92.2	641	2 I54542	dnak-type molecula
21	47	92.2	641	2 A45871	dnak-type molecula
22	47	92.2	642	1 HHBYA1	dnak-type molecula
23	47	92.2	642	2 JH0095	dnak-type molecula
24	47	92.2	642	2 B35590	dnak-type molecula
25	47	92.2	644	2 A45635	dnak-type molecula
26	47	92.2	645	2 I51129	dnak-type molecula
27	47	92.2	646	2 T46650	heat shock protein
28	47	92.2	647	1 HHXL70	dnak-type molecula
29	47	92.2	647	2 T41121	heat shock protein

30	46	90.2	209	2 A44261	dnak-type molecula
31	46	90.2	214	2 A03309	dnak-type molecula
32	46	90.2	372	2 P00138	dnak-type molecula
33	46	90.2	379	2 I46588	dnak-type molecula
34	46	90.2	467	2 T45473	heat-shock protein
35	46	90.2	467	2 T45474	heat-shock protein
36	46	90.2	641	2 JN0668	dnak-type molecula
37	46	90.2	641	2 PC7036	heat shock protein
38	46	90.2	643	2 S25585	dnak-type molecula
39	46	90.2	651	2 S09036	dnak-type molecula
40	46	90.2	651	2 T45517	heat shock protein
41	46	90.2	651	2 JCI732	heat shock protein
42	44	86.3	209	2 S48024	dnak-type molecula
43	44	86.3	209	2 S48025	dnak-type molecula
44	44	86.3	630	2 A34041	dnak-type molecula
45	44	86.3	636	2 T45468	dnak-type molecula

## ALIGNMENTS

```

RESULT 1
B44261
dnak-type molecular chaperone HSC70 - California sea hare (fragment)
N:Alternate names: heat shock protein 70 homolog HSC70
C:Species: Aplysia californica (California sea hare)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 13-Aug-1999
C:Accession: B44261
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.
J. Cell Biol. 119, 1069-1076, 1992
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr
A:Reference number: A44261; MUID:93077669
A:Accession: B44261
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-208 <KUN>
A>Note: sequence extracted from NCBI backbone (NCBIP:118950)
C:Gene(s):
A:Gene: HSC70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP, molecular chaperone

Query Match          92.2%; Score 47; DB 2; Length 208;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10
DB 132 SLEFGIDLYT 141

RESULT 2
I51344
dnak-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment)
N:Alternate names: 70K heat shock protein
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C:Accession: I51344
R:Kotahary, R.K.; Jones, D.; Candido, E.P.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A:Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization o
A:Reference number: I51344; MUID:85036330
A:Accession: I51344
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-278 <KOT>
C:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70

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C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 278;  
Best Local Similarity 90.0%; Pred. No. 0.085;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDLYT 10  
|||||  
Db 156 SLFEGIDFYT 165

## RESULT 3

T45477  
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)  
C:Species: Chondrosia reniformis  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45477  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45477  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDLYT 10  
|||||  
Db 252 SLFEGIDFYT 261

## RESULT 4

T45479  
heat-shock protein 70 [imported] - Euniceella cavolini (fragment)  
C:Species: Euniceella cavolini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45479  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10  
|||||  
Db 252 SLFEGIDFYT 261

## RESULT 5

T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
C:Species: Funiculina quadrangularis  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45476  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45476  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-468 <BOR>  
A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 468;  
Best Local Similarity 90.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDLYT 10  
|||||  
Db 253 SLFEGIDFYT 262

## RESULT 6

T45478  
heat-shock protein 70 [imported] - Euniceella cavolini (fragment)  
C:Species: Euniceella cavolini  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45478  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45478  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-469 <BOR>  
A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 92.2%; Score 47; DB 2; Length 469;  
Best Local Similarity 90.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDLYT 10  
|||||  
Db 254 SLFEGIDFYT 263

## RESULT 7

T45471  
dnak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum  
N:Alternate names: heat shock cognate protein 70  
C:Species: Dictyostelium discoideum  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T45471  
R:Boyes, H.; Mintert, U.; Dittich, W.; Faix, J.; Gerisch, G.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22980  
A:Accession: T45471  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-632 <BOV>  
A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
A:Experimental source: strain AX3  
C:Genetics:  
A:Gene: hsc70  
A:Note: localized to filopodias and cortex  
C:Superfamily: heat shock protein 70



Query Match 92.2%; Score 47; DB 2; Length 632;  
 Best Local Similarity 90.0%; Pred. No. 0.21;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDLYT 10  
 ||||||| ||  
 Db 285 SLEEGIDFYT 294

RESULT 8  
 A:Accession: A25646  
 A:Molecule type: mRNA  
 A:Residues: 1-634 <MON>  
 A:Cross-references: GB:J02579; NID:9211940; PIDN:AAA48825.1; PID:9211941  
 A:Note: the authors translated the codon TCG for residue 583 as Trp  
 C:Function: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 634;  
 Best Local Similarity 90.0%; Pred. No. 0.21;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDLYT 10  
 ||||||| ||  
 Db 289 SLEEGIDFYT 298

RESULT 9  
 A:Accession: A48872  
 A:Molecule type: mRNA  
 A:Residues: 1-636 <EDD>  
 A:Cross-references: GB:LA22736; NID:9433179; PIDN:AAA33219.1; PID:9433180  
 A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va  
 C:Function: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 636;  
 Best Local Similarity 90.0%; Pred. No. 0.21;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDLYT 10  
 ||||||| ||  
 Db 280 SLEEGIDFYT 289

RESULT 10

S31766  
 dnak-type molecular chaperone hsp70 - green monkey  
 N:Alternate names: heat shock protein 70  
 C:Species: Cercopithecus aethiops (green monkey, griwet)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
 C:Accession: S31766; I36927  
 R:Salais, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 submitted to the EMBL Data Library, January 1993

A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock prot  
 A:Reference number: S31766  
 A:Accession: S31766  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <SAI>  
 R:Salais, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FBS Lett. 355, 282-286, 1994  
 A:Title: The hsc70 gene which is slightly induced by heat is the main virus inducible  
 A:Reference number: I36927; MUID:95080396  
 A:Accession: I36927  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <RES>  
 A:Cross-references: EMBL:X70684; NID:922781; PIDN:CAA50019.1; PID:922782  
 A:Experimental source: kidney; cell line COS-1  
 C:Genetics:  
 A:Gene: hsp70  
 C:Function: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDLYT 10  
 ||||||| ||  
 Db 284 SLEEGIDFYT 293

RESULT 11  
 JCI1391  
 dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
 N:Alternate names: heat shock protein 70IV, hsp70IV protein  
 C:Species: Paracentrotus lividus (common urchin)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C:Accession: JCI1391  
 R:Sconzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp  
 A:Reference number: JCI1391; MUID:93077053  
 A:Accession: JCI1391  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SCO>  
 A:Cross-references: EMBL:X61379; NID:9312916; PIDN:CAA43653.1; PID:9312917  
 C:Genetics:  
 A:Gene: hsp70IV  
 A:Introns: 61/2  
 C:Function: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 92.2%; Score 47; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDLYT 10  
 ||||||| ||  
 Db 286 SLEEGIDFYT 295



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RESULT 12
220139
dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: heat shock protein YG102; protein L0911; protein YLL024c
C:Species: Saccharomyces cerevisiae
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Jun-2000
C:Accession: S20139; S64772; S64775; S69383
R:Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A:Reference number: S20139; MUID:89128457
A:Accession: S20139
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-639 <SRA>
A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546
R:Goffeau, A.; Purnelle, B.
Submitted to the Protein Sequence Database, May 1996
A:Reference number: S64772
A:Accession: S64772
A:Molecule type: DNA
A:Residues: 1-639 <GOF>
A:Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL02
A:Experimental source: strain S288C
R:Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
Submitted to the Protein Sequence Database, May 1996
A:Reference number: S64775
A:Accession: S64775
A:Molecule type: DNA
A:Residues: 72-639 <DOE>
A:Cross-references: EMBL:Z73129; MIPS:YLL024c
A:Experimental source: strain S288C
R:Purnelle, B.; Goffeau, A.
Submitted to the EMBL Data Library, April 1996
A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
mily and a new ABC transporter homologous to the human multidrug resistance protein.
A:Reference number: S69383
A:Accession: S69383
A:Molecule type: DNA
A:Residues: 1-639 <PBR>
A:Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
C:Genetics:
A:Gene: SGD:SSA2
A:Cross-references: MIPS:YLL024c; SGD:S0003947
A:Map position: 12L
A:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match          92.2%  Score 47; DB 2; Length 639;
Best Local Similarity 90.0%  Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 SLFEGIDLYT 10
      |||||  ||
Db      283 SLFEGIDFYT 292

RESULT 13
HHKW7A
dnak-type molecular chaperone hsp70A - Caenorhabditis elegans
N:Alternate names: heat shock protein 70 A
C:Species: Caenorhabditis elegans
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C:Accession: J70285
R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat
A:Reference number: J70285; MUID:88297155
A:Accession: J70285
A:Molecule type: DNA; mRNA

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A:Residues: 1-640 <SNU>
A:Cross-references: GB:M18540; NID:g156351; PIDN:AA28078.1; PID:g156352
A:Note: genomic clones representing six distinct members of the hsp70 gene family wer
A:Note: transcripts of hsp70A are abundant in control worms and also increase two- to
A:Note: one of the three introns in hsp70A is in a position similar to an intron in D
C:Genetics:
A:Gene: hsp70A
A:Map position: IV
A:Introns: 69/1; 331/3; 558/3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match          92.2%  Score 47; DB 1; Length 640;
Best Local Similarity 90.0%  Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 SLFEGIDLYT 10
      |||||  ||
Db      287 SLFEGIDFYT 296

RESULT 14
A29160
dnak-type molecular chaperone HSPALL - human
N:Alternate names: heat shock protein, 70K
C:Species: Homo sapiens (hmn)
C:Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: A29160; I37561; I37562
R:Hunt, C.; Morimoto, R.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985
A:Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the
A:Reference number: A29160; MUID:86016721
A:Accession: A29160
A:Molecule type: DNA
A:Residues: 1-640 <HUN>
A:Cross-references: GB:M11717; GB:M15432; NID:g184416; PIDN:AA52697.1; PID:g386785
A:Note: the authors mistranslated residues 463, 491, and 492
R:Draebert, B.; Genthe, A.; Benecke, B.J.
Nucleic Acids Res. 14, 8933-8948, 1986
A:Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepare
A:Reference number: I37561; MUID:87066768
A:Accession: I37561
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481
A:Accession: I37562
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 616-640 <RE2>
A:Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
C:Genetics:
A:Gene: GDB:HSPALL; HSP70-HOM
A:Cross-references: GDB:I20058; OMIM:140559
A:Map position: 6p21.3-6p21.3
A:Introns: #status absent
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein co
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match          92.2%  Score 47; DB 2; Length 640;
Best Local Similarity 90.0%  Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 SLFEGIDLYT 10
      |||||  ||
Db      286 SLFEGIDFYT 295

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RESULT 15  
S37394  
dnaK-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)  
N:Alternate.names: heat shock cognate protein 70  
C:Species: Dictyostelium discoideum  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 20-Aug-1999  
C:Accession: S37394  
R:Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schl  
EMBO J. 12, 3763-3771, 1993  
A>Title: The heat shock cognate protein from Dictyostelium affects actin polymerization  
A:Reference.number: S37394; MUID:94008983  
A:Accession: S37394  
A:Molecule.type: mRNA  
A:Residues: 1-640 <HAU>  
A:Cross-references: EMBL:X75263; NID:g433874; PIDN:CA53039.1; PID:g433875  
C:Genetics:  
A:Gene: hsc70  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 92.2%; Score 47; DB 2; Length 640;  
Best Local Similarity 90.0%; Pred.No. 0.22;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 SLFEGIDLYT 10  
||| ||| ||  
Db 284 SLFEGIDFYT 293

Search completed: December 6, 2001, 07:58:27  
Job time: 275 sec

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DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191825; AAF12784.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 153  
FT SEQUENCE 153 AA; 17352 MW; E29EE20CACA934D CRC64;

Query Match 87.0%; Score 40; DB 5; Length 153;  
Best Local Similarity 88.9%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
DB 80 SLEEGIDAY 88

RESULT 3  
O9U669 PRELIMINARY; PRT; 155 AA.  
AC O9U669;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191826; AAF12785.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 155  
FT SEQUENCE 155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;

Query Match 87.0%; Score 40; DB 5; Length 155;  
Best Local Similarity 88.9%; Pred. No. 2.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
DB 82 SLEEGIDAY 90

RESULT 4  
O9U665 PRELIMINARY; PRT; 157 AA.

AC O9U665;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191830; AAF12789.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 157  
FT SEQUENCE 157 AA; 17834 MW; E8F7A3382B285EB2 CRC64;

Query Match 87.0%; Score 40; DB 5; Length 157;  
Best Local Similarity 88.9%; Pred. No. 2.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
DB 84 SLEEGIDAY 92

RESULT 5  
O9U671 PRELIMINARY; PRT; 158 AA.  
AC O9U671;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaenioglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191824; AAF12783.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 158  
FT SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 87.0%; Score 40; DB 5; Length 158;  
Best Local Similarity 88.9%; Pred. No. 2.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
DB 85 SLEEGIDAY 93

RESULT 6  
O9U668 PRELIMINARY; PRT; 158 AA.

AC O9U668;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)



DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 CC Neocoenoglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF191827; AAF12786.1; -  
 DR HSP; P19120; IBA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 87.0%; Score 40; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
 DB 85 SLEEGIDFY 93

RESULT 7  
 ID 090666 PRELIMINARY; PRT; 158 AA.  
 AC 090666;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 CC Neocoenoglossa; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF191829; AAF12788.1; -  
 DR HSP; P19120; IBA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41E5356BCAD2F CRC64;

Query Match 87.0%; Score 40; DB 5; Length 158;  
 Best Local Similarity 88.9%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
 DB 85 SLEEGIDFY 93

RESULT 8  
 ID P81159 PRELIMINARY; PRT; 220 AA.  
 AC P81159;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
 DE HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
 CC Aplysidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in the expression of b1p, the major protein chaperon of the ER."  
 RL J. Cell Biol. 119:1069-1076(1992)  
 CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
 CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15039; CAA78757.1; -  
 DR HSP; P19120; IBA1.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PR00012; HSP70\_1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1 220  
 SQ SEQUENCE 220 AA; 24684 MW; FA8557F2BB85C37A CRC64;

Query Match 87.0%; Score 40; DB 5; Length 220;  
 Best Local Similarity 88.9%; Pred. No. 3.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDAY 9  
 DB 138 SLEEGIDFY 146

RESULT 9  
 ID P81157 PRELIMINARY; PRT; 221 AA.  
 AC P81157;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).  
 GN HSP70A.  
 OS Aplysia californica (California sea hare).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
 CC Aplysidae; Aplysia.  
 OX NCBI\_TaxID=6500;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
 RT "Long-term sensitization training in Aplysia leads to an increase in the expression of b1p, the major protein chaperon of the ER."  
 RL J. Cell Biol. 119:1069-1076(1992).  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.  
 DR EMBL; Z15037; CAA78755.1; -  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PR00012; HSP70\_1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1 221  
 SQ SEQUENCE 221 AA; 24404 MW; 853F794106B83CC9 CRC64;



Query Match 87.0%; Score 40; DB 5; Length 221;  
 Best Local Similarity 88.9%; Pred. No. 3.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 DB 139 SLFEGIDY 147

RESULT 10  
 Q90520 PRELIMINARY; PRT; 278 AA.

AC Q90520;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-85036330; PubMed-6092938;  
 RA Kothary R.K., Jones D., Candido E.P.M.;  
 RT "70-Kilodalton heat shock polypeptides from rainbow trout:  
 RT Characterization of cDNA sequences.";  
 RL Mol. Cell. Biol. 4:1785-1791(1984).  
 DR EMBL; K02549; AAA49562.1; -.  
 DR HSSP; P08109; ICKR.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT SEQUENCE 278 278 EAC745DE5484C17A CRC64;

Query Match 87.0%; Score 40; DB 13; Length 278;  
 Best Local Similarity 88.9%; Pred. No. 4.9;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 DB 156 SLFEGIDY 164

RESULT 11  
 Q98899 PRELIMINARY; PRT; 367 AA.

AC Q98899;  
 DT 01-FEB-1997 (TREMblrel. 02, Created)  
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 GN HSP70-3.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontiidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP Llm E.H.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y08578; CAA69892.1; -.  
 DR HSSP; P19120; HSC.  
 DR InterPro; IPR001023; HSP70.

DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock.  
 FT NON\_TER 367  
 FT SEQUENCE 367 367 8CD3DD8DF6E3C2CA CRC64;

Query Match 87.0%; Score 40; DB 13; Length 367;  
 Best Local Similarity 88.9%; Pred. No. 6.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 DB 268 SLFEGIDY 276

RESULT 12  
 Q63718 PRELIMINARY; PRT; 455 AA.

AC Q63718;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HEAT SHOCK PROTEIN 70 (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,  
 RA D'Ambrosio E.;  
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z27118; CAA81642.1; -.  
 DR HSSP; P08107; ICKO.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock.  
 FT NON\_TER 1  
 FT SEQUENCE 455 455 0F45F12CBA1E2971 CRC64;

Query Match 87.0%; Score 40; DB 11; Length 455;  
 Best Local Similarity 88.9%; Pred. No. 8.7;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDAY 9  
 DB 254 SLFEGIDY 262

RESULT 13  
 Q44350 PRELIMINARY; PRT; 467 AA.

AC Q44350;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
 GN HSP70.  
 OS Chondrosia reinformis.  
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;  
 OC Chondrosida; Chondrillidae; Chondrosia.  
 OX NCBI\_TaxID=68574;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP Borchellini C., Le Parco Y.;



```

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026517; AAC05362.1; -.
DR HSSP: P08109; 1CKR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1 467 1
FT NON_TER 1 467 1
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match
Best Local Similarity 87.0%; Score 40; DB 5; Length 467;
Pred. No. 9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEEGIDAY 9
Db 252 SLEEGIDFY 260

RESULT 14
O44352 PRELIMINARY; PRT; 467 AA.
AC O44352;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petrobiona massillana.
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarea; Petrobionidae;
OC Petrobiona.
OX NCBI_TaxID=68578;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchgellini C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026520; AAC05364.1; -.
DR HSSP: P08109; 1CKR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1 467 1
FT NON_TER 1 467 1
SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match
Best Local Similarity 87.0%; Score 40; DB 5; Length 467;
Pred. No. 9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEEGIDAY 9
Db 252 SLEEGIDFY 260

RESULT 15
O9NJ92 PRELIMINARY; PRT; 467 AA.
AC O9NJ92;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).
OS Guancha lacunosa.
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcinea; Clathrinida;
OC Clathrinidae; Guancha.
OX NCBI_TaxID=115120;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RA Borchgellini C., Le Parco Y.;
RT "Sponges paraphyly and the origin of Metazoa.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF182195; AAF61297.1; -.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1 467 1
FT NON_TER 1 467 1
SQ SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match
Best Local Similarity 87.0%; Score 40; DB 5; Length 467;
Pred. No. 9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEEGIDAY 9
Db 252 SLEEGIDFY 260

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Search completed: December 6, 2001, 07:56:53  
Job time: 181 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:53:52 ; Search time 184.09 Seconds  
(without alignments)  
3.621 Million cell updates/sec

Title: US-09-673-795-1  
Perfect score: 46  
Sequence: 1 SLFEGIDIV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues  
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq.1101:\*

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- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	21	AAV44199
2	46	100.0	9	22	AAV44199
3	46	100.0	10	21	AAV44200
4	46	100.0	10	22	AAV44200
5	42	91.3	10	22	AAV44200
6	42	91.3	10	22	AAV44200
7	42	91.3	10	22	AAV44200
8	42	91.3	10	22	AAV44200
9	42	91.3	10	22	AAV44200
10	42	91.3	10	22	AAV44200
11	42	91.3	10	22	AAV44200

12	42	91.3	640	11	AAV44199
13	42	91.3	640	18	AAV44199
14	42	91.3	640	21	AAV44199
15	42	91.3	640	21	AAV44199
16	42	91.3	640	21	AAV44199
17	42	91.3	640	21	AAV44199
18	42	91.3	640	21	AAV44199
19	42	91.3	640	21	AAV44199
20	42	91.3	640	21	AAV44199
21	42	91.3	640	21	AAV44199
22	42	91.3	640	21	AAV44199
23	41	89.1	643	18	AAV44199
24	41	89.1	665	21	AAV44199
25	39	84.8	91	21	AAV44199
26	39	84.8	253	21	AAV44199
27	39	84.8	279	21	AAV44199
28	39	84.8	342	21	AAV44199
29	39	84.8	646	11	AAV44199
30	39	84.8	646	19	AAV44199
31	39	84.8	646	20	AAV44199
32	39	84.8	646	20	AAV44199
33	39	84.8	646	21	AAV44199
34	39	84.8	646	21	AAV44199
35	39	84.8	646	22	AAV44199
36	39	84.8	656	18	AAV44199
37	39	84.8	890	21	AAV44199
38	38	82.6	633	14	AAV44199
39	37	80.4	412	22	AAV44199
40	36	78.3	214	19	AAV44199
41	36	78.3	221	19	AAV44199
42	35	76.1	421	21	AAV44199
43	35	76.1	542	21	AAV44199
44	35	76.1	623	21	AAV44199
45	35	76.1	646	11	AAV44199

#### ALIGNMENTS

RESULT 1

ID AAV44199 standard; peptide; 9 AA.

AC AAV44199;

DT 15-FEB-2000 (First entry)

XX

DE Heat shock protein 70 amino acid residues 286-294.

XX

KW Human: heat shock protein 70; hsp70; Identification: tumour; mutation;

KW T cell response; amplification; vector; bacterium; cancer; allele;

KW cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;

KW Immune defence; immunogenicity; specificity; human leucocyte antigen.

XX

OS Homo sapiens.

XX

PN WO954464-A1.

XX

PD 28-OCT-1999.

XX

PF 22-APR-1999; 99MO-FR00957.

XX

PR 22-APR-1998; 98PR-0005033.

XX

PA (INSR) INSR ROUSSY GUSTAVE.

XX

PI Triebel F, Gaudin C;

XX

DR WPI; 2000-013251/01.

XX

PT Identifying mutant peptides from heat-shock protein 70, for treatment of cancer -

XX



PS Claim 10; Page 6; 56pp; French.

CC This peptide corresponds to amino acid residues 286-294 of the human  
CC heat shock protein 70 (hsp70). The invention relates to a method of  
CC identifying peptides, derived from hsp70 that stimulate a tumour-specific  
CC T cell response. Identification of the hsp70 peptides that have at least  
CC one mutation or alteration compared with the native sequence, and induce  
CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70  
CC encoding DNA from one or more tumours; (ii) cloning the amplified  
CC sequences into a vector that can be replicated in bacteria;  
CC (iii) sequencing fragments in each cultured bacterial colony to identify  
CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
CC mutant peptides identified. The peptides, optionally formulated with an  
CC agent that induces cellular stress, are used for treatment of cancer,  
CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
CC cancers of head and neck, particularly kidney cancer). The peptides may  
CC also be used to increase the proportion of tumour-specific cytotoxic  
CC T lymphocytes in a cell culture and/or induce these cells to secrete  
CC cytotoxic factors (specifically interleukin-2, interferon gamma and  
CC tumour necrosis factor), particularly where the cells are used to  
CC stimulate immune defences. The method identifies peptides with high  
CC immunogenicity and high specificity for particular HLA (human leucocyte  
CC antigen) alleles.

CC Sequence 9 AA:

Query Match 100.0%; Score 46; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFEGIDIV 9  
| | | | |  
Db 1 slfegidiv 9

RESULT 2

AAB97601 standard; peptide: 9 AA.

AC AAB97601:

XX 30-JUL-2001 (first entry)

DE Heat shock protein 70 (HSP70) peptidic fragment 1.

KM HSP; HSP70: heat shock protein 70; cancer; chronic infectious disease;

KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

XX cytotoxic response; epitope; antigen presenting cell; fragment 1.

OS Homo sapiens.

PN WO200129190-A1.

PD 26-APR-2001.

PF 29-SEP-2000; 2000WO-EP09530.

PR 15-OCT-1999; 99EP-0120484.

PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

DK WPI, 2001-290909/30.

XX Lymphocytes useful for treating cancer, recognizes specifically

PT transformed human cells with induced and increased membrane expression

XX of heat shock protein -

PS Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 1 relating to position 286-294 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates  
CC to lymphocytes which recognise cells of a patient in which overexpression  
CC of HSP has been induced. Overexpression of HSP leads to a substantial  
CC increase in the numbers of HSPs and HSP epitopes presented on the  
CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
CC response which kills the target cells. As a further embodiment of the  
CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells. (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumour or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

CC Sequence 9 AA:

Query Match 100.0%; Score 46; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFEGIDIV 9  
| | | | |  
Db 1 slfegidiv 9

RESULT 3

AAV44200 standard; peptide: 10 AA.

AC AAV44200:

XX 15-FEB-2000 (first entry)

DE Heat shock protein 70 amino acid residues 286-295.

KM Human; heat shock protein 70; hsp70; identification; tumour; mutation;

KW T cell response; amplification; vector; bacterium; cancer; allele; HLA;

XX cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;

XX immune defence; immunogenicity; specificity; human leucocyte antigen.

OS Homo sapiens.

PN WO9954464-A1.

PD 28-OCT-1999.

PF 22-APR-1999; 99WO-FR00957.

PR 22-APR-1998; 98FR-0005033.

PA (INSR) INST ROUSSY GUSTAVE.

PI Triebel F, Gaudin C;

DR WPI, 2000-013251/01.

XX Identifying mutant peptides from heat-shock protein 70, for treatment

XX of cancer -

PS Claim 10; Page 6; 56pp; French.

XX This peptide corresponds to amino acid residues 286-295 of the human

CC heat shock protein 70 (hsp70). The invention relates to a method of

CC identifying peptides, derived from hsp70 that stimulate a tumour-specific

CC T cell response. Identification of the hsp70 peptides that have at least

CC one mutation or alteration compared with the native sequence, and induce

CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70

CC encoding DNA from one or more tumours; (ii) cloning the amplified

CC sequences into a vector that can be replicated in bacteria;

CC (iii) sequencing fragments in each cultured bacterial colony to identify



CC any hsp70 mutations, and (iv) determining the immunogenicity of the  
 CC mutant peptides identified. The peptides, optionally formulated with an  
 CC agent that induces cellular stress, are used for treatment of cancer,  
 CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,  
 CC cancers of head and neck, particularly kidney cancer). The peptides may  
 CC also be used to increase the proportion of tumour-specific cytotoxic  
 CC T lymphocytes in a cell culture and/or induce these cells to secrete  
 CC cytotoxic factors (specifically interleukin-2, interferon-gamma and  
 CC tumour necrosis factor), particularly where the cells are used to  
 CC stimulate immune defences. The method identifies peptides with high  
 CC immunogenicity and high specificity for particular HLA (human leucocyte  
 CC antigen) alleles.

CC Sequence 10 AA;

Query Match 100.0%; Score 46; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0029;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEGLDIY 9  
 |||||  
 Db 1 slegldiy 9

#### RESULT 4

ID AAB97602 standard; peptide; 10 AA.

AC AAB97602;

DT 30-JUL-2001 (first entry)

DE Heat shock protein 70 (HSP70) peptidic fragment 2.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;

KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

KM cytotoxic response; epitope; antigen presenting cell; fragment 2.

XX Homo sapiens.

PN WO200129190-A1.

PD 26-APR-2001.

PF 29-SEP-2000; 2000WO-EP09530.

PR 15-OCT-1999; 99EP-0120484.

PA (IDM-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

PS WPI; 2001-290909/30.

PT Lymphocytes useful for treating cancer, recognizes specifically

PT transformed human cells with induced and increased membrane expression

PT of heat shock protein -

XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 2 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

CC Sequence 10 AA;

Query Match 100.0%; Score 46; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0029;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SFEGLDIY 9  
 |||||  
 Db 1 slegldiy 9

#### RESULT 5

ID AAB97603 standard; peptide; 10 AA.

AC AAB97603;

DT 30-JUL-2001 (first entry)

DE Heat shock protein 70 (HSP70) peptidic fragment 3.

XX HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease;

KW vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

KM cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX Homo sapiens.

PN WO200129190-A1.

PD 26-APR-2001.

PF 29-SEP-2000; 2000WO-EP09530.

PR 15-OCT-1999; 99EP-0120484.

PA (IDM-) IDM IMMUNO-DESIGNED MOLECULES.

PI Abastado JP, Bartholeyns J;

PS WPI; 2001-290909/30.

PT Lymphocytes useful for treating cancer, recognizes specifically

PT transformed human cells with induced and increased membrane expression

PT of heat shock protein -

XX Claim 8; Page 15; 21pp; English.

XX The amino acid sequence of fragment 3 relating to position 286-295 of  
 CC human heat shock protein 70 (HSP70) is given. The new invention relates  
 CC to lymphocytes which recognise cells of a patient in which overexpression  
 CC of HSP has been induced. Overexpression of HSP leads to a substantial  
 CC increase in the numbers of HSPs and HSP epitopes presented on the  
 CC pericellular membrane. Recognition of increased numbers of HSP epitopes  
 CC on cell pericellular membranes by lymphocytes elicits a cytotoxic  
 CC response which kills the target cells. As a further embodiment of the  
 CC invention, HSP70 epitopes are mutated prior to being loaded into antigen  
 CC presenting cells. This has the effect of increasing the immune response  
 CC to HSP and helps direct the immune response to specific cells, (e.g.  
 CC cancer cells). HSP70 fragments are useful for treating cancer or  
 CC intracellular infections by vaccination. The tolerance of the organism to  
 CC the tumour or to the virus associated HSP is broken using an immunogenic  
 CC mutated form of HSP and induction of a stress on the target tumoural or  
 CC intracellular infected cells.

CC Sequence 10 AA;



Query Match 91.3%; Score 42; DB 22; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDIT 9  
|||  
Db 1 slfegidit 9

## RESULT 6

AAV88409  
ID AAV88409 standard; Protein; 554 AA.

AC AAV88409;

XX 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI: 2000-264458/23.

XX N-PSDB: AAA15621.

XX Abnormal transcription of intracellular HSP70mRNA under acute and

XX chronic continuous load of stress in a human being and its application

XX Examples; Fig 2; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid

XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22

XX and 14q22-24. The invention relates to the abnormal transcription of

XX intracellular HSP70mRNA under acute and chronic stress load in a human.

XX The abnormal transcription of HSP70 can be used in the improvement of

XX stress and response and diagnosis of stress diseases including

XX rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

OY 1 SLFEGIDIT 9  
|||  
Db 200 slfegidit 208

RESULT 7  
AAV88410  
ID AAV88410 standard; Protein; 554 AA.

AC AAV88410;

XX 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI: 2000-264458/23.

XX N-PSDB: AAA15622.

XX Abnormal transcription of intracellular HSP70mRNA under acute and

XX chronic continuous load of stress in a human being and its application

XX Disclosure; Fig 3; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid

XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22

XX and 14q22-24. The invention relates to the abnormal transcription of

XX intracellular HSP70mRNA under acute and chronic stress load in a human.

XX The abnormal transcription of HSP70 can be used in the improvement of

XX stress and response and diagnosis of stress diseases including

XX rheumatism, schizophrenia, depression and nephrotic syndrome.

XX Sequence 554 AA;

OY 1 SLFEGIDIT 9  
|||  
Db 200 slfegidit 208

## RESULT 8

AAV88412  
ID AAV88412 standard; Protein; 554 AA.

AC AAV88412;

XX 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

XX JP2000069999-A.

XX 07-MAR-2000.

XX 01-JUN-1995; 99JP-0257146.

XX 01-JUN-1995; 95JP-0158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI: 2000-264458/23.



XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application  
 PT  
 XX  
 XX  
 PS  
 XX

Disclosure; Fig 5; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 CC  
 XX

Sequence 554 AA;

Query Match 91.3%; Score 42; DB 21; Length 554;  
 Best Local Similarity 88.9%; Pred. No. 1.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEPGIDY 9  
 |||||  
 Db 200 slfigidfy 208

RESULT 9  
 AAY88413

ID AAY88413 standard; Protein; 554 AA.

AC AAY88413;

DT 31-JUL-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KM chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

PN JP2000069999-A.

PD 07-MAR-2000.

PF 01-JUN-1995; 99JP-0257146.

PR 01-JUN-1995; 95JP-0158581.

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

DR WPI; 2000-264458/73.

PT Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application  
 PT  
 XX  
 XX

PS Disclosure; Fig 6; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 CC  
 XX

Sequence 554 AA;

Query Match 91.3%; Score 42; DB 21; Length 554;

Best Local Similarity 88.9%; Pred. No. 1.6;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEPGIDY 9  
 |||||  
 Db 200 slfigidfy 208

RESULT 10  
 AAB23252

ID AAB23252 standard; Protein; 624 AA.

AC AAB23252;

DT 29-JAN-2001 (first entry)

DE Human Hsp72 (heat shock protein 72).

XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
 KM expression modulator; JNK phosphatase inhibitor; antiproliferative;  
 KW drug screening; cancer; Leukemia; lymphoma; solid tumour; sarcoma;  
 KW carcinoma; breast cancer; prostate cancer; premalignant condition.  
 XX  
 XX

OS Homo sapiens.

PN WO200054814-A1.

PD 21-SEP-2000.

PF 17-MAR-2000; 2000WO-US07350.

PR 18-MAR-1999; 99US-0125046.

PA (PHYL-) PHYLOGENY INC.

PI Vollloch VZ, Sherman M;

DR WPI; 2000-647056/62.

DR N-PADB; AAA97541.

PT Identifying compounds that inhibit proliferation of cells and capable  
 PT of modulating the expression of heat shock protein 72 gene and/or  
 PT activity of Hsp72 useful for treating cancers such as leukemia.  
 PT Lymphoma  
 PT  
 XX  
 XX

PS Examples; Fig 16B; 77pp; English.

XX The invention relates to a novel method of identifying compounds that  
 CC inhibit proliferation of cells comprising contacting a test compound with  
 CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
 CC if the test compound inhibits activity or expression of Hsp72.  
 CC Optionally, Hsp72 is contacted with the test compound under optimum  
 CC conditions to allow the two components to interact and bind, forming a  
 CC complex which is detected. The invention also relates to a method of  
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
 CC activation, comprising contacting a test compound with a cell which  
 CC expresses Hsp72, exposing the cell to a heat induced stress and  
 CC determining if the compound inhibits JNK phosphatase activity. The  
 CC invention additionally encompasses compositions comprising an inhibitor  
 CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
 CC inhibiting the proliferation of cells. Modulation of the activity of the  
 CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcoma and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.  
 CC  
 XX

Sequence 624 AA;



Query Match 91.3%; Score 42; DB 21; Length 624;  
 Best Local Similarity 88.9%; Pred. No. 1.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDIV 9  
 |||||  
 Db 286 slfegidiv 294

RESULT 11  
 AAR03930  
 ID AAR03930 standard; Protein: 634 AA.  
 AC AAR03930;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Gallus gallus HSP (chhsp70).  
 XX  
 KM Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Gallus gallus.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 634  
 FT /note= "residue given as "O" in specification"  
 XX  
 XX WO9002564-A.  
 XX  
 XX 22-MAR-1990.  
 XX  
 XX 12-SEP-1989; 89WO-0003955.  
 XX  
 XX 12-SEP-1988; 88US-0243474.  
 XX  
 XX (CODON-)  
 XX  
 XX Dragon E, Faulds D, Sias S;  
 XX  
 XX WPI: 1990-115820/15.  
 XX  
 XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 XX Disclosure: Fig 2.1-2.14; 86pp; English.  
 XX  
 XX According to the legend of Fig 2, the G. gallus HSP sequence has  
 XX 635 amino acid residues, the sequence itself has only 634,  
 XX including "O" (?) at position 634.  
 XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 XX of organisms: 1. M.hypneumoniae (Mhysp70 - AAR03922);  
 XX 2. Bacillus megaterium (Bmehsp70 - AAR03923);  
 XX 3. E. coli (dnak - AAR03924);  
 XX 4. T. cruzi (tc70kd - AAR03925);  
 XX 5. T. cruzi (AAR03926);  
 XX 6. Rat rattus (rathsp70 - AAR03927);  
 XX 7. Xenopus laevis (xl70 - AAR03928);  
 XX 8. Homo sapiens (humhsp70 - AAR03929);  
 XX 9. Gallus gallus (chhsp70 - AAR03930);  
 XX 10. Zea mays (mzehsp70 - AAR03931);  
 XX 11. Serratia marcescens (smahsp70 - AAR03932).  
 XX The proteins having homology to hsp's of T. cruzi can be used in  
 XX vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 XX Mycobacteria species.  
 XX  
 XX Sequence 634 AA;

Query Match 91.3%; Score 42; DB 11; Length 634;  
 Best Local Similarity 88.9%; Pred. No. 1.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDIV 9  
 |||||  
 Db 289 slfegidiv 297

RESULT 12  
 AAR03929  
 ID AAR03929 standard; Protein: 640 AA.  
 AC AAR03929;  
 XX  
 DT 30-AUG-1990 (first entry)  
 XX  
 DE Homo sapiens HSP (humhsp70).  
 XX  
 KM Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 640  
 FT /note= "residue given as "O" in specification"  
 XX  
 XX WO9002564-A.  
 XX  
 XX 22-MAR-1990.  
 XX  
 XX 12-SEP-1989; 89WO-0003955.  
 XX  
 XX 12-SEP-1988; 88US-0243474.  
 XX  
 XX (CODON-)  
 XX  
 XX Dragon E, Faulds D, Sias S;  
 XX  
 XX WPI: 1990-115820/15.  
 XX  
 XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 XX in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.  
 XX  
 XX Disclosure: Fig 2.1-2.14; 86pp; English.  
 XX  
 XX According to the legend of Fig 2, the H. sapiens HSP sequence has  
 XX 641 amino acid residues, the sequence itself has only 640,  
 XX including "O" (?) at position 640.  
 XX Fig. 2 provides an alignment of heat shock proteins from a variety  
 XX of organisms: 1. M.hypneumoniae (Mhysp70 - AAR03922);  
 XX 2. Bacillus megaterium (Bmehsp70 - AAR03923);  
 XX 3. E. coli (dnak - AAR03924);  
 XX 4. T. cruzi (tc70kd - AAR03925);  
 XX 5. T. cruzi (AAR03926);  
 XX 6. Rat rattus (rathsp70 - AAR03927);  
 XX 7. Xenopus laevis (xl70 - AAR03928);  
 XX 8. Homo sapiens (humhsp70 - AAR03929);  
 XX 9. Gallus gallus (chhsp70 - AAR03930);  
 XX 10. Zea mays (mzehsp70 - AAR03931);  
 XX 11. Serratia marcescens (smahsp70 - AAR03932).  
 XX The proteins having homology to hsp's of T. cruzi can be used in  
 XX vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 XX Mycobacteria species.  
 XX  
 XX Sequence 640 AA;

Query Match 91.3%; Score 42; DB 11; Length 640;  
 Best Local Similarity 88.9%; Pred. No. 1.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



XX	AAW10065;
XX	AAW10065 standard; Protein; 640 AA.
ID	AAW10065
RESULT 13	
OS	Homo sapiens.
PN	JP08322577-A.
PD	10-DEC-1996.
PQ	01-JUN-1995; 95JP-0158581.
PR	01-JUN-1995; 95JP-0158581.
PS	(HOKE-) HOKEN KAGAKU KENKYUSHO KK.
PT	WP1; 1997-081088/08.
PT	N-PSDB; AAT58086.
PT	Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load
PS	Claim 1; Fig 1; 13pp; Japanese.
CC	The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24
CC	and 21. primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained stress load.
SQ	Sequence 640 AA;
Query Match	91.3%; Score 42; DB 18; Length 640;
Best Local Similarity	88.9%; Pred. No. 1.8;
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 SLFEGIDIV 9 
Db	286 slfegidiv 294
RESULT 14	
ID	AAB23653
AC	AAB23653 standard; protein; 640 AA.
AD	AAB23653;
DT	05-JAN-2001 (first entry)
DE	Human heat shock protein Hsp70 protein sequence SFO ID NO:5.
KM	Arpase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytosolic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
OS	Homo sapiens.
XX	MO200049041-A1.

```

PD    24-AUG-2000.
XX
XX    18-FEB-2000; 2000OMO-JP00941.
PF
XX    19-FEB-1999;   99JP-00A1535.
PR
XX    (SOME ) SUMITOMO ELECTRIC IND CO.
PA
XX    Shinbara N, Udono H, Yui K;
PI
DR    WPI; 2000-543748/49.
XX
PT    Fused protein capable of inducing cellular immune response, useful as
PT    active ingredient for drug compositions in preventing and/or treating
PT    infectious diseases such as malaria or cancer .
XX
PS    Claim 3; Page 49-52; 72pp; Japanese.
XX
CC    The present invention describes a fused protein (1) prepared from a
CC    peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC    cytotoxic T cells and a protein containing the Arpase domain of a heat
CC    shock protein. Also described are: (1) a drug composition containing (1)
CC    as active ingredient; (2) a DNA encoding (1); (3) an expression vector
CC    containing the DNA of (2); and (4) a transformant which can retain the
CC    expression vector of (3). (1) has cyostatic, immunostimulant and
CC    protooncogene activities, and can be used as a cellular immune response
CC    inducer. The protein is useful as an active ingredient for drug
CC    compositions in preventing and/or treating infectious diseases such as
CC    malaria or cancer e.g. to provide systemic immunity against leukaemia.
CC    The present sequence represents a specifically claimed heat shock
CC    protein for use in a fused protein of the present invention.
XX
SQ    Sequence      640 AA;

Query Match          91.3%; Score 42; DB 21; Length 640;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches      8; Conservative     0; Mismatches      1; Indels      0; Gaps      0;

OY      1 SLFEGIDIV 9
        ||||| |
DB      286 SLFEGIDV 294

RESULT 15
AAAY88408
XX    AAY88408 standard; Protein: 640 AA.
XX
XX    AAY88408;
AC
XX
DT      31-JUL-2000 (first entry)
DE
XX    Human heat shock protein HSP70 amino acid sequence.
XX
KW    Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW    Chromosome 1q42.2-24; transcription; rheumatism; schizophrenia;
KW    depression; nephrotic syndrome.
OS
XX    Homo sapiens.
XX
XX    JP2000069999-A.
PN
XX
PD      07-MAR-2000.
PP
XX    01-JUN-1995;   99JP-0257146.
XX
XX    01-JUN-1995;   95JP-0158581.
XX
XX    (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX    WPI; 2000-264458/23.
XX
XX    N-PSDB; AAA15620.

```



XX Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
XX  
PS Claim 2; Fig 1; 11pp; Japanese.  
XX  
CC This sequence represents the human heat shock protein HSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
XX  
SQ Sequence . 640 AA;

Query Match 91.3%; Score 42; DB 21; Length 640;  
Best Local Similarity 88.9%; Pred. No. 1.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLEFGIDY 9  
|||  
Db 286 slfegidfy 294

Search completed: December 6, 2001, 08:04:01  
Job time: 609 sec



RESULT		ALIGNMENTS	
ID	1		
AAV44200	standard; peptide; 10 AA.		
AAV44200;			
15-FEB-2000	(first entry)		
Heat shock protein 70	amino acid residues 286-295.		
Human; heat shock protein 70; hsp70; identification; tumour; mutation;			
T cell response; amplification; vector; bacterium; cancer; allele;			
cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA;			
immune defence; immunogenicity; specificity; human leucocyte antigen.			
Homo sapiens.			
MO9954464-AL.			
28-OCT-1999.			
22-APR-1999;	99MO-FR00957.		
22-APR-1998;	98PR-0005033.		
(INSR )	INST RODSSY GUSTAVE.		
Triebel F, Gaudin C;			
WPI; 2000-013251/01.			
Identifying mutant peptides from heat-shock protein 70, for treatment			
of cancer -			



PS Claim 10; Page 6; 56pp; French.

XX CC This peptide corresponds to amino acid residues 286-295 of the human

CC heat shock protein 70 (hsp70). The invention relates to a method of

CC identifying peptides, derived from hsp70 that stimulate a tumour-specific

CC T cell response. Identification of the hsp70 peptides that have at least

CC one mutation or alteration compared with the native sequence, and induce

CC a tumour-specific T-cell response, comprises: (i) amplifying hsp70

CC encoding DNA from one or more tumours; (ii) cloning the amplified

CC sequences into a vector that can be replicated in bacteria;

CC (iii) sequencing fragments in each cultured bacterial colony to identify

CC any hsp70 mutations; and (iv) determining the immunogenicity of the

CC mutant peptides identified. The peptides, optionally formulated with an

CC agent that induces cellular stress, are used for treatment of cancer,

CC particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma,

CC cancers of head and neck, particularly kidney cancer). The peptides may

CC also be used to increase the proportion of tumour-specific cytotoxic

CC T lymphocytes in a cell culture and/or induce these cells to secrete

CC cytotoxic factors (specifically interleukin-2, interferon-gamma and

CC tumour necrosis factor), particularly where the cells are used to

CC stimulate immune defences. The method identifies peptides with high

CC immunogenicity and high specificity for particular HLA (human leucocyte

CC antigen) alleles.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDITYT 10

|||||||

Db 1 slfegidlyt 10

RESULT 2

AAB97602

ID AAB97602 standard; peptide: 10 AA.

XX AC AAB97602;

XX DT 30-JUL-2001 (first entry)

XX DE Heat shock protein 70 (HSP70) peptidic fragment 2.

XX KW HSP: HSP70: heat shock protein 70; cancer; chronic infectious disease;

XX KM vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

XX KW cytotoxic response; epitope; antigen presenting cell; fragment 2.

XX OS Homo sapiens.

XX PN WO200129190-A1.

XX PD 26-APR-2001.

XX PF 29-SEP-2000; 2000WO-EP09530.

XX PR 15-OCT-1999; 99EP-0120484.

XX PA (IDM-) IDM IMMUNO-DESIGNED MOLECULES.

XX PI Abastado JP, Bartholeyns J;

XX DR WPI: 2001-290909/30.

XX PT Lymphocytes useful for treating cancer, recognizes specifically

XX PT transformed human cells with induced and increased membrane expression

XX PT of heat shock protein -

XX PS Claim 8; Page 15; 21pp; English.

XX CC The amino acid sequence of fragment 2 relating to position 286-295 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates

CC to lymphocytes which recognise cells of a patient in which overexpression

CC of HSP has been induced. Overexpression of HSP leads to a substantial

CC increase in the numbers of HSPs and HSP epitopes presented on the

CC pericellular membrane. Recognition of increased numbers of HSP epitopes

CC on cell pericellular membranes by lymphocytes elicits a cytotoxic

CC response which kills the target cells. As a further embodiment of the

CC invention, HSP70 epitopes are mutated prior to being loaded into antigen

CC presenting cells. This has the effect of increasing the immune response

CC to HSP and helps direct the immune response to specific cells, (e.g.

CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to

CC the tumour or to the virus associated HSP is broken using an immunogenic

CC mutated form of HSP and induction of a stress on the target tumoural or

CC intracellular infected cells.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFEGIDITYT 10

|||||||

Db 1 slfegidlyt 10

RESULT 3

AAB97603

ID AAB97603 standard; peptide: 10 AA.

XX AC AAB97603;

XX DT 30-JUL-2001 (first entry)

XX DE Heat shock protein 70 (HSP70) peptidic fragment 3.

XX KW HSP: HSP70: heat shock protein 70; cancer; chronic infectious disease;

XX KM vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte;

XX KW cytotoxic response; epitope; antigen presenting cell; fragment 3.

XX OS Homo sapiens.

XX PN WO200129190-A1.

XX PD 26-APR-2001.

XX PF 29-SEP-2000; 2000WO-EP09530.

XX PR 15-OCT-1999; 99EP-0120484.

XX PA (IDM-) IDM IMMUNO-DESIGNED MOLECULES.

XX PI Abastado JP, Bartholeyns J;

XX DR WPI: 2001-290909/30.

XX PT Lymphocytes useful for treating cancer, recognizes specifically

XX PT transformed human cells with induced and increased membrane expression

XX PT of heat shock protein -

XX PS Claim 8; Page 15; 21pp; English.

XX CC The amino acid sequence of fragment 3 relating to position 286-295 of

CC human heat shock protein 70 (HSP70) is given. The new invention relates

CC to lymphocytes which recognise cells of a patient in which overexpression

CC of HSP has been induced. Overexpression of HSP leads to a substantial

CC increase in the numbers of HSPs and HSP epitopes presented on the

CC pericellular membrane. Recognition of increased numbers of HSP epitopes

CC on cell pericellular membranes by lymphocytes elicits a cytotoxic

CC response which kills the target cells. As a further embodiment of the

CC invention, HSP70 epitopes are mutated prior to being loaded into antigen

CC presenting cells. This has the effect of increasing the immune response

CC to HSP and helps direct the immune response to specific cells, (e.g.

CC cancer cells). HSP70 fragments are useful for treating cancer or

CC intracellular infections by vaccination. The tolerance of the organism to

CC the tumour or to the virus associated HSP is broken using an immunogenic

CC mutated form of HSP and induction of a stress on the target tumoural or

CC intracellular infected cells.



CC presenting cells. This has the effect of increasing the immune response  
CC to HSP and helps direct the immune response to specific cells, (e.g.  
CC cancer cells). HSP70 fragments are useful for treating cancer or  
CC intracellular infections by vaccination. The tolerance of the organism to  
CC the tumour or to the virus associated HSP is broken using an immunogenic  
CC mutated form of HSP and induction of a stress on the target tumoural or  
CC intracellular infected cells.

SQ Sequence 10 AA;

Query Match 92.2%; Score 47; DB 22; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.0021; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDIVT 10  
| | | | | | | |  
DB 1 sifegidfyt 10

RESULT 4

AAV88409 standard; Protein; 554 AA.

AAV88409;

31-JUL-2000 (first entry)

Human heat shock protein SHSP70 amino acid sequence.

Human: heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

Homo sapiens.

JP2000069999-A.

07-MAR-2000.

01-JUN-1995; 99JP-0257146.

01-JUN-1995; 95JP-0158581.

(HOKE-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 2000-264458/23.

N-PSDB; AAA15621.

Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

Examples; Fig 2; 11pp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

SQ Sequence 554 AA;

Query Match 92.2%; Score 47; DB 21; Length 554;

Best Local Similarity 90.0%; Pred. No. 0.2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDIVT 10  
| | | | | | | |  
DB 200 sifegidfyt 209

RESULT 5

AAV88410 standard; Protein; 554 AA.

AAV88410;

31-JUL-2000 (first entry)

Human heat shock protein SHSP70 amino acid sequence.

Human: heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

Homo sapiens.

JP2000069999-A.

07-MAR-2000.

01-JUN-1995; 99JP-0257146.

01-JUN-1995; 95JP-0158581.

(HOKE-) HOKEN KAGAKU KENKYUSHO KK.

WPI; 2000-264458/23.

N-PSDB; AAA15622.

Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

Disclosure; Fig 3; 11pp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.

SQ Sequence 554 AA;

Query Match 92.2%; Score 47; DB 21; Length 554;

Best Local Similarity 90.0%; Pred. No. 0.2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDIVT 10  
| | | | | | | |  
DB 200 sifegidfyt 209

RESULT 6

AAV88412 standard; Protein; 554 AA.

AAV88412;

31-JUL-2000 (first entry)

Human heat shock protein SHSP70 amino acid sequence.

Human: heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
KW depression; nephrotic syndrome; SHSP70.

Homo sapiens.

OS



PN JP2000069999-A.  
XX  
PD 07-MAR-2000.  
XX  
PF 01-JUN-1995; 99JP-0257146.  
XX  
PR 01-JUN-1995; 95JP-0158581.  
XX  
PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
XX  
DR WPI; 2000-264458/23.  
XX  
PT Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application  
PT  
PS Disclosure; Fig 5; 11pp; Japanese.  
XX  
XX This sequence represents the human heat shock protein SHSP70 amino acid  
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
CC  
SQ Sequence 554 AA:

Query Match 92.2%; Score 47; DB 21; Length 554;  
Best Local Similarity 90.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDITYT 10  
|||  
DB 200 sltegidfyt 209

## RESULT 7

AAV88413  
ID AAV88413 standard; Protein; 554 AA.

XX AAV88413;

DT 31-JUN-2000 (first entry)

DE Human heat shock protein SHSP70 amino acid sequence.

KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

OS JP2000069999-A.

PN 07-MAR-2000.

PF 01-JUN-1995; 99JP-0257146.

PR 01-JUN-1995; 95JP-0158581.

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

DR WPI; 2000-264458/23.

PT Abnormal transcription of intracellular HSP70mRNA under acute and  
PT chronic continuous load of stress in a human being and its application

PS Disclosure; Fig 6; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
CC and 14q22-24. The invention relates to the abnormal transcription of  
CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
CC The abnormal transcription of HSP70 can be used in the improvement of  
CC stress and response and diagnosis of stress diseases including  
CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
CC  
SQ Sequence 554 AA:

Query Match 92.2%; Score 47; DB 21; Length 554;  
Best Local Similarity 90.0%; Pred. No. 0.2;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDITYT 10  
|||  
DB 200 sltegidfyt 209

## RESULT 8

AAB23252  
ID AAB23252 standard; Protein; 624 AA.

XX AAB23252;

DT 29-JAN-2001 (first entry)

DE Human Hsp72 (heat shock protein 72).

KW Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;  
KW expression modulator; JNK phosphatase inhibitor; antiproliferative;  
KW drug screening; cancer; Leukemia; lymphoma; solid tumour; sarcoma;  
KW carcinoma; breast cancer; prostate cancer; premalignant condition.

XX Homo sapiens.

OS WO200054814-A1.

PN 21-SEP-2000.

PF 17-MAR-2000; 2000WO-US07350.

PR 18-MAR-1999; 99US-0125046.

PA (PHYL-) PHYLOGENY INC.

PI Vollooch VZ, Sherman M;

DR WPI; 2000-647056/62.

DR N-PSDB; AAA97541.

PT Identifying compounds that inhibit proliferation of cells and capable  
PT of modulating the expression of heat shock protein 72 gene and/or  
PT activity of Hsp72 useful for treating cancers such as leukemia,  
PT lymphoma

PS Examples; Fig 16B; 77pp; English.

XX The invention relates to a novel method of identifying compounds that  
CC inhibit proliferation of cells comprising contacting a test compound with  
CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining  
CC if the test compound inhibits activity or expression of Hsp72.  
CC Optionally, Hsp72 is contacted with the test compound under optimum  
CC conditions to allow the two components to interact and bind, forming a  
CC complex which is detected. The invention also relates to a method of  
CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase  
CC activation, comprising contacting a test compound with a cell which  
CC expresses Hsp72, exposing the cell to a heat induced stress and  
CC determining if the compound inhibits JNK phosphatase activity. The  
CC invention additionally encompasses compositions comprising an inhibitor  
CC of Hsp72 or JNK phosphatase activity. The compounds identified as  
CC inhibitors of Hsp72 or JNK phosphatase activity are useful for  
CC inhibiting the proliferation of cells. Modulation of the activity of the



CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such  
 CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and  
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit  
 CC Hsp72 activity can also be administered to treat premalignant conditions  
 CC and to prevent progression to a neoplastic or malignant state. The  
 CC compounds that inhibit Hsp72 function are administered to a patient  
 CC having a disease or disorder mediated by an increase of Hsp72 expression  
 CC or activity relative to normal levels. The present sequence represents  
 CC human Hsp72 used in the exemplifications of the invention.

XX Sequence 624 AA;

Query Match 92.2%; Score 47; DB 21; Length 624;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDIVT 10  
 |||||  
 Db 286 slfegidlyt 295

RESULT 9  
 AAR03930  
 ID AAR03930 standard; Protein; 634 AA.

XX AAR03930;

XX 30-AUG-1990 (first entry)

XX Gallus gallus HSP (chhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Gallus gallus.

XX Key Location/Qualifiers

FT Misc-difference 634 /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the G. gallus HSP sequence has  
 CC 635 amino acid residues, the sequence itself has only 634,  
 CC including "O" (?) at position 634.

CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypneumoninae (Mhyhsp70 - AAR03922);

CC 2. Bacillus megaterium (Bmebsp70 - AAR03923);

CC 3. E. coli (dnak - AAR03924);

CC 4. T. cruzi (tc70kd - AAR03925);

CC 5. T. cruzi (AAR03926);

CC 6. Rat rattus (rathsp70 - AAR03927);

CC 7. Xenopus laevis (xl70 - AAR03928);

CC 8. Homo sapiens (humhsp70 - AAR03929);

CC 9. Gallus gallus (chhsp70 - AAR03930);

CC 10. Zea mays (mzhsp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).  
 CC The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.

XX Sequence 634 AA;

Query Match 92.2%; Score 47; DB 11; Length 634;  
 Best Local Similarity 90.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDIVT 10  
 |||||  
 Db 289 slfegidlyt 298

RESULT 10  
 AAR03929  
 ID AAR03929 standard; Protein; 640 AA.

XX AAR03929;

XX 30-AUG-1990 (first entry)

XX Homo sapiens HSP (humhsp70).

XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 640 /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1989; 89WO-0003955.

XX 12-SEP-1988; 88US-0243474.

XX (CODO-) CODON.

XX Dragon E, Faulds D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins from Trypanosoma cruzi - used  
 PT in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has  
 CC 641 amino acid residues, the sequence itself has only 640,  
 CC including "O" (?) at position 640.

CC Fig. 2 provides an alignment of heat shock proteins from a variety  
 CC of organisms: 1. M.hypneumoninae (Mhyhsp70 - AAR03922);

CC 2. Bacillus megaterium (Bmebsp70 - AAR03923);

CC 3. E. coli (dnak - AAR03924);

CC 4. T. cruzi (tc70kd - AAR03925);

CC 5. T. cruzi (AAR03926);

CC 6. Rat rattus (rathsp70 - AAR03927);

CC 7. Xenopus laevis (xl70 - AAR03928);

CC 8. Homo sapiens (humhsp70 - AAR03929);

CC 9. Gallus gallus (chhsp70 - AAR03930);

CC 10. Zea mays (mzhsp70 - AAR03931);

CC 11. Serratia marcescens (smahsp70 - AAR03932).

XX The proteins having homology to hsp's of T. cruzi can be used in  
 CC vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and  
 CC Mycobacteria species.







XX 07-MAR-2000.  
 XX 01-JUN-1995; 99JP-0257146.  
 XX 01-JUN-1995; 95JP-0158581.  
 XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.  
 XX WPI: 2000-264458/23.  
 XX N-PSDB: AAA15620.  
 CC Abnormal transcription of intracellular HSP70mRNA under acute and  
 CC chronic continuous load of stress in a human being and its application  
 CC Claim 2; Fig 1; 11pp; Japanese.  
 CC This sequence represents the human heat shock protein HSP70 amino acid  
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 CC Sequence 640 AA;  
 SQ

Query Match 92.2%; Score 47; DB 21; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDYIT 10  
 |||||  
 Db 286 slfegidfty 295

## RESULT 14

AAV88411  
 ID AAV88411 standard; Protein; 640 AA.

AC AAV88411;

DT 31-JUL-2000 (first entry)

DE Human heat shock protein LHSF70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;  
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;  
 KW depression; nephrotic syndrome; LHSF70.

OS Homo sapiens.

PN JP2000069999-A.

PD 07-MAR-2000.

PF 01-JUN-1995; 99JP-0257146.

PR 01-JUN-1995; 95JP-0158581.

PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

DR WPI: 2000-264458/23.

XX Abnormal transcription of intracellular HSP70mRNA under acute and  
 PT chronic continuous load of stress in a human being and its application

PS Disclosure; Fig 4; 11pp; Japanese.

CC This sequence represents the human heat shock protein LHSF70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22  
 CC and 14q22-24. The invention relates to the abnormal transcription of  
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.  
 CC The abnormal transcription of HSP70 can be used in the improvement of  
 CC stress and response and diagnosis of stress diseases including  
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.  
 CC Sequence 640 AA;  
 SQ

Query Match 92.2%; Score 47; DB 21; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDYIT 10  
 |||||  
 Db 286 slfegidfty 295

## RESULT 15

AAAR3004  
 ID AAR3004 standard; protein; 641 AA.

AC AAR3004;

DT 20-MAY-1994 (first entry)

DE Mature mouse sperm 70KD heat shock protein.

XX Sulphoglycolipid immobilising protein 1; sperm plasma membrane;  
 KW HSC70B; mammalian; infertility; mycoplasma; HSP70.

OS Mus musculus.

FN Key Location/Qualifiers  
 FT 1..385

FT /label= 44KD\_ATPase\_fragment  
 FT /note= "peptides comprising an intact domain from  
 the ATPase fragment of hsp70 are claimed;  
 the peptides are homologous to sequences  
 conserved between SLIP1 and 74.5kd  
 mycoplasma protein"

FT Domain

FT 1..39

FT /label= IA

FT /note= "part"

FT Domain

FT 40..115

FT /label= IB

FT Domain

FT 116..188

FT /label= IA

FT /note= "part"

FT Domain

FT 189..228

FT /label= IIA

FT /note= "part"

FT Domain

FT 229..306

FT /label= IIB

FT 307..385

FT /label= IIA

FT /note= "part"

PN MO9321954-A.

PD 11-NOV-1993.

PF 22-APR-1993; 93WO-US03816.

PR 24-APR-1992; 92US-0873961.

PA (BERL-) BERLEX LAB INC.

PA (OTTA-) OTTAWA CIVIC HOSPITAL.

XX Fauds DH, Lingwood CA, Tanphalchitr N;

XX WPI: 1993-368422/46.



XX Mammalian fertilisation decrease for detecting and treating  
PT infertility - using sulpho glyco lipid immobilising protein  
PT 1-sulphated-glyco moiety interfering compsn., for mycoplasma  
PT infection treatment  
XX  
XX Claim 2 and Claim 17; Page 60-62; 77pp; English.  
PS  
XX The likelihood of mammalian fertilisation is decreased by contacting  
CC a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/  
CC sulphated glyco-moiety interfering composition. The interfering  
CC compsn. is e.g. the heat shock 70kd protein, SLIP1 (or analogues  
CC such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid  
CC sequence AAR43002) or the 74.5kd mycoplasma protein (AAR43003).  
XX  
XX Sequence 641 AA;  
SQ

Query Match 92.2%; Score 47; DB 14; Length 641;  
Best Local Similarity 90.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDITYT 10  
|||  
|||  
Db 286 slfegidtyt 295

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Job time: 611 sec

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CC or send an email to license@sb-sib.ch).
CC EMBL: L16764; AAA17441.1; -
DR EMBL: X77208; CAA54423.1; -
DR EMBL: X77207; CAA54422.1; -
DR EMBL: X74271; CAA52328.1; -
DR HSSP: P19120; INGC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
FT CONFLICT 71 72 KR -> NG (IN REF. 3).
FT CONFLICT 227 227 D -> H (IN REF. 2 AND 3).
FT CONFLICT 408 408 G -> A (IN REF. 3).
SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10
Db 286 SLEFGIDFYT 295

RESULT 15
HS71_YEAST STANDARD; PRT; 641 AA.
AC P10591;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).
GN SSA1 OR YAL005C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=69128457; Pubmed=2644626;
RA Slater M.R.; Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX MEDLINE=95028152; Pubmed=7941740;
RA Clark M.W.; Keng T.; Storms R.K.; Zhong W.; Fortin N.; Zeng B.;
RA Delaney S.; Ouellette B.F.F.; Barton A.B.; Kaback D.B.; Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
the 42 kbp SP07-CENT-CDCl5 region.";
RL Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 590-641 FROM N.A.
RX MEDLINE=85087943; Pubmed=6096826;
RA Ogden R.C.; Lee M.-C.; Knapp G.;
RT "Transfer RNA splicing in Saccharomyces cerevisiae: defining the
substrates.";
RL Nucleic Acids Res. 12:9367-9382(1984).
RN [4]
RP REVISIONS TO 207; 417 AND 421.
RA Slater M.R.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=5288C;
RX MEDLINE=95203288; Pubmed=7895733;

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RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [6]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; Pubmed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [7]
RP ACETYLATION.
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
CC ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
CC ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL: X12926; CAA13393.1; -
DR EMBL: L22015; AAC04952.1; ALT_SEQ.
DR PIR: S25438; HHBYAI.
DR PIR: S42164; S42164.
DR HSSP: P19120; IATR.
DR SWISS-2DPAGE: P10591; YEAST.
DR YEPD: 9788; -
DR SGD: S0000004; SSA1.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
FT SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10
Db 282 SLEFGIDFYT 291

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Job time: 420 sec







NCBI\_TaxId=9606;  
 [1] SEQUENCE FROM N.A.  
 MEDLINE=91055806; PubMed=1700760;  
 RA Milner C.M., Campbell R.D.;  
 "Structure and expression of the three MHC-linked HSP70 genes.";  
 Immunogenetics 32:242-251(1990).  
 [2] SEQUENCE FROM N.A.  
 MEDLINE=86016721; PubMed=3931075;  
 RA Hunt C., Morimoto R.I.;  
 "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";  
 Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
 [3] SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).  
 RA Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,  
 Loretz C., Ratcliffe A., Abbasi N., Shafer T., Hood L.;  
 "Sequence of the human major histocompatibility complex class III region.";  
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 [4] SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
 RA MEDLINE=89184548; PubMed=2538825;  
 RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;  
 "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";  
 Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
 [5] SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
 RA MEDLINE=87066768; PubMed=3786141;  
 RA Drabant B., Genthe A., Benescke B.-J.;  
 "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";  
 Nucleic Acids Res. 14:8933-8949(1986).  
 [6] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
 RA Ostpluk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 "Structure of a new crystal form of human hsp70 ATPase domain.";  
 Acta Crystallogr. D 55:1105-1107(1999).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRYING FORCE FOR PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M59828; AAA63226.1; -  
 DR EMBL: M59830; AAA63227.1; -  
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 DR EMBL: AF134726; AAD21815.1; -  
 DR EMBL: M11717; AAA52697.1; -  
 DR EMBL: M24743; AAA59844.1; -  
 DR EMBL: M24744; AAA59845.1; -  
 DR EMBL: X04676; CAA28381.1; -  
 DR EMBL: X04677; CAA28382.1; -

DR PIR: A29160; A29160.  
 DR PIR: A45871; A45871.  
 DR PIR: A25773; A25773.  
 DR PDB: 1H3O; 21-OCT-98.  
 DR SWISS-2DPAGE: P08107; HUMAN.  
 DR MIM: 140550; -  
 DR MIM: 603012; -  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PRO0301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chapterone; Heat shock; Multigene family; MHC III;  
 KW 3D-structure.  
 FT CONFLICT 7 7 I -> V (IN REF. 2).  
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).  
 FT CONFLICT 370 370 A -> G (IN REF. 2).  
 FT CONFLICT 469 469 MISSING (IN REF. 2).  
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).  
 SQ SEQUENCE 641 AA; 70052 MW; 78F513118C96DE86 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10  
 |||||  
 Db 286 SLFEGIDFYT 295

RESULT 12  
 HS71\_MOUSE STANDARD; PRT; 641 AA.  
 ID HS71\_MOUSE  
 AC P17879; 061689;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN HSPA1 OR HSP70A1 OR HSP70-1 OR HCP70.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90236310; PubMed=2332169;  
 RA Hunt C., Calderwood S.;  
 "Characterization and sequence of a mouse hsp70 gene and its expression in mouse cell lines.";  
 Gene 87:199-204(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Auljane L., Shiang S., Moran L.A.;  
 "Structure and expression of an inducible HSP70-encoding gene from Mus musculus.";  
 Gene 146:273-278(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN-AX3;
RX MEDLINE=94043116; PubMed=8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Ablactin, an agonist-regulated F-actin capping activity is associated with an Hsc70 in Dictyostelium.";
RL J. Biol. Chem. 268:23267-23274(1993).
CC -1- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP2 AND CAP34.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -1- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL: X75263; CAA53039.1; -
DR EMBL: L22736; AAA33219.1; -
DR PIR: S37394; S37394.
DR HSSP: P19120; INGU.
DR SWISS-2DPAGE: P36415; DICTY.
DR DictyDb; DD01078; hspB.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF000012; HSP70.1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone.
KM ATP-binding; Chaperone.
FT CONFLICT 1 29 MSGSIGDICTVSCVGMWDREIITAND ->
FT FT IHHINGNMTWYVESPVSEVLSFN (IN REF. 2).
FT CONFLICT 32 32 N -> T (IN REF. 2).
FT CONFLICT 64 64 V -> A (IN REF. 2).
FT CONFLICT 180 180 R -> A (IN REF. 2).
FT CONFLICT 237 237 S -> A (IN REF. 2).
FT CONFLICT 240 240 V -> A (IN REF. 2).
FT CONFLICT 341 341 I -> L (IN REF. 2).
FT CONFLICT 352 352 F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 2E6BDC2DB96A9F5D CRC64;

Query Match 92.2%; Score 47; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10
DB 284 SLEFGIDFYT 293
|||||

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=95126904; PubMed=7826329;
RA Gutierrez J.A., Guerriero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (hsp70) mimics Hsp70 isoforms from tissues.";
RL Biochem. J. 305:197-203(1995).
CC [2]
RN SEQUENCE OF 212-641 FROM N.A.
RC STRAIN-ANGUS;
RX MEDLINE=95030563; PubMed=7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An Alu polymorphism at the bovine 70 kD heat-shock protein-1 (hsp70-1) locus.";
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
DR EMBL: U09861; AAA73914.1; -
DR EMBL: U02891; AAA03450.1; -
DR HSSP: P19120; INGU.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF000012; HSP70.1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KM ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10
DB 286 SLEFGIDFYT 295
|||||

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RESULT 10
HST1_BOVIN
ID HST1_BOVIN STANDARD; PRT; 641 AA.
AC 027975; 027964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;

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RESULT 11
HST1_HUMAN
ID HST1_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9UQO0; Q9UQJ9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1) (HSP70-1/HSP70-2).
GN (HSPA1A OR HSPA1) AND HSPA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KM Heat shock; ATP-binding; Multigene family; Acetylation;  
 KW Phosphorylation.  
 FT INIT\_MET 0  
 FT MOD\_RES 1  
 SO SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEPGIDLYT 10  
 |||||  
 DB 282 SLEPGIDFYT 291

## RESULT 7

HS7A\_PARLI STANDARD; PRT; 639 AA.  
 AC 006248;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).  
 OS HSP70IV.  
 OS Paracentrotus lividus (Common sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;  
 OC Paracentrotus.  
 OX NCBI\_TaxID=7656;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9077053; PubMed=1339375;  
 RA Sconzo G., Scardina G., Ferraro M.G.;  
 RT "Characterization of a new member of the sea urchin Paracentrotus  
 RT lividus hsp70 gene family and its expression.";  
 RL Gene 121:353-358(1992).  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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CC EMBL: X61379; CAA43653.1; -.  
 DR PIR; JCI391; JCI391.  
 DR HSSP; P19120; INGI.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70\_1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KM ATP-binding; Heat shock; Multigene family.  
 SO SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match 92.2%; Score 47; DB 1; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEPGIDLYT 10  
 |||||  
 DB 286 SLEPGIDFYT 295

RESULT 8

HS7A\_CAEEL STANDARD; PRT; 640 AA.  
 ID HS7A\_CAEEL  
 AC P09446;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN A.  
 GN HSP-1 OR HSP70A.  
 OS Caenorhabditis elegans.  
 OS Caenorhabditis elegans.  
 OS Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88297155; PubMed=2841196;  
 RA Snutch T.P., Heschl M.F.P., Baillie D.L.;  
 RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic  
 RT characterization.";  
 RL Gene 64:241-255(1989).  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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CC EMBL: M18540; AAA28078.1; -.  
 DR PIR; JTD285; HKW7A.  
 DR HSSP; P19120; INGI.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70\_1.  
 DR PRINTS; PR00301; HEATSHOCK70.  
 DR PROSITE; PS00297; HSP70\_1; 1.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KM ATP-binding; Heat shock; Multigene family.  
 SO SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 640;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEPGIDLYT 10  
 |||||  
 DB 287 SLEPGIDFYT 296

## RESULT 9

HS7C\_DICDI STANDARD; PRT; 640 AA.  
 ID HS7C\_DICDI  
 AC P36415;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).  
 GN HSPB OR HSC70.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX3;  
 RX MEDLINE=94008983; PubMed=8404847;  
 RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F.,  
 RA Noegel A.A., Schleicher M.;  
 RT "The heat shock cognate protein from Dictyostelium affects actin  
 RT polymerization through interaction with the actin-binding protein  
 RT cap32/34.";  
 RL EMBO J. 12:3763-3771(1993).



```

RESULT 5
HS71_CERAE STANDARD: PRT: 638 AA.
AC Q28222:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1.
GN HSPAL.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC
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CC
CC EMBL: X70684; CAA50019.1; -.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70.1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70.1; 1.
CC PROSITE: PS00329; HSP70.2; 1.
CC PROSITE: PS01036; HSP70.3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
KW SEQUENCE 638 AA; 69920 MW; D55076A0FFABAB3 CRC64;

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Query Match 92.2%; Score 47; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 SLEFEGIDLYT 10
   |||||
Db 284 SLEFEGIDFYT 293

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RESULT 6
HS72_YEAST STANDARD: PRT: 638 AA.
AC P10592:
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

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DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HEAT SHOCK PROTEIN SSA2.
GN SSA2 OR YL1024C OR I0931.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=89128457; PubMed=2644626;
RA Slater M.R., Craig E.A.;
RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 17:805-806(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Purnelle B., Goffeau A.;
RT Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 71-638 FROM N.A.
RA Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
RT Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 91-97 AND 325-341.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 186-195.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACETYLATION, AND PHOSPHORYLATION.
RA Garels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT Submitted (Sep-1994) to the SWISS-PROT data bank.
RN -1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
RN BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
RN ENOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
RN SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
RN ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
RN -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
RN -1- PTM: PHOSPHORYLATED.
RN -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
RN
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RN
RN EMBL: X12927; CAA31394.1; -.
RN EMBL: Z73129; CAA97472.1; -.
RN EMBL: X97560; CAA66167.1; -.
RN PIR: S20139; S20139.
RN HSSP: P19120; 1NG1.
RN SWISS-2DPAGE; P10592; YEAST.
RN YEPD; 9800; -.
RN SGD: S0003947; SSA2.
RN InterPro: IPR001023; HSP70.
RN Pfam: PF00012; HSP70.1.
RN PRINTS: PR00301; HEATSHOCK70.

```



OS Onchocerca volvulus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 CC Onchocercidae; Onchocerca.  
 OX NCBI\_TaxID=6282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89201313; PubMed=2704388;  
 RA Rothstein N.M., Higashi G., Yates J., Rajan T.V.;  
 RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in  
 amicrofilaremic individuals from a filariasis-endemic area."  
 RL Mol. Biochem. Parasitol. 33:229-236(1989).  
 CC -1- DISEASE: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A  
 MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
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 CC -----

DR EMBL: J04006; AAA29417.1; -.  
 DR HSSP: P19120; IATR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PROSITE: PS00297; HSP70\_1; PARTIAL.  
 DR PROSITE: PS00329; HSP70\_2; PARTIAL.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Heat shock.  
 KW NON\_TER 1  
 FT NON\_TER 322 322  
 SQ SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 322;  
 Best Local Similarity 90.0%; Pred. No. 0.059;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10  
 |||||  
 DB 43 SLFEGIDFYT 52

RESULT 3  
 HS70\_PENCI STANDARD; PRT; 503 AA.  
 AC 092260;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).  
 GN HSP70.  
 OS Penicillium citrinum.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 CC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
 OX NCBI\_TaxID=5077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;  
 RT "Molecular cloning and expression of a penicillium citrinum  
 RT allergen with sequence homology and antigenic cross-reactivity to  
 RT a hsp70 human heat shock protein."  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC -----

Query Match 92.2%; Score 47; DB 1; Length 322;  
 Best Local Similarity 90.0%; Pred. No. 0.059;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 CC -----

DR EMBL: U64207; AAB06397.1; -.  
 DR HSSP: P19120; 3HSC.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chapterone; Heat shock; Allergen.  
 KW NON\_TER 1  
 FT NON\_TER 503 503  
 SQ SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;

Query Match 92.2%; Score 47; DB 1; Length 503;  
 Best Local Similarity 90.0%; Pred. No. 0.097;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10  
 |||||  
 DB 154 SLFEGIDFYT 163

RESULT 4  
 HS70\_CHICK STANDARD; PRT; 634 AA.  
 ID HS70\_CHICK  
 AC P08106;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN (HSP70).  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86304452; PubMed=3017985;  
 RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;  
 RT "Organization, nucleotide sequence, and transcription of the chicken  
 RT HSP70 gene."  
 RL J. Biol. Chem. 261:12692-12699(1986).  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: J02579; AAA48825.1; -.  
 DR PIR: A25646; A25646.  
 DR HSSP: P19120; IATR.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Heat shock; Multigene family.  
 KW ATP-binding; Heat shock; Multigene family.  
 SQ SEQUENCE 634 AA; 69750 MW; 4270F7F0BD365AEB CRC64;

Query Match 92.2%; Score 47; DB 1; Length 634;  
 Best Local Similarity 90.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLYT 10  
 |||||  
 DB 269 SLFEGIDFYT 298







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RN      (1)
RP      SEQUENCE FROM N.A.
RA      Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RL      D'Amoroso E.;
RL      Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR      EMBL; 227118; CAAB1642.1; -.
DR      HSSP; P08107; 1HQO.
DR      InterPro; IPR001023; HSP70.
DR      Pfam; PF000012; HSP70; 1.
DR      PRINTS; PR00301; HEATSHOCK70.
DR      PROSITE; PS00329; HSP70_2; 1.
DR      PROSITE; PS01036; HSP70_3; 1.
KW      Heat shock.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;

Query Match
Best Local Similarity 92.2%; Score 47; DB 11; Length 455;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLEPGIDLYT 10
DB      254 SLEPGIDFYT 263

RESULT 14
O44350
ID      O44350      PRELIMINARY;      PRT; 467 AA.
AC      O44350;
DT      01-JUN-1998 (TREMBlrel. 06, Created)
DT      01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN      HSP70.
OS      Chondrosia reniformis.
OC      Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC      Chondrosida; Chondrillidae; Chondrosia.
OX      NCBI_TaxID=68574;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      Borchiellini C., Le Parco Y.;
RL      Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF026517; AAC05362.1; -.
DR      HSSP; P08109; 1CKR.
DR      InterPro; IPR001023; HSP70.
DR      Pfam; PF00012; HSP70; 1.
DR      PRINTS; PR00301; HEATSHOCK70.
DR      PROSITE; PS00329; HSP70_2; 1.
DR      PROSITE; PS01036; HSP70_3; 1.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 467 AA; 51707 MW; 0DBE6920F2E6EA96 CRC64;

Query Match
Best Local Similarity 92.2%; Score 47; DB 5; Length 467;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLEPGIDLYT 10
DB      252 SLEPGIDFYT 261

RESULT 15
O44352
ID      O44352      PRELIMINARY;      PRT; 467 AA.
AC      O44352;
DT      01-JUN-1998 (TREMBlrel. 06, Created)
DT      01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).

```

```

GN      HSP70.
OS      Petrobiona massilliana.
OC      Eukaryota; Metazoa; Porifera; Calcarea; Calcarenea; Petrobionidae;
OC      Petrobiona.
OX      NCBI_TaxID=68578;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      Borchiellini C., Le Parco Y.;
RL      Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF026520; AAC05364.1; -.
DR      HSSP; P08109; 1CKR.
DR      InterPro; IPR001023; HSP70.
DR      Pfam; PF00012; HSP70; 1.
DR      PRINTS; PR00301; HEATSHOCK70.
DR      PROSITE; PS01036; HSP70_3; 1.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 467 AA; 51458 MW; 23EB28FPD1873DA6 CRC64;

Query Match
Best Local Similarity 92.2%; Score 47; DB 5; Length 467;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SLEPGIDLYT 10
DB      252 SLEPGIDFYT 261

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Search completed: December 6, 2001, 07:56:53  
Job time: 181 sec



Best Local Similarity 90.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10  
| | | | | | | |  
Db 85 SLFEGIDFYT 94

RESULT 10  
ID P81159 PRELIMINARY; PRT; 220 AA.

AC P81159;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
DE HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).  
GN HSC70.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasplidea;  
OC Aplysiidae; Aplysia.  
OX NCBI\_TaxID=6500;

RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93077669; Pubmed=1360013;  
RA Kuhl D., Kennedy T., Barzilai A., Kandel E.;  
RT "Long-term sensitization training in Aplysia leads to an increase in  
the expression of R1p, the major protein chaperon of the ER.";  
RL J. Cell Biol. 119:1069-1076(1992).  
CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.  
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

DR EMBL: Z15039; CAAT8757.1; -.  
DR HSSP: P19120; IBA1.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70.1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT SEQUENCE 220 AA; 24684 MW; FA8557F2B85C37A CRC64;

Query Match 92.2%; Score 47; DB 5; Length 220;  
Best Local Similarity 90.0%; Pred. No. 0.28;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10  
| | | | | | | |  
Db 138 SLFEGIDFYT 147

RESULT 11  
ID Q90520 PRELIMINARY; PRT; 278 AA.

AC Q90520;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;

RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=85036330; Pubmed=6092938;  
RA Kohary R.K., Jones D., Candido E.P.M.;  
RT "70-kilodalton heat shock polypeptides from rainbow trout:  
characterization of cDNA sequences.";  
RL Mol. Cell. Biol. 4:1785-1791(1984).  
DR EMBL: K02549; AAA49562.1; -.

DR HSSP: P08109; 1CKR.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70.1.

DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00329; HSP70\_2; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 1  
FT SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

QY 1 SLFEGIDLYT 10  
| | | | | | | |  
Db 156 SLFEGIDFYT 165

Query Match 92.2%; Score 47; DB 13; Length 278;  
Best Local Similarity 90.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10  
| | | | | | | |  
Db 156 SLFEGIDFYT 165

RESULT 12  
ID Q98899 PRELIMINARY; PRT; 367 AA.

AC Q98899;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
GN HSP70-3.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Lim E.H.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y08578; CA69892.1; -.  
DR HSSP: P19120; 3HSC.  
DR InterPro: IPR001023; HSP70.  
DR Pfam: PF00012; HSP70.1.  
DR PRINTS: PR00301; HEATSHOCK70.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
KW Heat shock.

FT NON\_TER 367  
FT SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6B3C2CA CRC64;

Query Match 92.2%; Score 47; DB 13; Length 367;  
Best Local Similarity 90.0%; Pred. No. 0.5;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLFEGIDLYT 10  
| | | | | | | |  
Db 268 SLFEGIDFYT 277

RESULT 13  
ID Q63718 PRELIMINARY; PRT; 455 AA.

AC Q63718;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE HEAT SHOCK ROTEIN 70 (FRAGMENT).  
OS Rattus norvegicus (rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;



QY 1 SLEFGIDLYT 10  
 |||||||  
 DB 82 SLEFGIDFYT 91

## RESULT 6

Q90665 PRELIMINARY; PRT; 157 AA.  
 AC Q90665; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF191830; AAF12789.1; -  
 DR HSSP: P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 157  
 FT NON\_TER 1 157  
 SQ SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 92.2%; Score 47; DB 5; Length 157;  
 Best Local Similarity 90.0%; Pred. No. 0.19;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10  
 |||||||  
 DB 84 SLEFGIDFYT 93

RESULT 7  
 Q90671 PRELIMINARY; PRT; 158 AA.  
 AC Q90671; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina scutallata.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF191824; AAF12783.1; -  
 DR HSSP: P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 158  
 FT NON\_TER 1 158  
 SQ SEQUENCE 158 AA; 17887 MW; B41B5356A24CAD2F CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;  
 Best Local Similarity 90.0%; Pred. No. 0.19;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SLEFGIDLYT 10  
 |||||||  
 DB 85 SLEFGIDFYT 94

## RESULT 8

Q90668 PRELIMINARY; PRT; 158 AA.  
 AC Q90668; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF191827; AAF12786.1; -  
 DR HSSP: P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 158  
 FT NON\_TER 1 158  
 SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;  
 Best Local Similarity 90.0%; Pred. No. 0.19;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDLYT 10  
 |||||||  
 DB 85 SLEFGIDFYT 94

RESULT 9  
 Q90666 PRELIMINARY; PRT; 158 AA.  
 AC Q90666; 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HEAT-SHOCK PROTEIN (FRAGMENT).  
 GN HSC70.  
 OS Littorina plena.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
 OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
 OX NCBI\_TaxID=31219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hohenlohe P.A.;  
 RT "Heat-shock genes in the heat-stressed genus Littorina."  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF191829; AAF12788.1; -  
 DR HSSP: P19120; 1BA1.  
 DR InterPro: IPR001023; HSP70.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 FT NON\_TER 1 158  
 FT NON\_TER 1 158  
 SQ SEQUENCE 158 AA; 17891 MW; B41B5356BCECAD2F CRC64;

Query Match 92.2%; Score 47; DB 5; Length 158;  
 Best Local Similarity 90.0%; Pred. No. 0.19;



RESULT 2  
ID 094104 PRELIMINARY; PRT: 647 AA.

AC 094104;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).

GN HSP70.  
OS Pneumocystis carinii.  
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;  
OC Pneumocystis.  
DE NCBI\_TaxID=4754;  
GN [1]  
RN SEQUENCE FROM N.A.  
RP Paul S.P., Graves D.C.;  
RT "Phylogeny and sequence analysis of Pneumocystis carinii HSP70.";  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U71151; AAD09565.1; -.  
DR HSSP; P19120; 3HSC.  
DR Interpro; IPR001023; HSP70.  
DR Interpro; IPR00169; Thiolprot\_act\_site.  
DR Pfam; PF00012; HSP70; 1.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS00297; HSP70\_1; UNKNOWN\_1.  
DR PROSITE; PS00329; HSP70\_2; 1.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; UNKNOWN\_1.  
DR Heat shock.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 647 AA; 71176 MW; 92F9496399380F9 CRC64;

Query Match  
Best Local Similarity 94.1%; Score 48; DB 3; Length 647;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFEGIDLTY 10  
||:|||||  
DB 288 SLFEGIDLTY 297

RESULT 3  
ID 090667 PRELIMINARY; PRT: 146 AA.  
AC 090667;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plana.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191828; AAF12787.1; -.  
DR HSSP; P19120; 1BA1.  
DR Interpro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR NON\_TER  
FT NON\_TER  
SQ SEQUENCE 146 AA; 16607 MW; 3CF3556A1AF438BB CRC64;

Query Match  
Best Local Similarity 92.2%; Score 47; DB 5; Length 146;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 SLFEGIDLTY 10  
|||||||  
DB 79 SLFEGIDFYT 88

RESULT 4  
ID 090670 PRELIMINARY; PRT: 153 AA.  
AC 090670;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191825; AAF12784.1; -.  
DR HSSP; P19120; 1BA1.  
DR Interpro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR NON\_TER  
FT NON\_TER  
SQ SEQUENCE 153 AA; 17352 MW; E29EE20C4CAF934D CRC64;

Query Match  
Best Local Similarity 92.2%; Score 47; DB 5; Length 153;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDLTY 10  
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DB 80 SLFEGIDFYT 89

RESULT 5  
ID 090669 PRELIMINARY; PRT: 155 AA.  
AC 090669;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutulata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotaeniolossia; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191826; AAF12785.1; -.  
DR HSSP; P19120; 1BA1.  
DR Interpro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
DR NON\_TER  
FT NON\_TER  
SQ SEQUENCE 155 AA; 17676 MW; C191FE5B1F346C2 CRC64;

Query Match  
Best Local Similarity 92.2%; Score 47; DB 5; Length 155;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:56:53 ; Search time 170.25 Seconds  
(without alignments)  
8.592 Million cell updates/sec

Title: PEP2-MOD81  
Perfect score: 51  
Sequence: 1 SLFEGIDLYT 10

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP:REMBL\_17:\*  
2: sp.archaea:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	94.1	645	3	094106	094106 pneumocysti
2	48	94.1	647	3	094104	094104 pneumocysti
3	47	92.2	146	5	090667	090667 littorina p
4	47	92.2	153	5	090670	090670 littorina s
5	47	92.2	155	5	090669	090669 littorina s
6	47	92.2	157	5	090665	090665 littorina p
7	47	92.2	158	5	090671	090671 littorina s
8	47	92.2	158	5	090668	090668 littorina p
9	47	92.2	158	5	090666	090666 littorina p
10	47	92.2	220	5	P81159	P81159 aplysia cal
11	47	92.2	278	13	090520	090520 oncorhynch
12	47	92.2	367	13	098899	098899 fungu rubrip
13	47	92.2	455	11	063718	063718 rattus norv
14	47	92.2	467	5	044350	044350 chondrosia
15	47	92.2	467	5	044352	044352 petrobiona
16	47	92.2	467	5	09N92	09N92 guancha lac
17	47	92.2	468	5	044349	044349 funiculina
18	47	92.2	469	5	044351	044351 eunicella c
19	47	92.2	526	13	Q98897	Q98897 fungu rubrip

20	47	92.2	632	5	015766	015766 dictyostell
21	47	92.2	639	13	098900	098900 fungu rubrip
22	47	92.2	639	13	0918P9	0918P9 oryzias lat
23	47	92.2	640	5	093601	093601 caenorhabd
24	47	92.2	640	13	093240	093240 paralicthy
25	47	92.2	641	11	063256	063256 rattus norv
26	47	92.2	641	11	09QWJ5	09QWJ5 mus musculu
27	47	92.2	645	5	096541	096541 setaria dig
28	47	92.2	645	5	09NJB7	09NJB7 wuchereria
29	47	92.2	645	5	09NGK9	09NGK9 wuchereria
30	47	92.2	647	3	059855	059855 schizosacch
31	47	92.2	650	10	09XS55	09XS55 arabidopsis
32	47	92.2	650	10	09LHA8	09LHA8 arabidopsis
33	47	92.2	652	10	P93937	P93937 ascophyllum
34	47	92.2	653	5	094805	094805 trichoplusi
35	47	92.2	659	5	09XJ22	09XJ22 crassostrea
36	46	90.2	190	5	0909B4	0909B4 mytilus edu
37	46	90.2	221	5	P81157	P81157 aplysia cal
38	46	90.2	467	5	044346	044346 asbestoplum
39	46	90.2	467	5	044347	044347 petrosia fl
40	46	90.2	467	5	09GPM5	09GPM5 monosiga ov
41	46	90.2	639	13	073922	073922 oreochromis
42	46	90.2	642	3	090VM0	090VM0 rhizopus st
43	46	90.2	643	6	09NIU2	09NIU2 saginatus oe
44	46	90.2	651	3	09UVM1	09UVM1 rhizopus st
45	46	90.2	651	10	022664	022664 spinacia ol

## ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	645 AA.
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AC	094106			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	HEAT SHOCK PROTEIN 70 (FRAGMENT).			
GN	PCSA1.			
OS	Pneumocystis carinii f. sp. carinii.			
OC	Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;			
OC	Pneumocystis.			
OX	NCBI_TaxID=38081;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97045128; PubMed=8890193;			
RA	Stedman T.T., Buck G.A.;			
RT	"Identification, characterization, and expression of the BIP			
RT	endoplasmic reticulum resident chaperonins in Pneumocystis carinii.",			
RL	Infect. Immun. 64:4463-4471(1996).			
DR	EMBL; U80967; AAD00455.1; -.			
DR	HSSP; P19120; 3HSC.			
DR	InterPro; IPR001023; HSP70.			
DR	InterPro; IPR000169; Thiolprot_act_site.			
DR	Pfam; PF000012; HSP70. 1.			
DR	PRINTS; PR00301; HEATSHOCK70.			
DR	PROSITE; PS00297; HSP70_1; UNKNOWN_1.			
DR	PROSITE; PS00329; HSP70_2; 1.			
DR	PROSITE; PS01036; HSP70_3; 1.			
DR	PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.			
KW	Heat shock.			
FT	NON_TER			
SQ	SEQUENCE 645 AA; 70884 MW; 6D8CF90433BB163F CRC64;			

Query Match 94.1%; Score 48; DB 3; Length 645;  
Best Local Similarity 90.0%; Pred. No. 0.61;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLFEGIDLYT 10  
|:|:|:|:|:|:|  
DB 286 SLFEGIDLYT 295



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2001, 07:59:58 : Search time 81.43 Seconds  
(without alignments)  
2.764 Million cell updates/sec

Title: PEP2-MOD8V  
Perfect score: 51  
Sequence: 1 SLFEGIDVYT 10

Scoring table:  
BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	643	4	US-08-797-358B-3 Sequence 3, Appl1
2	43	84.3	646	1	US-08-441-139-14 Sequence 14, Appl1
3	34	66.7	332	2	US-08-637-763B-6 Sequence 6, Appl1
4	34	66.7	332	2	US-08-637-763B-8 Sequence 8, Appl1
5	34	66.7	332	3	US-09-170-354-6 Sequence 6, Appl1
6	34	66.7	332	3	US-09-170-354-8 Sequence 8, Appl1
7	34	66.7	789	3	US-08-727-308-1 Sequence 1, Appl1
8	33	64.7	36	1	US-08-487-890A-19 Sequence 19, Appl1
9	33	64.7	36	2	US-08-478-435-19 Sequence 19, Appl1
10	33	64.7	36	2	US-08-337-483-19 Sequence 19, Appl1
11	33	64.7	36	2	US-08-478-373-19 Sequence 19, Appl1
12	33	64.7	36	3	US-08-474-671-19 Sequence 19, Appl1
13	33	64.7	36	3	US-08-483-577A-19 Sequence 19, Appl1
14	33	64.7	36	4	US-08-897-438-19 Sequence 19, Appl1
15	33	64.7	301	5	PCT-US95-13975-72 Sequence 72, Appl1
16	33	64.7	435	3	US-08-911-321-8 Sequence 8, Appl1
17	33	64.7	458	4	US-09-457-046B-61 Sequence 61, Appl1
18	33	64.7	911	1	US-08-487-890A-107 Sequence 107, Appl1
19	33	64.7	911	2	US-08-478-435-107 Sequence 107, Appl1
20	33	64.7	911	2	US-08-337-483-107 Sequence 107, Appl1
21	33	64.7	911	3	US-08-478-373-107 Sequence 107, Appl1
22	33	64.7	911	3	US-08-474-671-107 Sequence 107, Appl1
23	33	64.7	911	3	US-08-483-577A-107 Sequence 107, Appl1
24	33	64.7	911	4	US-08-897-438-107 Sequence 107, Appl1
25	33	64.7	913	1	US-08-487-890A-5 Sequence 5, Appl1
26	33	64.7	913	2	US-08-478-435-5 Sequence 5, Appl1
27	33	64.7	913	2	US-08-337-483-5 Sequence 5, Appl1

28	33	64.7	913	2	US-08-478-373-5 Sequence 5, Appl1
29	33	64.7	913	3	US-08-474-671-5 Sequence 5, Appl1
30	33	64.7	913	3	US-08-483-577A-5 Sequence 5, Appl1
31	33	64.7	913	4	US-08-897-438-5 Sequence 5, Appl1
32	32	62.7	230	2	US-08-537-400-16 Sequence 16, Appl1
33	32	62.7	230	2	US-08-706-702-18 Sequence 18, Appl1
34	32	62.7	230	3	US-08-706-706-18 Sequence 18, Appl1
35	32	62.7	339	2	US-08-928-692-52 Sequence 52, Appl1
36	32	62.7	494	3	US-08-484-661A-39 Sequence 39, Appl1
37	32	62.7	494	3	US-08-656-664-39 Sequence 39, Appl1
38	32	62.7	494	5	PCT-US96-09641-39 Sequence 39, Appl1
39	32	62.7	495	3	US-09-079-415-4 Sequence 4, Appl1
40	32	62.7	533	2	US-08-225-488-2 Sequence 2, Appl1
41	32	62.7	571	3	US-08-484-661A-37 Sequence 37, Appl1
42	32	62.7	571	3	US-08-656-664-37 Sequence 37, Appl1
43	32	62.7	578	5	PCT-US96-09641-37 Sequence 37, Appl1
44	32	62.7	578	3	US-08-484-661A-11 Sequence 11, Appl1
45	32	62.7	578	3	US-08-656-664-11 Sequence 11, Appl1

## ALIGNMENTS

```
RESULT 1
US-08-797-358B-3
; Sequence 3, Application US/08797358B
; Patent No. 6268478
;
GENERAL INFORMATION:
; APPLICANT: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 11-Feb-1997
; CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
;
ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CE 3165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
;
INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
Query Match 88.2% Score 45; DB 4; Length 643;
Best Local Similarity 80.0%; Pred. No. 0.6;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;
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Db 288 SLEGEVDFT 297

RESULT 2  
US-08-441-139-14  
; Sequence 14, Application US/08441139  
; Patent No. 5773245

GENERAL INFORMATION:

APPLICANT: Wittrop, Dr. Karl D.

APPLICANT: Robinson, Anne S.  
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF  
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City

STATE: NY

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,139  
FILING DATE: 15-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/089,997  
FILING DATE: 06-JUL-1993  
ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8646

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 646 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-441-139-14

Query Match 84.3%; Score 43; DB 1; Length 646;

Best Local Similarity 80.0%; Pred. No. 1.5;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEGEVDFT 10

Db 286 SLEGEVDFT 295

RESULT 3  
US-08-637-763B-6

; Sequence 6, Application US/08637763B

; Patent No. 5849559

GENERAL INFORMATION:

APPLICANT: VAN DER WOUW, Monique J.A. et al

APPLICANT: ARABINOXYLAN DEGRADING ENZYME

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,763B

FILING DATE: 25-AUG-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 4615-0066.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030 MRSNFORSMH

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-637-763B-6

Query Match 66.7%; Score 34; DB 2; Length 332;

Best Local Similarity 66.7%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LFEAGVDFT 10

Db 212 LFEAGVDFT 220

RESULT 4  
US-08-637-763B-8

; Sequence 8, Application US/08637763B

; Patent No. 5849559

GENERAL INFORMATION:

APPLICANT: VAN DER WOUW, Monique J.A. et al

APPLICANT: ARABINOXYLAN DEGRADING ENZYME

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,763B

FILING DATE: 25-AUG-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 4615-0066.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

TELEX: 90-4030 MRSNFORSMH

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 amino acids

TYPE: amino acid

TOPOLOGY: linear



MOLECULE TYPE: protein  
US-08-637-763B-8

Query Match 66.7%; Score 34; DB 2; Length 332;  
Best Local Similarity 66.7%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LFEQIDVYT 10  
111 : 111  
DB 212 LFEAVQVYT 220

RESULT 5  
US-09-170-354-6  
; Sequence 6, Application US/09170354  
; Patent No. 6066356  
; GENERAL INFORMATION:  
; APPLICANT: VAN DER WOUW, Monique J.A. et al  
; TITLE OF INVENTION: ARABINOXYLAN DEGRADING ENZYME  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
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; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/637,763  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 4615-0066.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030 MRSNFORSMH  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-170-354-6

Query Match 66.7%; Score 34; DB 3; Length 332;  
Best Local Similarity 66.7%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LFEQIDVYT 10  
111 : 111  
DB 212 LFEAVQVYT 220

RESULT 6  
US-09-170-354-8  
; Sequence 8, Application US/09170354  
; Patent No. 6066356  
; GENERAL INFORMATION:  
; APPLICANT: VAN DER WOUW, Monique J.A. et al  
; TITLE OF INVENTION: ARABINOXYLAN DEGRADING ENZYME

NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/170,354  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/637,763  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 4615-0066.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030 MRSNFORSMH  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 332 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-170-354-8

Query Match 66.7%; Score 34; DB 3; Length 332;  
Best Local Similarity 66.7%; Pred. No. 39;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LFEQIDVYT 10  
111 : 111  
DB 212 LFEAVQVYT 220

RESULT 7  
US-08-727-308-1  
; Sequence 1, Application US/08727308  
; Patent No. 6020176  
; GENERAL INFORMATION:  
; APPLICANT: YUJI KAMIYA et al.  
; TITLE OF INVENTION: KAURENE SYNTHASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/727,308  
; FILING DATE: October 8, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:



ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 789 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-727-308-1

Query Match 66.7%; Score 34; DB 3; Length 789;  
Best Local Similarity 70.0%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
||| |::|||  
Db 23 SLFPGVDVDT 32

RESULT 8  
US-08-487-890A-19  
Sequence 19, Application US/08487890A  
Patent No. 5708149  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-ping  
APPLICANT: Murdin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,890A  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-890A-19

Query Match 64.7%; Score 33; DB 1; Length 36;  
Best Local Similarity 62.5%; Pred. No. 5.3;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 PEGIDVYT 10  
|||::|||  
Db 28 PEGVAVYT 35

RESULT 9  
US-08-478-435-19  
Sequence 19, Application US/08478435  
Patent No. 5922323  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-ping  
APPLICANT: Murdin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,435  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-478-435-19



Query Match 64.7%; Score 33; DB 2; Length 36;  
Best Local Similarity 62.5%; Pred. No. 5.3;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDVYT 10  
| | | : | |  
Db 28 FEGVAIYT 35

RESULT 10  
US-08-337-483-19

; Sequence 19, Application US/08337483  
; Patent No. 5922562  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Slim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,483  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-337-483-19

Query Match 64.7%; Score 33; DB 2; Length 36;  
Best Local Similarity 62.5%; Pred. No. 5.3;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDVYT 10  
| | | : | |  
Db 28 FEGVAIYT 35

RESULT 11

; US-08-478-373-19  
; Sequence 19, Application US/08478373  
; Patent No. 5922841  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Slim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,373  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,483  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,968  
; FILING DATE: 08-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-478-373-19

Query Match 64.7%; Score 33; DB 2; Length 36;  
Best Local Similarity 62.5%; Pred. No. 5.3;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDVYT 10  
| | | : | |  
Db 28 FEGVAIYT 35

RESULT 12  
US-08-474-671-19  
; Sequence 19, Application US/08474671  
; Patent No. 6008326

; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Mordin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147



```

CORRESPONDENCE ADDRESS:
ADDRESSEE:  Sim & McBurney
STREET:  Suite 701, 330 University Avenue
CITY:  Toronto
STATE:  Ontario
COUNTRY:  Canada
ZIP:  M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE:  floppy disk
COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/474,671
FILING DATE:  07-JUN-1995
CLASSIFICATION:  530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/337,483
FILING DATE:  08-NOV-1994
CLASSIFICATION:  530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/175,116
FILING DATE:  29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/148,968
FILING DATE:  08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME:  Stewart, Michael I
REGISTRATION NUMBER:  24,973
REFERENCE/DOCKET NUMBER:  1038-465 MIS:VG
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (416) 595-1155
TELEFAX:  (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH:  36 amino acids
TYPE:  amino acid
STRANDEDNESS:  single
TOPOLOGY:  linear
US-08-474-671-19

Query Match      64.7%; Score 33; DB 3; Length 36;
Best Local Similarity 62.5%; Pred. No. 5.3;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3  PEGIDVYT 10
      |||: |||
Db      28  FEGVAIYT 35

RESULT 13
US-08-483-577A-19
; Sequence 19, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT:  Loosmore, Sheena
; APPLICANT:  Harkness, Robin
; APPLICANT:  Schryvers, Anthony
; APPLICANT:  Chong, Pele
; APPLICANT:  Gray-Owen, Scott
; APPLICANT:  Yang, Yan-ping
; APPLICANT:  Murdin, Andrew
; APPLICANT:  Kleio, Michel
; TITLE OF INVENTION:  Transferrin Receptor Genes
; NUMBER OF SEQUENCES:  160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Sim & McBurney
; STREET:  Suite 701, 330 University Avenue
; CITY:  Toronto
; STATE:  Ontario
; COUNTRY:  Canada
; ZIP:  M5G 1R7
```

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COMPUTER READABLE FORM:
MEDIUM TYPE:  floppy disk
COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/483,577A
FILING DATE:  07-JUN-1995
CLASSIFICATION:  435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/337,483
FILING DATE:  08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/175,116
FILING DATE:  29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/148,968
FILING DATE:  08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME:  Stewart, Michael I
REGISTRATION NUMBER:  24,973
REFERENCE/DOCKET NUMBER:  1038-511
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (416) 595-1155
TELEFAX:  (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH:  36 amino acids
TYPE:  amino acid
STRANDEDNESS:  single
TOPOLOGY:  linear
US-08-483-577A-19
```

```

Query Match      64.7%; Score 33; DB 3; Length 36;
Best Local Similarity 62.5%; Pred. No. 5.3;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3  PEGIDVYT 10
      |||: |||
Db      28  FEGVAIYT 35
```

```

RESULT 14
US-08-897-438-19
; Sequence 19, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT:  Loosmore, Sheena
; APPLICANT:  Harkness, Robin
; APPLICANT:  Schryvers, Anthony
; APPLICANT:  Chong, Pele
; APPLICANT:  Gray-Owen, Scott
; APPLICANT:  Yang, Yan-ping
; APPLICANT:  Murdin, Andrew
; APPLICANT:  Kleio, Michel
; TITLE OF INVENTION:  Transferrin Receptor Genes
; NUMBER OF SEQUENCES:  160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Sim & McBurney
; STREET:  6th Floor, 330 University Avenue
; CITY:  Toronto
; STATE:  Ontario
; COUNTRY:  Canada
; ZIP:  M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE:  floppy disk
COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/897,438
FILING DATE:
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CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,577  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-897-438-19

Query Match 64.7%; Score 33; DB 4; Length 36;  
Best Local Similarity 62.5%; Pred. No. 5.3;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDVYT 10  
|||: |||  
DB 28 FEGVAIYT 35

RESULT 15  
PCT-US95-13975-72  
Sequence 72, Application PC/RTUS9513975  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: McDONELL, Michael W.  
TITLE OF INVENTION: Recombinant Feline Herpes virus  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13975  
FILING DATE: 26-OCT-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/329,883  
FILING DATE: 26-OCT-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 39118-PCY  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)391-0400  
TELEFAX: (212)391-0525

INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-13975-72

Query Match 64.7%; Score 33; DB 5; Length 301;  
Best Local Similarity 62.5%; Pred. No. 54;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEGIDVYT 10  
|||: |||  
DB 1 FEGITVYT 8

Search completed: December 6, 2001, 07:59:58  
Job time: 366 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 07:58:27 ; Search time 88.19 Seconds  
(without alignments)  
8.638 Million cell updates/sec

Title: PEP2-MOD8V  
Perfect score: 51  
Sequence: 1 SLEFGIDVYT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	46	90.2	208	2	B44261 dnak-type molecula
2	46	90.2	209	2	A44261 dnak-type molecula
3	46	90.2	278	2	I51344 dnak-type molecula
4	46	90.2	372	2	P00138 dnak-type molecula
5	46	90.2	467	2	T45477 heat-shock protein
6	46	90.2	467	2	T45479 heat-shock protein
7	46	90.2	468	2	T45476 heat-shock protein
8	46	90.2	469	2	T45478 heat-shock protein
9	46	90.2	632	2	T45471 dnak-type molecula
10	46	90.2	634	2	A25646 dnak-type molecula
11	46	90.2	636	2	A48872 dnak-type molecula
12	46	90.2	638	2	A31766 dnak-type molecula
13	46	90.2	639	2	UC1391 dnak-type molecula
14	46	90.2	639	2	S20139 dnak-type molecula
15	46	90.2	640	1	HHKW7A dnak-type molecula
16	46	90.2	640	2	A29160 dnak-type molecula
17	46	90.2	640	2	S37394 dnak-type molecula
18	46	90.2	640	2	T21394 hypothetical prote
19	46	90.2	640	2	T43724 dnak-type molecula
20	46	90.2	641	2	S33357 dnak-type molecula
21	46	90.2	641	2	S35718 dnak-type molecula
22	46	90.2	641	2	I54542 dnak-type molecula
23	46	90.2	641	2	A45871 dnak-type molecula
24	46	90.2	642	1	HHRYA1 dnak-type molecula
25	46	90.2	642	2	JH0095 dnak-type molecula
26	46	90.2	642	2	B36590 dnak-type molecula
27	46	90.2	644	2	A45635 dnak-type molecula
28	46	90.2	645	2	I51129 dnak-type molecula
29	46	90.2	646	2	T46650 heat shock protein

30	46	90.2	647	1	HHXL70 dnak-type molecula
31	46	90.2	647	2	T41121 heat shock protein
32	45	88.2	214	2	A03309 dnak-type molecula
33	45	88.2	379	2	I46588 dnak-type molecula
34	45	88.2	467	2	T45473 heat-shock protein
35	45	88.2	467	2	T45474 heat-shock protein
36	45	88.2	641	2	JN0668 dnak-type molecula
37	45	88.2	641	2	PC7036 heat shock protein
38	45	88.2	643	2	S25585 dnak-type molecula
39	45	88.2	643	2	S09036 dnak-type molecula
40	45	88.2	651	2	T45517 heat shock protein
41	45	88.2	651	2	JC7132 heat shock protein
42	43	84.3	209	2	S48024 dnak-type molecula
43	43	84.3	209	2	S48025 dnak-type molecula
44	43	84.3	209	2	C44261 dnak-type molecula
45	43	84.3	630	2	A34041 dnak-type molecula

## ALIGNMENTS

RESULT 1  
B44261  
dnak-type molecular chaperone HSC70 - California sea hare (fragment)  
N:Alternate names: heat shock protein 70 homolog HSC70  
C:Species: Aplysia californica (California sea hare)  
C:Date: 04-Sep-1998 #sequence\_reviston 04-Sep-1998 #text\_change 13-Aug-1999  
C:Accession: B44261  
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.  
J. Cell Biol. 119, 1069-1076, 1992  
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr  
A:Reference number: A44261; MVID:93077669  
A:Accession: B44261  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-208 <RUH>  
A>Note: sequence extracted from NCBI backbone (NCBIP:118950)  
C:Genetics:  
A:Gene: HSC70  
C:Function:  
A:Description: Involved in protein folding and assembling/disassembling of protein co  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 208;  
Best Local Similarity 90.0%; Pred. No. 0.088;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLEFGIDVYT 10  
DB 132 SLEFGIDVYT 141  
RESULT 2  
A44261  
dnak-type molecular chaperone HSP70a - California sea hare (fragment)  
N:Alternate names: heat shock protein 70  
C:Species: Aplysia californica (California sea hare)  
C:Date: 04-Sep-1998 #sequence\_reviston 04-Sep-1998 #text\_change 13-Aug-1999  
C:Accession: A44261  
R:Kuhl, D.; Kennedy, T.E.; Barzilai, A.; Kandel, E.R.  
J. Cell Biol. 119, 1069-1076, 1992  
A:Title: Long-term sensitization training in Aplysia leads to an increase in the expr  
A:Reference number: A44261; MVID:93077669  
A:Accession: A44261  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-209 <RUH>  
A>Note: sequence extracted from NCBI backbone (NCBIP:118951)  
C:Genetics:  
A:Gene: HSP70a  
C:Function:



A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 209;  
Best Local Similarity 90.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
| | | | | | | |  
Db 133 SLFEGIDVYT 142

RESULT 3  
I51344  
dnak-type molecular chaperone (clone PTHS70.7) - rainbow trout (fragment)  
N:Alternate names: 70K heat shock protein  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Aug-1999  
C:Accession: I51344  
R:Kothary, R.K.; Jones, D.; Cardido, E.P.M.  
Mol. Cell. Biol. 4, 1785-1791, 1984  
A:Title: 70-Kilodalton heat shock polypeptides from rainbow trout: Characterization of  
A:Reference number: I51344; MUID:85036330  
A:Accession: I51344  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-278 <KOT>  
A:Cross-references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 278;  
Best Local Similarity 90.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
| | | | | | | |  
Db 156 SLFEGIDVYT 165

RESULT 4  
P00138  
dnak-type molecular chaperone hsp70 II - sea urchin (Paracentrotus lividus) (fragment)  
N:Alternate names: heat shock protein 70  
C:Species: Paracentrotus lividus (common urchin)  
C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 20-Aug-1999  
C:Accession: P00138  
R:Rosa, M.L.; Scomzo, G.; Giudice, G.; Roccheri, M.G.; Carlo, M.D.  
Gene 96, 295-300, 1990  
A:Title: Sequence of a sea urchin hsp70 gene and its 5' flanking region.  
A:Reference number: P00138; MUID:91099690  
A:Accession: P00138  
A:Molecule type: DNA  
A:Residues: 1-372 <ROS>  
A:Cross-references: EMBL:X16544; NID:g10000; PIDN:CAA34544.1; PID:g10001  
C:Genetics:  
A:Gene: hsp70 II  
A:Introns: 68/1; 137/1; 188/3; 281/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 372;  
Best Local Similarity 90.0%; Pred. No. 0.17;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
| | | | | | | |  
Db 286 SLFEGIDVYT 295

RESULT 5  
T45477  
heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)  
C:Species: Chondrosia reniformis  
C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45477  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45477  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026517; PIDN:AAC05362.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 90.2%; Score 46; DB 2; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
| | | | | | | |  
Db 252 SLFEGIDVYT 261

RESULT 6  
T45479  
heat-shock protein 70 [imported] - Eunicella cavolini (fragment)  
C:Species: Eunicella cavolini  
C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45479  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-467 <BOR>  
A:Cross-references: EMBL:AF026520; PIDN:AAC05364.1  
C:Genetics:  
A:Gene: Hsp70  
C:Superfamily: heat shock protein 70

Query Match 90.2%; Score 46; DB 2; Length 467;  
Best Local Similarity 90.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
| | | | | | | |  
Db 252 SLFEGIDVYT 261

RESULT 7  
T45476  
heat-shock protein 70 [imported] - Funiculina quadrangularis (fragment)  
C:Species: Funiculina quadrangularis  
C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T45476  
R:Borchelliini, C.; Le Parco, Y.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z22983  
A:Accession: T45476  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA



A:Residues: 1-468 <BOR>  
 A:Cross-references: EMBL:AF026516; PIDN:AAC05361.1  
 C:Genetics:  
 A:Gene: hsp70  
 C:Superfamily: heat shock protein 70

Query Match 90.2%; Score 46; DB 2; Length 468;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10  
 |||||||  
 Db 253 SLEFGIDFYT 262

RESULT 8  
 T45478  
 heat-shock protein 70 [imported] - Euniceella cavolinii (fragment)  
 C:Species: Euniceella cavolinii  
 C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 21-Jul-2000  
 C:Accession: T45478  
 R:Borchellini, C.; Le Parco, Y.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: 222983  
 A:Accession: T45478  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-469 <BOR>  
 A:Cross-references: EMBL:AF026518; PIDN:AAC05363.1  
 C:Genetics:  
 A:Gene: hsp70  
 C:Superfamily: heat shock protein 70

Query Match 90.2%; Score 46; DB 2; Length 469;  
 Best Local Similarity 90.0%; Pred. No. 0.22;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10  
 |||||||  
 Db 254 SLEFGIDFYT 263

RESULT 9  
 T45471  
 dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)  
 N:Alternate names: heat shock cognate protein 70  
 C:Species: Dictyostelium discoideum  
 C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 18-Feb-2000  
 C:Accession: T45471  
 R:Boves, H.; Miltert, U.; Dittlich, W.; Faix, J.; Gerisch, G.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: 222980  
 A:Accession: T45471  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-632 <BOV>  
 A:Cross-references: EMBL:AF025951; PIDN:AAB81865.1  
 A:Experimental source: strain AX3  
 C:Genetics:  
 A:Gene: hsc70  
 A:Note: localized to filopodias and cortex  
 C:Superfamily: heat shock protein 70

Query Match 90.2%; Score 46; DB 2; Length 632;  
 Best Local Similarity 90.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10  
 |||||||  
 Db 285 SLEFGIDFYT 294

RESULT 10  
 A25646  
 dnaK-type molecular chaperone - chicken  
 N:Alternate names: heat shock protein 70  
 C:Species: Gallus gallus (chicken)  
 C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
 C:Accession: A25646  
 R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.  
 J. Biol. Chem. 261, 12692-12699, 1986

A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene  
 A:Reference number: A25646; MID:86304452  
 A:Accession: A25646  
 A:Molecule type: DNA

A:Residues: 1-634 <MOR>  
 A:Cross-references: GB:J02579; NID:q211940; PIDN:AAA48825.1; PID:q211941  
 A:Note: the authors translated the codon TCG for residue 583 as Trp  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 634;  
 Best Local Similarity 90.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10  
 |||||||  
 Db 289 SLEFGIDFYT 298

RESULT 11  
 A48872  
 dnaK-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment)  
 N:Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein  
 C:Species: Dictyostelium discoideum  
 C:Date: 19-May-1995 #sequence\_revision 19-May-1995 #text\_change 20-Aug-1999  
 C:Accession: A48872  
 R:Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.  
 J. Biol. Chem. 268, 23267-23274, 1993  
 A:Title: Aginactin, an agonist-regulated F-actin capping activity is associated with  
 A:Reference number: A48872; MID:94043116  
 A:Accession: A48872  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-636 <RDD>  
 A:Cross-references: GB:I22736; NID:q433179; PIDN:AAA33219.1; PID:q433180  
 A:Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 636;  
 Best Local Similarity 90.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10  
 |||||||  
 Db 280 SLEFGIDFYT 289

RESULT 12  
 S31766  
 dnaK-type molecular chaperone hsp70 - green monkey  
 N:Alternate names: heat shock protein 70  
 C:Species: Cercopithecus aethiops (green monkey, grivet)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
 C:Accession: S31766; 136927  
 R:Sains, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.



submitted to the EMBL Data Library, January 1993  
 A:Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein  
 A:Reference number: S31766  
 A:Accession: S31766  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <SAI>  
 R:Sains, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.  
 FEBS Lett. 355, 282-286, 1994  
 A:Title: The hsc70 gene which is slightly induced by heat is the main virus-inducible me  
 A:Reference number: I36927; MUID:95080396  
 A:Accession: I36927  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-638 <RES>  
 A:Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782  
 A:Experimental source: kidney, cell line COS-1  
 C:Genetics:  
 A:Gene: hsp70  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDVYT 10  
 ||||| ||  
 Db 284 SLEEGIDFYT 293

RESULT 13  
 JC1391  
 dnak-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)  
 N:Alternate names: heat shock protein 70IV; hsp70IV protein  
 C:Species: Paracentrotus lividus (common urchin)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 20-Aug-1999  
 C:Accession: JC1391  
 R:Scanzo, G.; Scardina, G.; Ferraro, M.G.  
 Gene 121, 353-358, 1992  
 A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70  
 A:Reference number: JC1391; MUID:93070753  
 A:Accession: JC1391  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SCG>  
 A:Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917  
 C:Genetics:  
 A:Gene: hsp70IV  
 A:Introns: 61/2  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein comp  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 90.2%; Score 46; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDVYT 10  
 ||||| ||  
 Db 286 SLEEGIDFYT 295

RESULT 14  
 S20139  
 dnak-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: heat shock protein YG102; protein I0971; protein YLL024c  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 20-Jun-2000  
 C:Accession: S20139; S64772; S64775; S69383

R:Slater, M.R.; Craig, E.A.  
 Nucleic Acids Res. 17, 805-806, 1989  
 A:Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.  
 A:Reference number: S20139; MUID:89128457  
 A:Accession: S20139  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-639 <SLA>  
 A:Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA1394.1; PID:g4546  
 R:Goffeau, A.; Purnelle, B.  
 Submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64761  
 A:Accession: S64772  
 A:Molecule type: DNA  
 A:Residues: 1-639 <GOF>  
 A:Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YL  
 R:Goffeau, A.; Purnelle, B.  
 Submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64775  
 A:Accession: S64775  
 A:Molecule type: DNA  
 A:Residues: 72-639 <DUE>  
 A:Cross-references: EMBL:Z73129; MIPS:YLL024c  
 A:Experimental source: strain S288C  
 R:Purnelle, B.; Goffeau, A.  
 Submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals  
 mly and a new ABC transporter homologous to the human multidrug resistance protein.  
 A:Reference number: S69380  
 A:Accession: S69383  
 A:Molecule type: DNA  
 A:Residues: 1-639 <PDR>  
 A:Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007  
 C:Genetics:  
 A:Gene: SGD:SSA2  
 A:Cross-references: MIPS:YLL024c; SGD:S0003947  
 A:Map position: 12L  
 C:Function:  
 A:Description: involved in protein folding and assembling/disassembling of protein co  
 C:Superfamily: heat shock protein 70  
 C:Keywords: ATP; molecular chaperone

Query Match 90.2%; Score 46; DB 2; Length 639;  
 Best Local Similarity 90.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEEGIDVYT 10  
 ||||| ||  
 Db 283 SLEEGIDFYT 292

RESULT 15  
 HKW7A  
 dnak-type molecular chaperone hsp70A - Caenorhabditis elegans  
 N:Alternate names: heat shock protein 70 A  
 C:Species: Caenorhabditis elegans  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 22-Jun-1999  
 C:Accession: J0285  
 R:Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.  
 Gene 64, 241-255, 1988  
 A:Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characteri  
 A:Reference number: J0285; MUID:88297155  
 A:Accession: J0285  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-640 <SND>  
 A:Cross-references: GB:M18540; NID:g156351; PIDN:AA28078.1; PID:g156352  
 A:Note: genomic clones representing six distinct members of the hsp70 gene family wer  
 A:Note: transcripts of hsp70A are abundant in control worms and also increase two- to  
 C:Note: one of the three introns in hsp70A is in a position similar to an intron in D  
 C:Genetics:  
 A:Gene: hsp70A



A:Map position: IV  
A:Introns: 69/1; 331/3; 558/3  
C:Function:  
A:Description: involved in protein folding and assembling/disassembling of protein comp  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 90.2%; Score 46; DB 1; Length 640;  
Best local similarity 90.0%; Pred. No. 0.32;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SLFEGIDVYT 10  
|||||||  
Db 287 SLFEGIDFYT 296

Search completed: December 6, 2001, 07:58:28  
Job time: 276 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 6, 2001, 08:00:52 ; Search time 50.21 Seconds  
(without alignments)  
7.302 Million cell updates/sec

Title: PEP2-MOD8V  
Perfect score: 51  
Sequence: 1 SLFEGIDVYT 10

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSProt\_39:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	90.2	322	1 HS70_ONCYO	P11503 onchocerca
2	46	90.2	372	1 HS72_PARLI	P22623 paracentrot
3	46	90.2	503	1 HS70_PENCI	Q92260 penicillium
4	46	90.2	634	1 HS70_CHICK	P08106 gallus gall
5	46	90.2	638	1 HS71_CERAE	Q28222 cercopitheca
6	46	90.2	638	1 HS72_YEAST	P15922 saccharomyc
7	46	90.2	639	1 HS74_PARLI	Q06248 paracentrot
8	46	90.2	640	1 HS7A_CAEEL	P09446 caenorhabdi
9	46	90.2	640	1 HS7C_DICDI	P36415 dictyosteli
10	46	90.2	641	1 HS71_BOVIN	Q27975 bos taurus
11	46	90.2	641	1 HS71_HUMAN	P08107 homo sapien
12	46	90.2	641	1 HS71_MOUSE	P17879 mus musculu
13	46	90.2	641	1 HS71_PIG	P34930 sus scrofa
14	46	90.2	641	1 HS71_RAT	Q07439 rattus norv
15	46	90.2	641	1 HS71_YEAST	P10591 saccharomyc
16	46	90.2	641	1 HS72_BOVIN	Q27965 bos taurus
17	46	90.2	641	1 HS74_YEAST	P22202 saccharomyc
18	46	90.2	644	1 HS70_BRUMA	P27541 brugia mala
19	46	90.2	644	1 HS70_ONCTS	Q91233 oncorhynch
20	46	90.2	645	1 HS70_PLENA	Q91291 pleurodeles
21	46	90.2	646	1 HS70_NEUCR	Q01233 neuropept
22	46	90.2	647	1 HS70_XENLA	P02827 xenopus lae
23	46	90.2	649	1 HS70_BLAEM	P48720 blastoclad
24	46	90.2	652	1 HS7D_MANSE	Q94639 manduca sex
25	45	88.2	214	1 HS7A_DROSI	P02826 saccharomyc
26	45	88.2	379	1 HS7X_PIG	P34934 sus scrofa
27	45	88.2	638	1 HS70_CERCA	P31902 ceratilis c
28	45	88.2	643	1 HS7A_DROME	P29843 drosophila
29	45	88.2	643	1 HS76_HUMAN	P17066 homo sapien
30	45	88.2	643	1 HS76_PIG	Q04967 sus scrofa
31	45	88.2	648	1 HS71_PUCGR	Q01877 puccinia gr
32	43	84.3	641	1 HS73_RAT	P55063 rattus norv
33	43	84.3	641	1 HS7H_HUMAN	P34931 homo sapien

34	43	84.3	641	1 HS7T_MOUSE	P16627 mus musculu
35	43	84.3	642	1 HS72_PICAN	P53623 pichia angu
36	43	84.3	643	1 HS71_SCHRO	Q10265 schizosacch
37	43	84.3	644	1 HS71_PICAN	P53421 pichia angu
38	43	84.3	646	1 HS7C_CRIGR	P19378 cricetulus
39	43	84.3	646	1 HS7C_HUMAN	P11142 homo sapien
40	43	84.3	646	1 HS7C_HUMAN	P08109 mus musculu
41	43	84.3	649	1 HS70_PARRR	P87047 paracoccidi
42	43	84.3	649	1 HS73_YEAST	P09435 saccharomyc
43	43	84.3	649	1 HS7C_BRARE	Q90473 brachydantio
44	43	84.3	650	1 HS7C_BOVIN	P19120 bos taurus
45	43	84.3	651	1 HS70_ONCMY	P08108 oncorhynch

## ALIGNMENTS

RESULT 1					
HS70_ONCYO	STANDARD:	PRT:	322 AA.		
AC P11503:					
DT 01-OCT-1989 (Rel. 12, Created)					
DT 01-FEB-1996 (Rel. 33, Last sequence update)					
DT 01-FEB-1996 (Rel. 33, Last annotation update)					
DE HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).					
OS Onchocerca volvulus.					
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;					
OC Onchocercidae; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;					
OX NCBI_TaxID=6282;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=89201313; PubMed=2704388;					
RA Rottstein N.M., Hiyashi G., Yates J., Rajan T.V.;					
RT "Onchocerca volvulus heat shock protein 70 is a major immunogen in					
RT amicrofilaricidal individuals from a filariasis-endemic area.";					
RL Mol. Biochem. Parasitol. 33:229-236(1989).					
CC -!- DISSEM: HEAT SHOCK PROTEIN 70 IS A MAJOR IMMUNOGEN IN A					
CC MICROFILAREMIC INDIVIDUALS FROM A FILARIASIS-ENDEMIC AREA.					
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.					
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CC or send an email to <a href="mailto:license@sib.ch">license@sib.ch</a> ).					
CC -----					
DR EMBL: J04006; AAA29417.1; -					
DR HSSP: P19120; IATR.					
DR InterPro: IPR001023; HSP70.					
DR Pfam: PF00012; HSP70; 1.					
DR PROSITE: PS00297; HSP70.1; PARTIAL.					
DR PROSITE: PS00329; HSP70.2; PARTIAL.					
DR PROSITE: PS01036; HSP70.3; 1.					
KW ATP-binding; Heat shock.					
KW ATP-binding; Heat shock.					
FT NON_TER 1					
FT NON_TER 322					
SO SEQUENCE 322 AA; 35614 MW; 2BA3A2E8155A7180 CRC64;					
Query Match	90.2%;	Score 46;	DB 1;	Length 322;	
Best local Similarity	90.0%;	Pred. No. 0.087;			
Matches 9;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY 1 SLFEGIDVYT 10					
DB 43 SLFEGIDVYT 52					
RESULT 2					
HS72_PARLI	STANDARD:	PRT:	372 AA.		
ID HS72_PARLI					



```
AC P22623;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN II (HSP70 II) (FRAGMENT).
GN HSP70II.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gonad;
RX MEDLINE=9109960; PubMed=2269441;
RA la Rosa M., Sconzo G., Giudice G., Roccheri M.C., di Carlo M.;
RT Sequence of a sea urchin hsp70 gene and its 5' flanking region.;
RL Gene 96:295-300(1990).
CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: X16544; CA34544.1; -.
CC PIR: P00138; P00138.
CC HSSP: P19120; INGSJ.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70_1; 1.
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; PARTIAL.
CC PROSITE: PS01036; HSP70_3; 1.
CC ATP-binding; Heat shock; Multigene family.
CC KW NON_TER 372 372
CC FT SEQUENCE 372 AA; 41347 MW; 5F8C1C590527A659 CRC64;
CC -----
Query Match 90.2%; Score 46; DB 1; Length 372;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDVYT 10
DB 286 SLFESIDYIT 295
RESULT 3
ID HS70_PENCI STANDARD; PRT; 503 AA.
AC Q92260;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (ALLERGEN PEN C 19) (FRAGMENT).
GN HSP70.
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
RP SEQUENCE FROM N.A.
RA Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
RT Molecular cloning and expression of a penicillium citrinum
RT allergen with sequence homology and antigenic cross-reactivity to
RT a hsp70 human heat shock protein.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: U64207; AAB06397.1; -.
CC HSSP: P19120; 3HSC.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70_1; 1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Allergen.
CC KW NON_TER 1 1
CC FT SEQUENCE 503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
CC -----
Query Match 90.2%; Score 46; DB 1; Length 503;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SLFEGIDVYT 10
DB 154 SLFEGIDVYT 163
RESULT 4
ID HS70_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699(1986).
CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: J02579; AAA48825.1; -.
CC PIR: A25646; A25646.
CC HSSP: P19120; IATR.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70_1; 1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC ATP-binding; Heat shock; Multigene family.
CC KW SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB CRC64;
CC -----
Query Match 90.2%; Score 46; DB 1; Length 634;
Best Local Similarity 90.0%; Pred. No. 0.16;
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Matches 9: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

OY 1 SLEEGIDVYT 10  
Db 289 SLEEGIDVYT 298

## RESULT 5

HS71\_CERAE STANDARD: PRT; 638 AA.

AC Q28222; 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE HEAT SHOCK 70 KDA PROTEIN 1.

GN HSP71.

OS Cercopithecus aethiops (Green monkey) (Givet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

NCBI\_TaxID=9534;

OX NCBI\_TaxID=9534;

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=95080396; PubMed=7988690;

RA Sahas I., Angelidis C., Pagoulatos G., Lazaridis I.;

RT "The hsc70 gene which is slightly induced by heat is the main virus

inducible member of the hsp70 gene family."

FEBS Lett. 355:282-286(1994).

-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

PREEXISTENT PROTEIN AGAINST AGGREGATION AND MEDATE THE FOLDING

OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN

ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC

RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR

PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION

PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE

PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE

CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE

SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES

DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING

STRESS-INDUCED DAMAGE.

-1- INDUCTION: BY HEAT SHOCK.

-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

-----

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CC EMBL: X70684; CAA50019.1; -

DR InterPro: IPR001023; HSP70.1.

DR Pfam: PF00012; HSP70.1.

DR PRINTS: PR00301; HEATSHOCK70.

DR PROSITE: PS00297; HSP70.1; 1.

DR PROSITE: PS00329; HSP70.2; 1.

DR PROSITE: PS01036; HSP70.3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.

SEQUENCE 638 AA: 69920 MW; D55076A0FPA86AB3 CRC64;

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OY 1 SLEEGIDVYT 10

Db 284 SLEEGIDVYT 293

RESULT 6

HS72\_YEAST STANDARD: PRT; 638 AA.

AC P10592; 01-JUL-1989 (Rel. 11, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE HEAT SHOCK PROTEIN SSA2.

SSA2 OR YL024C OR L0931.

GN Saccharomyces cerevisiae (Baker's yeast).

OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI\_TaxID=4932;

OX NCBI\_TaxID=4932;

RP SEQUENCE FROM N.A.

RC STRAIN=S288C;

RX MEDLINE=89128457; PubMed=2644626;

RA Slater M.R., Craig E.A.;

RT "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae";

Nucleic Acids Res. 17:805-806(1989).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C;

RA Purnelle B., Goffeau A.;

RT Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.

[3]

RP SEQUENCE OF 71-638 FROM N.A.

RA Duesterhoeft A., Fleeth M., Heuss-Neltzel D., Hilbert H., Moestl D.;

RT Submitted (May-1996) to the EMBL/Genbank/DBJ databases.

[4]

RP SEQUENCE OF 91-97 AND 325-341.

RC STRAIN=S288C;

RX MEDLINE=95203288; PubMed=7895733;

RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.;

RT "Protein identifications for a Saccharomyces cerevisiae protein

database";

Electrophoresis 15:1466-1486(1994).

[5]

RP SEQUENCE OF 186-195.

RC STRAIN=ATCC 38531 / Y41;

RX MEDLINE=97089742; PubMed=8935650;

RA Norbeck J., Blomberg A.;

RT "Protein expression during exponential growth in 0.7 M NaCl medium of

Saccharomyces cerevisiae";

FEMS Microbiol. Lett. 137:1-8(1996).

[6]

RP ACETYLATION, AND PHOSPHORYLATION.

RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.;

RT Submitted (Sep-1994) to the SWISS-PROT data bank.

-1- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES

BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE

ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST

SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE

ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC.

-1- PTM: PHOSPHORYLATED.

-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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CC EMBL: X12927; CAA31394.1; -

DR EMBL: 273129; CAA97472.1; -

DR EMBL: X97560; CAA66167.1; -

DR PIR: S20139; S20139.

DR HSP; P19120; INGT.

DR SWISS-2DPAGE; P10592; YEAST.



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DR YEPD; 9800;
DR SGD: S0003947; SSA2.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; ATP-binding; Multigene family; Acetylation;
FT Phosphorylation.
FT INIT_MET 0
FT MOD_RES 1 0 ACETYLATION.
SQ SEQUENCE 638 AA; 69338 MW; 23BDD120C194912 CRC64;

Query Match          90.2%; Score 46; DB 1; Length 638;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10
DB 282 SLFEGIDVYT 291

RESULT 7
HS74_PARLI STANDARD; PRT; 639 AA.
AC O06246;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN IV (HSP70 IV).
GN HSP70IV.
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Euechinozoa; Echinacea; Echinozoa; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93077053; PubMed=1339375;
RA Sconzo G., Scardina G., Ferraro M.G.;
RT "Characterization of a new member of the sea urchin Paracentrotus
RT lividus hsp70 gene family and its expression.";
RL Gene 121:353-358(1992).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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-----
DR EMBL; X61379; CAA43653.1;
DR PIR; J01391; J01391.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 639 AA; 69749 MW; 40E2F29570808DCC CRC64;

Query Match          90.2%; Score 46; DB 1; Length 639;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10

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DB 286 SLFEGIDVYT 295

RESULT 8
HS7A_CAEL STANDARD; PRT; 640 AA.
AC P09446;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A.
GN HSP-1 OR HSP70A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297155; PubMed=2841196;
RA Snutch T.P., Heschl M.F.P., Baillie D.L.;
RT "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
RT characterization.";
RL Gene 64:241-255(1988).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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-----
DR EMBL; M18540; AAA28078.1;
DR PIR; J0285; HKK7A.
DR HSP; P19120; INGI.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;

Query Match          90.2%; Score 46; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10
DB 287 SLFEGIDVYT 296

RESULT 9
HS7C_DICDI STANDARD; PRT; 640 AA.
AC P36415;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK COGNATE PROTEIN (AGINACTIN).
GN HSPB OR HSC70.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008983; PubMed=8404847;
RA Haus U., Trommler P., Fisher P.R., Hartmann H., Lotzspeich F.,

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RA Noegel A.A., Schleicher M.:
RT "The heat shock cognate protein from Dictyostelium affects actin
RT polymerization through interaction with the actin-binding protein
RT CAP32/34."
RL EMBO J. 12:3763-3771(1993).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
RC STRAIN-AX3;
RX MEDLINE-94043116; PubMed-8226849;
RA Eddy R.J., Sauterer R.A., Condeelis J.S.;
RT "Aglactin, an agonist-regulated F-actin capping activity is
RT associated with an Hsc70 in Dictyostelium."
RL J. Biol. Chem. 268:23267-23274(1993)
CC -1- FUNCTION: AFFECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH
CC THE ACTIN-BINDING PROTEIN CAP32/34. ACTS AS A CHAPERONE BY
CC STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS
CC OF THE CELL CORTEX AND CELL PROTRUSIONS.
CC -1- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED
CC CONSTITUTIVELY DURING NORMAL DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
DR EMBL: X75263; CAA53039.1; -
DR EMBL: L22736; AAA33219.1; -
DR PIR: S37394; S37394.
DR HSSP: P19120; ING3.
DR SWISS-2DPAGE: P36415; DICTY.
DR DICTYDB: DP01078; hspb.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone.
KW ATP-binding; Chaperone.
FT FT 1 29 MSGSIGDICTYSCGVGMNDREITAND ->
FT FT 32 32 IMHNGNMTWYVESPVSEVLSFN (IN REF. 2).
FT FT 64 64 N -> T (IN REF. 2).
FT FT 180 180 V -> A (IN REF. 2).
FT FT 237 237 R -> A (IN REF. 2).
FT FT 240 240 S -> A (IN REF. 2).
FT FT 341 341 V -> A (IN REF. 2).
FT FT 352 352 I -> L (IN REF. 2).
FT FT 352 352 F -> P (IN REF. 2).
SQ SEQUENCE 640 AA; 70499 MW; 2E6BD3DB96A9F5D CRC64;

Query Match 90.2%; Score 46; DB 1; Length 640;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10
Db 284 SLEFGIDVYT 293

RESULT 10
HST1_BOVIN STANDARD; PRT; 641 AA.
AC 027975; 027964;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70-1).
GN HSP70-1.

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```

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE-95126904; PubMed-7826329;
RA Gutierrez J.A., Guertero V.;
RT "Chemical modifications of a recombinant bovine stress-inducible 70
RT kDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."
RL Biochem. J. 305:197-203(1995).
RN [2]
RP SEQUENCE OF 212-641 FROM N.A.
RC STRAIN-ANGUS;
RX MEDLINE-95030563; PubMed-7943958;
RA Grosz M.D., Skow L.C., Stone R.T.;
RT "An Alu polymorphism at the bovine 70 kD heat-shock protein-1
RT (HSP70-1) locus."
RL Anim. Genet. 25:196-196(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U09861; AAA73914.1; -
DR EMBL: U02891; AAA03450.1; -
DR HSSP: P19120; INGC.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70.1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;

Query Match 90.2%; Score 46; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10
Db 286 SLEFGIDVYT 295

RESULT 11
HST1_HUMAN STANDARD; PRT; 641 AA.
AC P08107; P19790; Q9U0M0; Q9U0L9;
DT 01-AUG-1988 (Rel. 09UOM0; Q9U0L9;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
GN HSP70-1.

```



DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN (HSPAL OR HSPAL) AND HSPALB.  
 OS Homo sapiens (human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91055806; PubMed=1700760;  
 RT "Structure and expression of the three MHC-linked HSP70 genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:242-251(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=86016721; PubMed=3931075;  
 RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A. (HSPAL AND HSPALB).  
 RA Kowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III region.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.  
 RA MEDLINE=89184548; PubMed=2538825;  
 RT Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;  
 RL "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).  
 RN [5]  
 RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.  
 RA MEDLINE=87066768; PubMed=3786141;  
 RT Diebent B., Genthe A., Benescke B.-J.;  
 RL "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";  
 RL Nucleic Acids Res. 14:8933-8949(1986).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.  
 RA MEDLINE=99234376; PubMed=10216320;  
 RT Osipjuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;  
 RL "Structure of a new crystal form of human hsp70 ATPase domain.";  
 RL Acta Crystallogr. D 55:1105-1107(1999).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
 CC -1- INDUCTION: BY HEAT SHOCK.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: M59828; AAA63226.1; -  
 CC EMBL: M59830; AAA63227.1; -  
 CC EMBL: AF134726; AAD21816.1; -  
 CC EMBL: AF134726; AAD21815.1; -  
 CC DR

DR EMBL: M11717; AAA52697.1; -  
 DR EMBL: M24743; AAA59844.1; -  
 DR EMBL: M24744; AAA59845.1; -  
 DR EMBL: X04676; CAA28381.1; -  
 DR EMBL: X04677; CAA28382.1; -  
 DR PIR: A29160; A29160.  
 DR PIR: A45871; A45871.  
 DR PIR: A25773; A25773.  
 DR PDB: 1HJO; 21-OCT-98.  
 DR SWISS-2DPAGE: P08107; HUMAN.  
 DR MIM: 140550; -  
 DR MIM: 603012; -  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70, 1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 DR ATP-binding; Chaperone; Heat shock; Multigene family; MHC III;  
 KW 3D-structure.  
 FT CONFLICT 7 7 I -> V (IN REF. 2).  
 FT CONFLICT 110 110 E -> D (IN REF. 3; AAD21816).  
 FT CONFLICT 370 370 A -> G (IN REF. 2).  
 FT CONFLICT 469 469 MISSING (IN REF. 2).  
 FT CONFLICT 499 499 N -> S (IN REF. 3; AAD21815).  
 FT SEQUENCE 641 AA; 70052 MW; 78F513118C90DE66 CRC64;  
 SQ  
 QY 1 SLFEGIDVYT 10  
 Db 286 SLFEGIDVYT 295  
 ID HS71\_MOUSE STANDARD; PRT; 641 AA.  
 AC P17879; 061689;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).  
 GN HSPAL OR HSP70A1 OR HSP70-1 OR HCP70.1.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90236310; PubMed=2332169;  
 RT Hunt C., Calderwood S.;  
 RL "Characterization and sequence of a mouse hsp70 gene and its expression in mouse cell lines.";  
 RL Gene 87:199-204(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Liver;  
 RA MEDLINE=94357449; PubMed=8076831;  
 RA Perry M.D., Anjane L., Shtang S., Moran L.A.;  
 RT "Structure and expression of an inducible HSP70-encoding gene from Mus musculus.";  
 RL Gene 146:273-278(1994).  
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.  
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CC -----
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M35021; AAA57864.1; -
CC EMBL: M76613; AAA57233.1; -
CC PIR: JH0095; JH0095.
CC HSP: P19120; INGC.
CC MGD: MGI:99517; HSP70-1.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70.1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.
CC CONFLICT 342 342 A -> R (IN REF. 1).
CC CONFLICT 627 627 P -> PP (IN REF. 1).
CC SEQUENCE 641 AA; 69994 MW; 41475360f6749f2f CRC64;

Query Match          90.2%; Score 46; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SFEIGIDVYT 10
Db 286 SFEIGIDVYT 295

RESULT 13
HS7L_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1).
GN HSPA1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
RA Bouquet Y.H.;
RT *Complete nucleotide sequence of a porcine HSP70 gene.*;
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC -----
CC EMBL: M69100; -; NOT_ANNOTATED_CDS.
CC PIR: S35718; S35718.
CC HSP: P19120; INGC.
CC InterPro: IPR001023; HSP70.
CC Pfam: PF00012; HSP70.1.
CC PRINTS: PR00301; HEATSHOCK70.
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;

Query Match          90.2%; Score 46; DB 1; Length 641;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SFEIGIDVYT 10
Db 286 SFEIGIDVYT 295

RESULT 14
HS7L_RAT STANDARD; PRT; 641 AA.
AC O07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN 1/2 (HSP70.1/2).
GN HSP70-1 AND HSP70-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=94096443; PubMed=8271311;
RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
RA Massa S.M., Sharp F.R.;
RT *CDNA cloning and expression of stress-inducible rat hsp70 in normal
RT and injured rat brain.*;
RL J. Neurosci. Res. 36:325-335(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=LEW.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter U., Raun F., Guenther E.;
RT *Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (hsp70) genes of the rat.*;
RL Immunogenetics 40:325-330(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94368874; PubMed=8086479;
RA Lisowska K., Krawczyk Z., Wlidlak W., Wolniczka P., Wisniewski J.;
RT *Cloning, nucleotide sequence and expression of rat heat inducible
RT hsp70 gene.*;
RL Biochim. Biophys. Acta 1219:64-72(1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
CC -1- SIMILARITY: BY HEAT SHOCK.
CC -----
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CC -----  
 CC EMBL: L16764; AAA17441.1; -;  
 CC EMBL: X77208; CAA54423.1; -;  
 CC EMBL: X77207; CAA54422.1; -;  
 CC EMBL: X74271; CAA52328.1; -;  
 CC HSSP: P19120; INGC.  
 CC InterPro: IPR001023; HSP70.  
 CC Pfam: PF00012; HSP70.1.  
 CC PRINTS: PR00301; HEATSHOCK70.  
 CC PROSITE: PS00297; HSP70\_1; 1.  
 CC PROSITE: PS00329; HSP70\_2; 1.  
 CC PROSITE: PS01036; HSP70\_3; 1.  
 CC ATP-binding; Chaperone; Heat shock; Multigene family; MHC III.  
 FT CONFLICT 71 72 KR -> NG (IN REF. 3).  
 FT CONFLICT 408 408 G -> A (IN REF. 3).  
 FT CONFLICT 408 408 G -> A (IN REF. 3).  
 SQ SEQUENCE 641 AA; 70163 MW; D02D96751C868583 CRC64;

Query Match 90.2%; Score 46; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
 |||||  
 Db 286 SLFEGIDVYT 295

RESULT 15  
 HS71\_YEAST STANDARD; PRT; 641 AA.  
 AC P10591;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DE 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE HEAT SHOCK PROTEIN SSA1 (HEAT SHOCK PROTEIN YG100).  
 GN SSA1 OR YAL005C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 CC Saccharomycetes;  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CX NCBI\_TaxID=4932;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SS288C;  
 RX MEDLINE=89128457; PubMed=2644626;  
 RA Slater M.R., Craig E.A.;  
 RL "The SSA1 and SSA2 genes of the yeast *Saccharomyces cerevisiae*.";  
 RL Nucleic Acids Res. 17:805-806(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SS288C / AB972;  
 RX MEDLINE=95028152; PubMed=7941740;  
 RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,  
 RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;  
 RT "Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of  
 RL the 42 kbp SP07-CENT-CO15 region.";  
 RL Yeast 10:535-541(1994).  
 RN [3]  
 RP SEQUENCE OF 590-641 FROM N.A.  
 RX MEDLINE=85087943; PubMed=6096826;  
 RA Ogen R.C., Lee M.-C., Knapp G.;  
 RT "Transfer RNA splicing in *Saccharomyces cerevisiae*: defining the  
 RL substrates";  
 RL Nucleic Acids Res. 12:9367-9382(1984).  
 RN [4]  
 RP REVISIONS TO 207; 417 AND 421.  
 RA Slater M.R.;

RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 91-97 AND 325-341.  
 RC STRAIN=SS288C;  
 RX MEDLINE=95203288; PubMed=7895733;  
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein  
 RL database";  
 RL Electrophoresis 15:1466-1486(1994).  
 RN [6]  
 RP SEQUENCE OF 186-195.  
 RC STRAIN=ATCC 38531 / Y41;  
 RX MEDLINE=97089742; PubMed=8935650;  
 RA Norbeck J., Blomberg A.;  
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of  
 RL *Saccharomyces cerevisiae*.";  
 RL FEBS Microbiol. Lett. 137:1-8(1996).  
 RN [7]  
 RP ACETYLATION.  
 RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe T., Warner J.R., McLaughlin C.S.;  
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES  
 CC BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE  
 CC ENDOPLASTIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST  
 CC SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE  
 CC APP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

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CC -----  
 CC EMBL: X12926; CAA31393.1; -;  
 CC EMBL: L22015; AAC04952.1; ALT\_SEQ.  
 DR PIR: S25438; HHRVY1.  
 DR PIR: S42164; S42164.  
 DR HSSP: P19120; IATR.  
 DR SWISS-2DPAGE: P10591; YEAST.  
 DR YEPD: 9788; -;  
 DR SGD: S0000004; SSA1.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70.1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW Heat shock; ATP-binding; Multigene family; Acetylation.  
 FT INIT\_MKT 0 0  
 FT MOD\_RES 1 1 ACETYLATION.  
 SQ SEQUENCE 641 AA; 69526 MW; FA9389BAE9B1D7DA CRC64;

Query Match 90.2%; Score 46; DB 1; Length 641;  
 Best Local Similarity 90.0%; Pred. No. 0.18;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLFEGIDVYT 10  
 |||||  
 Db 282 SLFEGIDVYT 291

Search completed: December 6, 2001, 08:00:52  
 Job time: 420 sec



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DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutolata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotenoglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191825; AAF12784.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 153 1  
FT SEQUENCE 153 AA; 17352 MW; E29EE20C4CA934D CRC64;

Query Match 90.28; Score 46; DB 5; Length 153;  
Best Local Similarity 90.08; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10  
DB 80 SLEFGIDVYT 89

RESULT 3  
ID Q9U669 PRELIMINARY; PRT; 155 AA.

AC Q9U669;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutolata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotenoglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191826; AAF12785.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 155 1  
FT SEQUENCE 155 AA; 17676 MW; C191P6E5B1F346C2 CRC64;

Query Match 90.28; Score 46; DB 5; Length 155;  
Best Local Similarity 90.08; Pred. No. 0.34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10  
DB 82 SLEFGIDVYT 91

RESULT 4  
ID Q9U665 PRELIMINARY; PRT; 157 AA.

AC Q9U665;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina plena.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotenoglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191830; AAF12789.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 157 1  
FT SEQUENCE 157 AA; 17834 MW; E8F743382B285EB2 CRC64;

Query Match 90.28; Score 46; DB 5; Length 157;  
Best Local Similarity 90.08; Pred. No. 0.35;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10  
DB 84 SLEFGIDVYT 93

RESULT 5  
ID Q9U671 PRELIMINARY; PRT; 158 AA.

AC Q9U671;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN HSC70.  
OS Littorina scutolata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  
OC Neotenoglossa; Littorinoidea; Littorinidae; Littorina.  
OX NCBI\_TaxID=31221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hohenlohe P.A.;  
RT "Heat-shock genes in the heat-stressed genus Littorina."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF191824; AAF12783.1; -.  
DR HSSP; P19120; 1BA1.  
DR InterPro; IPR001023; HSP70.  
DR PRINTS; PR00301; HEATSHOCK70.  
DR PROSITE; PS01036; HSP70\_3; 1.  
FT NON\_TER 1 158 1  
FT SEQUENCE 158 AA; 17887 MW; B41E5356A24CAD2F CRC64;

Query Match 90.28; Score 46; DB 5; Length 158;  
Best Local Similarity 90.08; Pred. No. 0.35;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10  
DB 85 SLEFGIDVYT 94

RESULT 6  
ID Q9U668 PRELIMINARY; PRT; 158 AA.

AC Q9U668;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)



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DT 01-JUN-2001 (TReMBLrel. 17, last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Litorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotenoglossa; Littorinoidea; Littorinidae; Litorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Litorina.";
RL Submitted (OCr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191827; AAF12786.1; -.
DR HSSP; P19120; 1BA1.
DR InterPro; IPR001023; HSP70.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1 158
SQ SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;

Query Match
Best Local Similarity 90.2%; Score 46; DB 5; Length 158;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10
DB 85 SLEFGIDVYT 94

RESULT 7
Q90666 PRELIMINARY; PRT; 158 AA.
AC Q90666;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN HSC70.
OS Litorina plena.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neotenoglossa; Littorinoidea; Littorinidae; Litorina.
OX NCBI_TaxID=31219;
RN [1]
RP SEQUENCE FROM N.A.
RA Hohenlohe P.A.;
RT "Heat-shock genes in the heat-stressed genus Litorina.";
RL Submitted (OCr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191829; AAF12788.1; -.
DR HSSP; P19120; 1BA1.
DR InterPro; IPR001023; HSP70.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; HSP70_3; 1.
FT NON_TER 1 158
SQ SEQUENCE 158 AA; 17891 MW; B41B5356BCECAD2F CRC64;

Query Match
Best Local Similarity 90.0%; Score 46; DB 5; Length 158;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10
DB 85 SLEFGIDVYT 94

RESULT 8
P81159 PRELIMINARY; PRT; 220 AA.
AC P81159;
DT 01-JUN-1998 (TReMBLrel. 06, Created)

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DT 01-JUN-1998 (TReMBLrel. 06, last sequence update)
DE HEAT SHOCK COGNATE 71 KDA PROTEIN (FRAGMENT).
GN HSC70.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93077669; PubMed=1360013;
RT "Long-term sensitization training in Aplysia leads to an increase in
the expression of BiP, the major protein chaperon of the ER.";
RL J. Cell Biol. 119:1069-1076(1992).
CC -1- INDUCTION: CONSTITUTIVELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; Z15039; CAA78757.1; -.
DR HSSP; P19120; 1BA1.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; Multigene family.
FT NON_TER 1 220
SQ SEQUENCE 220 AA; 24684 MW; FA8557F2B8B5C37A CRC64;

Query Match
Best Local Similarity 90.0%; Score 46; DB 5; Length 220;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLEFGIDVYT 10
DB 138 SLEFGIDVYT 147

RESULT 9
P81157 PRELIMINARY; PRT; 221 AA.
AC P81157;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, last annotation update)
DE HEAT SHOCK 70 KDA PROTEIN A (HSP70A) (FRAGMENT).
GN HSP70A.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93077669; PubMed=1360013;
RT "Long-term sensitization training in Aplysia leads to an increase in
the expression of BiP, the major protein chaperon of the ER.";
RL J. Cell Biol. 119:1069-1076(1992).
CC -1- INDUCTION: BY HEAT SHOCK
CC -1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; Z15037; CAA78753.1; -.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Heat shock; Multigene family.
FT NON_TER 1 221
SQ SEQUENCE 221 AA; 24404 MW; 853F794106B83C9C CRC64;

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Query Match	90.28;	Score 46;	DB 5;	Length 221;
Best Local Similarity	90.08;	Pred. No. 0.52;		
Matches	9;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY	1	SLEEGIDVYT	10
Db	139	SLEEGIDYYT	148

RESULT 10	
Q90520	
ID Q90520	PRELIMINARY; PRT; 278 AA

DT 01-NOV-1996 (TREMBL:rel. 01, Created)  
DT 01-NOV-1996 (TREMBL:rel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBL:rel. 17, Last annotation update)  
DE RAINBOW TROUT 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Proteolanchopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
NCBI\_TaxId=8022;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85036330; PubMed=6092938;  
 RA Kohary R.K., Jones D., Candido E.P.M.;  
 RT "70-kDolalton heat shock polypeptides from rainbow trout  
 RT characterization of cDNA sequences.";   
 RL Mol. Cell. Biol. 4,1785-1791(1984).  
 DR EMBL; K02949; AAA49562.1; --  
 DR HSSP; P08109; ICRK.  
 DR InterPro; IPR001023; HSP70.  
 DR Pfam; PF00012; HSP70; 1.  
 DR PRINTS; PR00301; HEATSHCK70.  
 DR PROSITE; PS00329; HSP70\_2; 1.  
 DR PROSITE; PS01036; HSP70\_3; 1.  
 KW Heat shock; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SO SEQUENCE 278 AA; 30327 MW; E4C745DE5484C17A CRC64;

Query Match	90.28;	Score 46;	DB 13;	Length 278;
Best Local Similarity	90.08;	Pred. No. 0.68;		
Matches	9;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0

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QY      1 SLEEGIDVYT 10
          |||||
Db     156 SLEEGIDFYT 16
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RESULT	11
Q98899	
ID	Q98899
PRELIMINARY;	
PRT;	367
AA	

DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE 70 KDA HEAT SHOCK PROTEIN (FRAGMENT).  
 GN HSP70-3.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei  
 OC Acanthopterygii; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 OC NCBI\_TaxId=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jim E.H.;  
 RL Submitted (0CT-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; 108578; CA69892.1; -.  
 DR HSSP; P19120; 3HSC.  
 DR InterPro; IPR001023; HSP70.

DR Pfam: PF00012; HSP70\_1.  
DR PRINTS: P00301; HEATSHOCK70.  
DR PROSITE: PS00297; HSP70\_1; 1.  
DR PROSITE: PS01036; HSP70\_3; 1.  
DR Heat shock.  
KW  
FT NON\_TER 367 367  
SQ SEQUENCE 367 AA; 40405 MW; 8CD3DD8DF6E3C2CA CRR64

Query Match	90.28;	Score 46;	DB 13;	Length 367;
Best Local Similarity	90.08;	Pred. No. 0.95;		
Matches	9;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0.

QY	1	SLEEGIDVYT	10
Db	268	SLEEGIDFYT	277

RESULT	12	
Q63718		
ID	Q63718	PRELIMINARY; PRT; 455 AA

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HEAT SHOCK PROTEIN 70 (FRAGMENT) .  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Cniariata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,  
 RA D'Ambrosio E.;  
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z27118; CAAB1642.1; -.  
 DR HSP: P08107; IHQO.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70.1.  
 DR PRINTS: PR00301; HEATSHOCK70.  
 DR PROSITE: PS00329; HSP70.2; 1.  
 DR PROSITE: PS01036; HSP70\_3; 1.  
 KW Heat shock.  
 FT NON\_TER 1  
 FT NON\_TER 455  
 SQ SEQUENCE 455 AA; 50404 MW; 0F45F12CBA1E2971 CRC64;

Query Match	90.28;	Score 46;	DB 11;	length 455;
Best Local Similarity	90.08;	Pred. No. 1.2;		
Matches	9;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0.

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QY      1 SLEEGIDVYT 10
          |||||
Db      254 SLEEGIDFYT 26

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RESULT	13		
044350			
ID	044350	PRELIMINARY;	PRT; 467 AA

DT 01-JUN-1998 (TEMBREl, 06, Created)  
DT 01-JUN-1998 (TEMBREl, 06, Last sequence update)  
DT 01-JUN-2001 (TEMBREl, 17, Last annotation update)  
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).  
GN HSP70.  
OS Chondrosta reniformis.  
OC Eukaryota; Metazoa; Polifera; Demospongiae; Tetractinomorpha;  
OC Chondrosida; Chondrillidae; Chondrosta.  
OX NCBI\_TaxID=68574;  
RN [1]  
RP SEQUENCE FROM N.A. Borchellini C., Le Parco Y.,



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RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026517; AAC05362.1; -.
DR HSP: P08109; 1CKR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1 467 1
SQ SEQUENCE 467 AA; 51707 MW; 0DBE6920F2B6EA96 CRC64;

Query Match
Best Local Similarity 90.0%; Score 46; DB 5; Length 467;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10
Db 252 SLEFGIDVYT 261

RESULT 14
O44352 PRELIMINARY; PRT; 467 AA.
AC 044352;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
DE HEAT-SHOCK PROTEIN HSP70 (FRAGMENT).
GN HSP70.
OS Petroblona massiliens.
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarenea; Petrobloniidae;
OC Petroblonia.
OX NCBI_TaxID=68578;
RN [1]
RP SEQUENCE FROM N.A.
RA Borchelliini C., Le Parco Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026520; AAC05364.1; -.
DR HSP: P08109; 1CKR.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1 467 1
SQ SEQUENCE 467 AA; 51458 MW; 23EB28FFD1873DA6 CRC64;

Query Match
Best Local Similarity 90.0%; Score 46; DB 5; Length 467;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10
Db 252 SLEFGIDVYT 261

RESULT 15
O9NJ92 PRELIMINARY; PRT; 467 AA.
ID O9NJ92;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DE HEAT SHOCK PROTEIN 70 (FRAGMENT).
OS Guancha lacunosa.
OC Eukaryota; Metazoa; Porifera; Calcarea; Calcarenea; Clathrinida;
OC Clathrinidae; Guancha.
OX NCBI_TaxID=115120;
RN [1]
RP SEQUENCE FROM N.A.

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RA Borchelliini C., Le Parco Y.;
RT "sponges paraphyly and the origin of Metazoa.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF182195; AAF61297.1; -.
DR InterPro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70; 1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
FT NON_TER 1 467 1
SQ SEQUENCE 467 AA; 51318 MW; F36FC06CB1DEE131 CRC64;

Query Match
Best Local Similarity 90.0%; Score 46; DB 5; Length 467;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLEFGIDVYT 10
Db 252 SLEFGIDVYT 261

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Search completed: December 6, 2001, 07:56:54  
Job time: 182 sec



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